



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2026 – 06:33 PM JST

PDB ID : 9V60 / pdb_00009v60
Title : Crystal structure of myrcene synthase
Authors : Song, T.; Jiang, H.; Xiao, J.
Deposited on : 2025-05-26
Resolution : 2.61 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

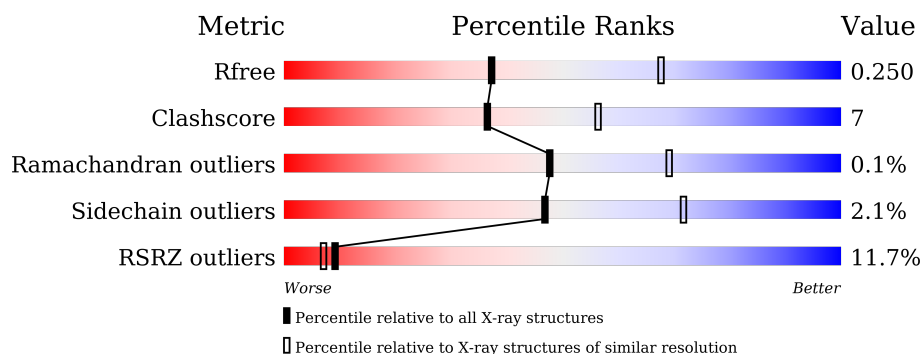
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	557	<div> <div>11%</div> <div> <div></div> <div>80%</div> <div>17%</div> <div>..</div> </div> </div>
1	B	557	<div> <div>12%</div> <div> <div></div> <div>76%</div> <div>17%</div> <div>6%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9052 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Myrcene synthase TPS3FN, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	544	Total	C	N	O	S	0	0	0
			4547	2922	752	849	24			
1	B	526	Total	C	N	O	S	0	1	0
			4408	2837	731	816	24			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Mg	0	0
			2	2		

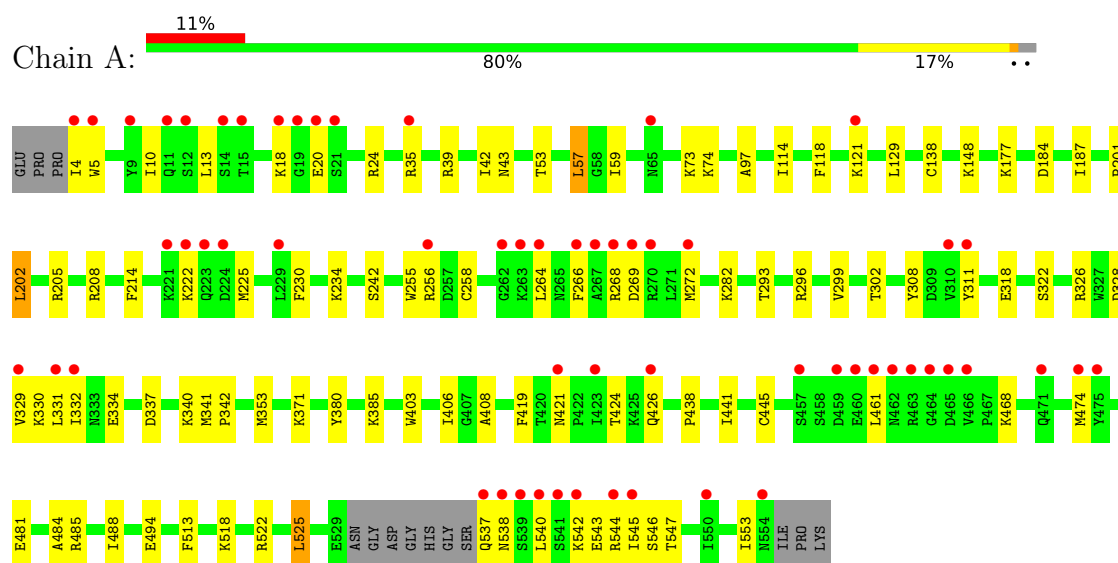
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	46	Total	O	0	0
			46	46		
3	B	49	Total	O	0	0
			49	49		

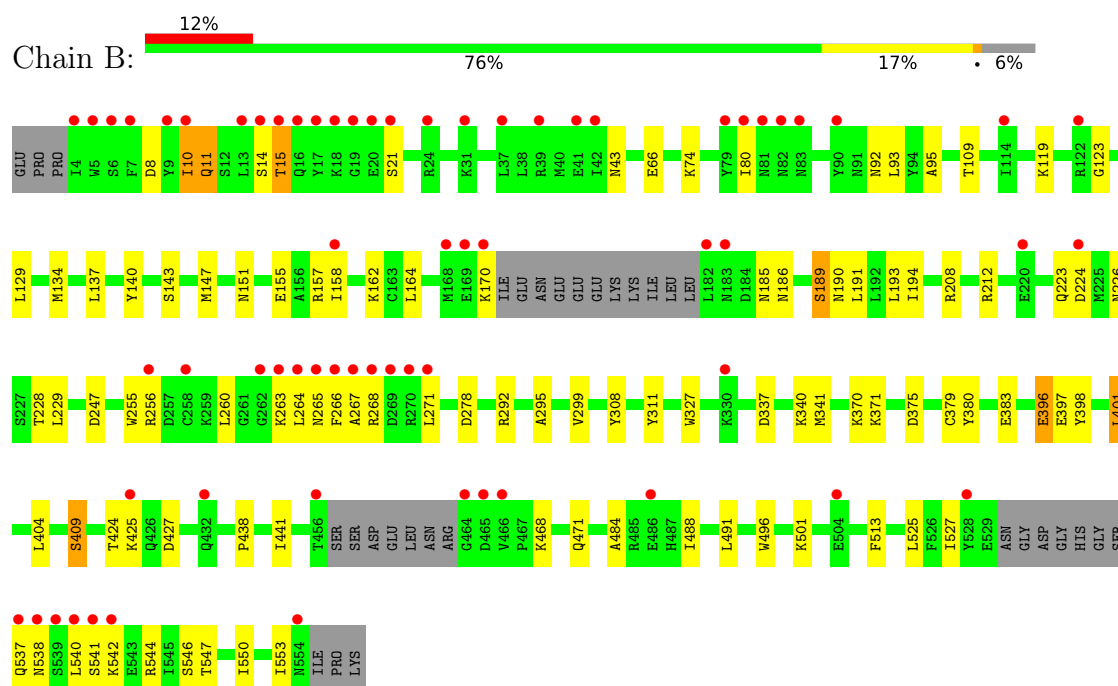
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Myrcene synthase TPS3FN, chloroplastic



- Molecule 1: Myrcene synthase TPS3FN, chloroplastic



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.83Å 124.83Å 193.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.20 – 2.61 44.20 – 2.61	Depositor EDS
% Data completeness (in resolution range)	97.9 (44.20-2.61) 97.8 (44.20-2.61)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.225 , 0.250 0.226 , 0.250	Depositor DCC
R_{free} test set	2006 reflections (3.73%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9052	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.15	0/4646	0.38	0/6273
1	B	0.16	0/4505	0.36	1/6081 (0.0%)
All	All	0.15	0/9151	0.37	1/12354 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	15	THR	CA-CB-OG1	-5.98	100.64	109.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	421	ASN	Peptide
1	B	256[B]	ARG	Mainchain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4547	0	4483	63	0
1	B	4408	0	4343	65	0
2	B	2	0	0	0	0
3	A	46	0	0	2	0
3	B	49	0	0	1	0
All	All	9052	0	8826	128	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (128) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:GLU:OE2	1:B:66:GLU:N	2.13	0.81
1:A:334:GLU:N	1:A:334:GLU:OE2	2.19	0.75
1:A:337:ASP:HA	1:A:340:LYS:HD2	1.71	0.72
1:A:121:LYS:H	1:A:121:LYS:HD2	1.60	0.67
1:A:264:LEU:HD11	1:A:342:PRO:HG3	1.77	0.67
1:B:337:ASP:HA	1:B:340:LYS:HD2	1.75	0.67
1:B:223:GLN:CD	1:B:223:GLN:H	2.04	0.63
1:B:424:THR:HG22	1:B:427:ASP:H	1.63	0.63
1:B:496:TRP:HE1	1:B:525:LEU:HD11	1.65	0.61
1:B:170:LYS:HD2	1:B:191:LEU:HD11	1.83	0.61
1:A:485:ARG:NH1	3:A:601:HOH:O	2.34	0.60
1:A:438:PRO:HD2	1:A:441:ILE:HD12	1.83	0.60
1:A:18:LYS:HA	1:A:18:LYS:HE2	1.83	0.60
1:B:119:LYS:NZ	1:B:123:GLY:O	2.34	0.60
1:B:438:PRO:HD2	1:B:441:ILE:HD12	1.86	0.58
1:B:157:ARG:O	1:B:158:ILE:HB	2.04	0.57
1:B:147:MET:HE3	1:B:501:LYS:HA	1.86	0.57
1:B:224:ASP:OD1	1:B:224:ASP:N	2.33	0.57
1:A:371:LYS:NZ	3:A:602:HOH:O	2.38	0.56
1:B:137:LEU:HD22	1:B:194:ILE:HD12	1.87	0.56
1:A:222:LYS:HB3	1:A:225:MET:HB3	1.88	0.55
1:A:326:ARG:HD3	1:A:331:LEU:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:GLU:OE2	1:A:24:ARG:NE	2.40	0.55
1:B:271:LEU:HD23	1:B:299:VAL:HG21	1.89	0.54
1:A:57:LEU:HB3	1:A:59:ILE:HG12	1.89	0.54
1:A:118:PHE:HB3	1:A:129:LEU:HD11	1.89	0.53
1:A:269:ASP:OD1	1:A:269:ASP:N	2.41	0.52
1:A:42:ILE:HG12	1:A:73:LYS:HD3	1.91	0.52
1:B:93:LEU:HD22	1:B:129:LEU:HD22	1.90	0.52
1:A:441:ILE:HD11	1:A:513:PHE:HZ	1.75	0.51
1:A:329:VAL:HA	1:A:332:ILE:HD11	1.92	0.51
1:B:265:ASN:HA	1:B:268:ARG:NH2	2.24	0.51
1:A:299:VAL:O	1:A:302:THR:HG22	2.11	0.51
1:B:396:GLU:C	1:B:398:TYR:H	2.19	0.51
1:A:256:ARG:O	1:A:256:ARG:HD3	2.11	0.51
1:B:441:ILE:HD11	1:B:513:PHE:HZ	1.76	0.50
1:B:8:ASP:OD1	1:B:11:GLN:N	2.44	0.50
1:B:409:SER:HB2	3:B:706:HOH:O	2.10	0.50
1:A:332:ILE:HD12	1:A:332:ILE:H	1.77	0.49
1:B:43:ASN:HA	1:B:74:LYS:HE2	1.95	0.49
1:B:327:TRP:HB2	1:B:370:LYS:HE3	1.94	0.49
1:A:545:ILE:H	1:A:545:ILE:HD12	1.78	0.48
1:B:212:ARG:HD2	1:B:553:ILE:HD11	1.94	0.48
1:A:518:LYS:O	1:A:522:ARG:HG3	2.12	0.48
1:B:383:GLU:HG3	1:B:401:LEU:HD23	1.95	0.48
1:A:474:MET:HE3	1:A:481:GLU:HA	1.95	0.48
1:B:255:TRP:CH2	1:B:260:LEU:HB3	2.48	0.48
1:A:234:LYS:HD3	1:A:553:ILE:CG2	2.43	0.48
1:A:255:TRP:CD1	1:A:268:ARG:HD2	2.48	0.47
1:A:293:THR:HG22	1:A:353:MET:HE2	1.97	0.47
1:B:185:ASN:O	1:B:189:SER:HB2	2.14	0.47
1:B:268:ARG:H	1:B:268:ARG:HE	1.60	0.47
1:A:318:GLU:OE2	1:A:385:LYS:HE3	2.13	0.47
1:B:140:TYR:O	1:B:143:SER:OG	2.33	0.47
1:A:484:ALA:O	1:A:488:ILE:HG12	2.15	0.47
1:B:471:GLN:OE1	1:B:471:GLN:N	2.39	0.47
1:B:190:ASN:O	1:B:194:ILE:HD13	2.15	0.47
1:B:247:ASP:HA	1:B:292:ARG:HE	1.80	0.47
1:B:425:LYS:H	1:B:425:LYS:CD	2.28	0.46
1:B:264:LEU:HD13	1:B:266:PHE:CZ	2.51	0.46
1:A:5:TRP:HZ2	1:A:542:LYS:HG3	1.80	0.45
1:A:10:ILE:O	1:A:13:LEU:HB2	2.16	0.45
1:A:230:PHE:CZ	1:A:234:LYS:HE3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:ALA:HB3	1:A:138:CYS:HB3	1.99	0.45
1:A:184:ASP:HB3	1:A:187:ILE:HB	1.99	0.45
1:B:268:ARG:NE	1:B:268:ARG:N	2.64	0.45
1:B:425:LYS:H	1:B:425:LYS:HE2	1.81	0.45
1:B:164:LEU:HD22	1:B:194:ILE:HG13	2.00	0.45
1:B:255:TRP:HZ2	1:B:267:ALA:HB1	1.82	0.45
1:A:53:THR:HG22	1:A:57:LEU:HD22	1.99	0.44
1:A:266:PHE:HE2	1:A:311:TYR:HE2	1.63	0.44
1:B:208:ARG:HD2	1:B:208:ARG:HA	1.68	0.44
1:B:80:ILE:HD12	1:B:80:ILE:HA	1.90	0.44
1:B:151:ASN:O	1:B:155:GLU:HG2	2.18	0.44
1:B:260:LEU:HG	1:B:264:LEU:HD12	2.00	0.44
1:B:541:SER:HB2	1:B:544:ARG:NH2	2.32	0.44
1:A:543:GLU:OE2	1:A:546:SER:OG	2.31	0.44
1:B:484:ALA:O	1:B:488:ILE:HG12	2.17	0.44
1:B:370:LYS:HB3	1:B:370:LYS:HE2	1.76	0.43
1:B:226:ASN:HB3	1:B:229:LEU:HB2	1.99	0.43
1:A:43:ASN:HA	1:A:74:LYS:NZ	2.33	0.43
1:A:201:PRO:O	1:A:205:ARG:HG3	2.19	0.43
1:A:4:ILE:HD12	1:A:542:LYS:HE3	2.00	0.43
1:A:225:MET:HE1	1:A:230:PHE:CD2	2.54	0.43
1:A:537:GLN:HG2	1:A:538:ASN:H	1.84	0.43
1:B:268:ARG:HE	1:B:268:ARG:N	2.16	0.43
1:B:546:SER:HA	1:B:550:ILE:HB	2.00	0.43
1:A:341:MET:HE2	1:A:341:MET:HB3	1.74	0.43
1:B:212:ARG:HG2	1:B:547:THR:CG2	2.49	0.43
1:B:266:PHE:HB3	1:B:311:TYR:OH	2.19	0.43
1:A:208:ARG:HA	1:A:208:ARG:HD2	1.80	0.43
1:A:540:LEU:C	1:A:542:LYS:H	2.27	0.43
1:A:57:LEU:HD13	1:A:214:PHE:HD2	1.84	0.43
1:A:544:ARG:HA	1:A:547:THR:HG22	2.01	0.42
1:B:267:ALA:H	1:B:268:ARG:HH21	1.67	0.42
1:B:341:MET:HB3	1:B:341:MET:HE2	1.71	0.42
1:B:537:GLN:HG2	1:B:538:ASN:H	1.84	0.42
1:A:18:LYS:HE3	1:A:242:SER:OG	2.20	0.42
1:B:134:MET:HE3	1:B:190:ASN:CG	2.44	0.42
1:A:177:LYS:HB3	1:A:177:LYS:HE2	1.68	0.42
1:B:143:SER:HB2	1:B:157:ARG:HB2	2.01	0.42
1:A:121:LYS:HD2	1:A:121:LYS:N	2.31	0.42
1:B:396:GLU:C	1:B:397:GLU:HG3	2.44	0.42
1:B:8:ASP:OD1	1:B:10:ILE:HG13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:LYS:HB3	1:B:162:LYS:HE2	1.54	0.42
1:A:35:ARG:NH2	1:A:39:ARG:HH11	2.19	0.41
1:A:328:ASP:OD1	1:A:330:LYS:HE3	2.20	0.41
1:A:406:ILE:HG23	1:A:408:ALA:H	1.86	0.41
1:A:424:THR:HG22	1:A:426:GLN:N	2.36	0.41
1:A:272:MET:HE2	1:A:272:MET:HB2	1.93	0.41
1:A:293:THR:O	1:A:296:ARG:HB2	2.20	0.41
1:A:424:THR:HG22	1:A:426:GLN:H	1.85	0.41
1:B:308:TYR:CG	1:B:380:TYR:HB3	2.56	0.41
1:B:468:LYS:HZ2	1:B:468:LYS:HG2	1.77	0.41
1:A:282:LYS:HG3	1:A:419:PHE:CZ	2.56	0.41
1:B:371:LYS:NZ	1:B:375:ASP:OD2	2.51	0.41
1:A:468:LYS:HD3	1:A:468:LYS:HA	1.85	0.41
1:B:263:LYS:HA	1:B:263:LYS:HD3	1.90	0.41
1:B:379:CYS:SG	1:B:404:LEU:HB3	2.61	0.41
1:B:278:ASP:OD2	1:B:295:ALA:HA	2.22	0.40
1:B:425:LYS:H	1:B:425:LYS:HD3	1.86	0.40
1:A:148:LYS:NZ	1:A:494:GLU:OE1	2.54	0.40
1:A:308:TYR:CG	1:A:380:TYR:HB3	2.57	0.40
1:B:540:LEU:C	1:B:542:LYS:H	2.29	0.40
1:A:202:LEU:HD12	1:A:202:LEU:HA	1.86	0.40
1:A:403:TRP:O	1:A:445:CYS:HB3	2.21	0.40
1:A:525:LEU:HD12	1:A:525:LEU:HA	1.91	0.40
1:B:92:ASN:HB3	1:B:95:ALA:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	540/557 (97%)	524 (97%)	16 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	519/557 (93%)	489 (94%)	29 (6%)	1 (0%)	43	64
All	All	1059/1114 (95%)	1013 (96%)	45 (4%)	1 (0%)	48	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	14	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	504/515 (98%)	497 (99%)	7 (1%)	59	80
1	B	487/515 (95%)	473 (97%)	14 (3%)	37	63
All	All	991/1030 (96%)	970 (98%)	21 (2%)	47	72

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LEU
1	A	114	ILE
1	A	202	LEU
1	A	258	CYS
1	A	322	SER
1	A	461	LEU
1	A	525	LEU
1	B	10	ILE
1	B	11	GLN
1	B	15	THR
1	B	21	SER
1	B	109	THR
1	B	186	ASN
1	B	189	SER
1	B	193	LEU

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Mol	Chain	Res	Type
1	B	228	THR
1	B	396	GLU
1	B	401	LEU
1	B	409	SER
1	B	491	LEU
1	B	527	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	55	GLN
1	A	91	ASN
1	A	392	GLN
1	A	435	HIS
1	A	487	HIS
1	A	537	GLN
1	B	43	ASN
1	B	55	GLN
1	B	68	ASN
1	B	81	ASN
1	B	105	GLN
1	B	106	HIS
1	B	249	GLN
1	B	347	HIS
1	B	351	ASN
1	B	392	GLN
1	B	436	HIS
1	B	477	ASN
1	B	537	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	544/557 (97%)	0.54	59 (10%) 11 8	36, 51, 100, 157	0
1	B	526/557 (94%)	0.70	66 (12%) 8 6	29, 53, 93, 125	1 (0%)
All	All	1070/1114 (96%)	0.62	125 (11%) 9 7	29, 52, 97, 157	1 (0%)

All (125) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	256[A]	ARG	7.0
1	A	540	LEU	6.6
1	A	465	ASP	5.9
1	A	464	GLY	5.9
1	B	16	GLN	5.4
1	B	80	ILE	5.4
1	A	266	PHE	5.3
1	B	541	SER	4.9
1	A	4	ILE	4.8
1	A	5	TRP	4.8
1	B	182	LEU	4.7
1	A	541	SER	4.7
1	A	264	LEU	4.5
1	A	267	ALA	4.5
1	A	268	ARG	4.5
1	A	11	GLN	4.5
1	B	168	MET	4.4
1	B	17	TYR	4.4
1	B	82	ASN	4.3
1	B	170	LYS	4.3
1	B	456	THR	4.3
1	B	13	LEU	4.3
1	B	464	GLY	4.2
1	A	461	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
1	B	5	TRP	4.1
1	B	266	PHE	4.0
1	A	475	TYR	3.9
1	A	14	SER	3.9
1	A	463	ARG	3.9
1	A	538	ASN	3.8
1	A	539	SER	3.8
1	A	256	ARG	3.8
1	B	504	GLU	3.7
1	B	262	GLY	3.6
1	A	537	GLN	3.6
1	B	21	SER	3.6
1	A	272	MET	3.5
1	B	220	GLU	3.5
1	A	269	ASP	3.4
1	A	544	ARG	3.4
1	B	268	ARG	3.3
1	A	329	VAL	3.3
1	B	10	ILE	3.3
1	B	9	TYR	3.3
1	A	19	GLY	3.3
1	A	466	VAL	3.3
1	A	15	THR	3.3
1	B	4	ILE	3.2
1	B	540	LEU	3.2
1	B	7	PHE	3.2
1	B	269	ASP	3.2
1	A	221	LYS	3.2
1	A	421	ASN	3.1
1	A	311	TYR	3.1
1	B	169	GLU	3.1
1	A	545	ILE	3.1
1	A	554	ASN	3.1
1	B	20	GLU	3.1
1	B	258	CYS	3.1
1	B	466	VAL	3.1
1	B	267	ALA	3.0
1	A	332	ILE	3.0
1	B	158	ILE	2.9
1	A	262	GLY	2.9
1	A	263	LYS	2.8
1	B	538	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	426	GLN	2.8
1	A	457	SER	2.8
1	A	65	ASN	2.8
1	A	460	GLU	2.8
1	A	550	ILE	2.7
1	A	542	LYS	2.7
1	A	462	ASN	2.7
1	B	18	LYS	2.7
1	B	24	ARG	2.7
1	A	12	SER	2.7
1	B	79	TYR	2.6
1	A	20	GLU	2.6
1	B	6	SER	2.6
1	B	81	ASN	2.6
1	A	222	LYS	2.6
1	A	310	VAL	2.6
1	A	21	SER	2.6
1	A	35	ARG	2.6
1	A	223	GLN	2.5
1	A	229	LEU	2.5
1	A	474	MET	2.5
1	B	265	ASN	2.5
1	B	122	ARG	2.5
1	B	554	ASN	2.5
1	B	330	LYS	2.4
1	B	537	GLN	2.4
1	B	183	ASN	2.4
1	A	224	ASP	2.4
1	A	423	ILE	2.4
1	B	83	ASN	2.4
1	A	459	ASP	2.4
1	B	465	ASP	2.4
1	B	90	TYR	2.4
1	B	31	LYS	2.3
1	B	19	GLY	2.3
1	A	121	LYS	2.3
1	B	14	SER	2.3
1	B	224	ASP	2.3
1	B	37	LEU	2.3
1	B	486	GLU	2.2
1	B	528	TYR	2.2
1	B	270	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	331	LEU	2.2
1	A	18	LYS	2.2
1	B	539	SER	2.2
1	B	264	LEU	2.2
1	B	42	ILE	2.2
1	A	270	ARG	2.1
1	A	9	TYR	2.1
1	B	432	GLN	2.1
1	B	542	LYS	2.1
1	B	114	ILE	2.1
1	B	41	GLU	2.1
1	A	471	GLN	2.1
1	B	425	LYS	2.1
1	B	39	ARG	2.1
1	B	263	LYS	2.1
1	B	15	THR	2.0
1	B	271	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

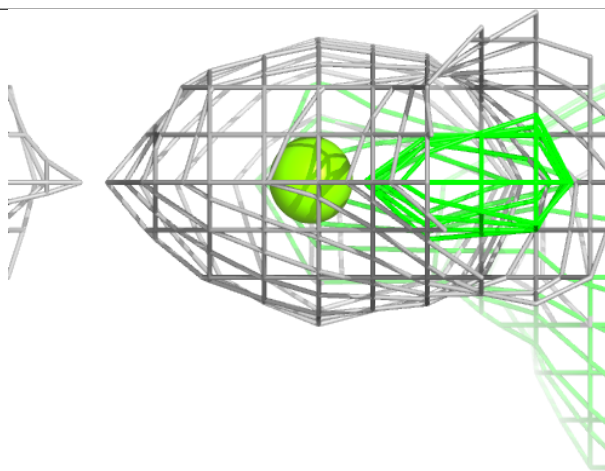
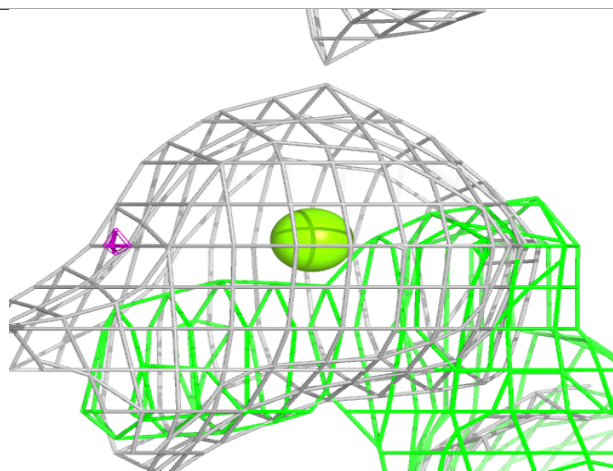
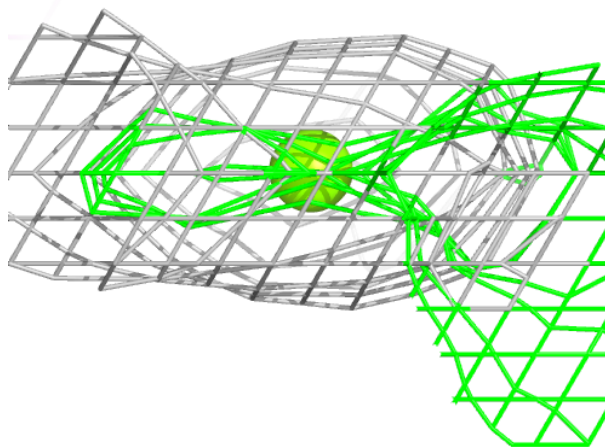
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	B	602	1/1	0.91	0.32	73,73,73,73	0
2	MG	B	601	1/1	0.98	0.27	30,30,30,30	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

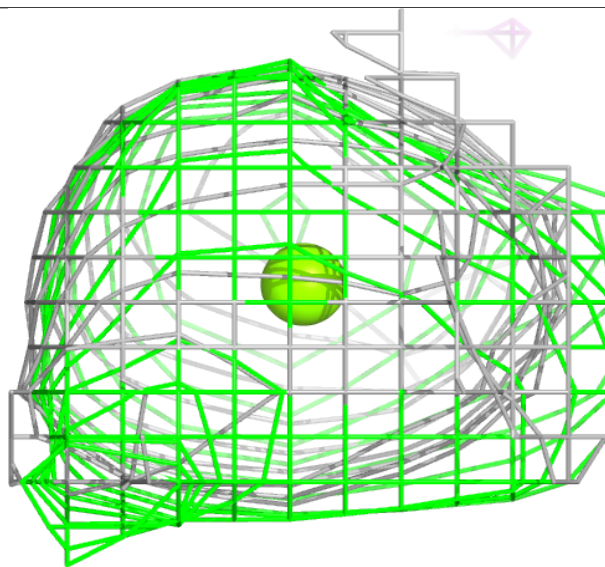
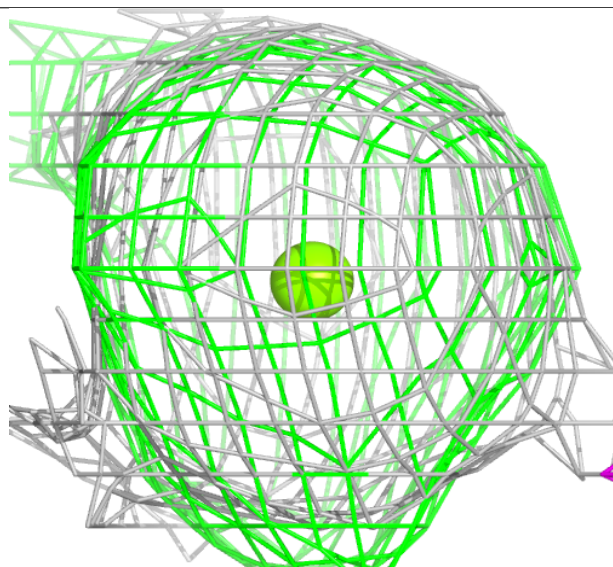
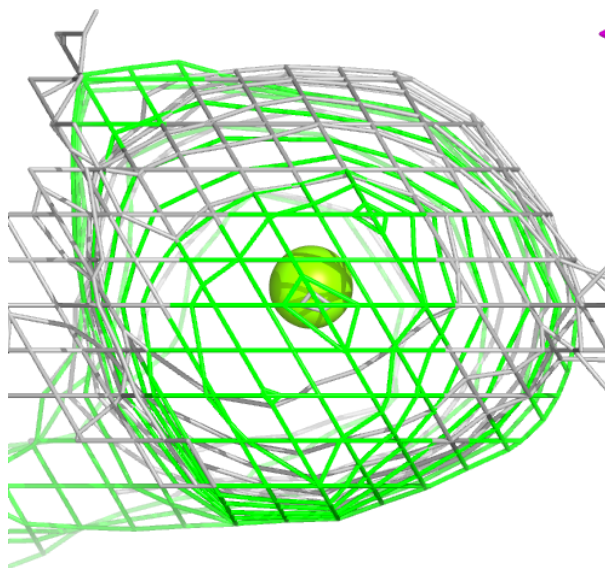
Electron density around MG B 602:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG B 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.