Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2024 – 06:15 AM EDT

PDB ID	:	5M4Y
Title	:	Crystal structure of the Sec3/Sso2 complex at 2.20 angstrom resolution
Authors	:	Zhang, Y.B.; Dong, G.
Deposited on	:	2016-10-19
Resolution	:	2.20 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 (i) 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 (1)) were used in the production of this report:

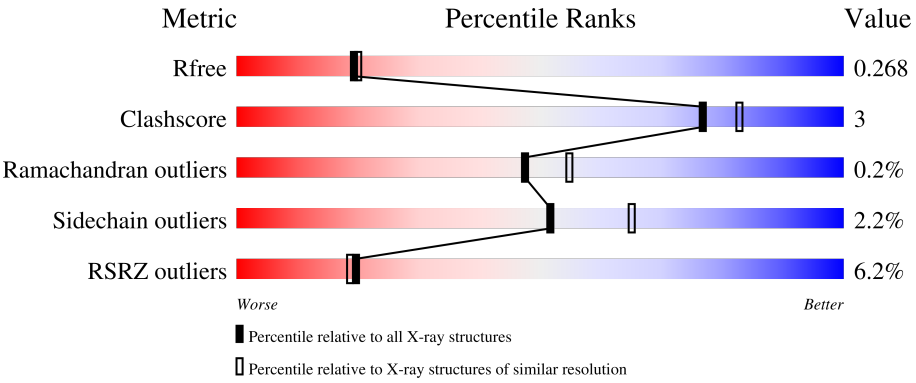
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	210	9% 74% 10% • 16%
1	C	210	6% 79% 7% 14%
1	E	210	13% 75% 10% • 14%
2	B	250	2% 65% • 31%
2	D	250	% 62% 7% 31%

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Mol	Chain	Length	Quality of chain
2	F	250	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	D	401	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9010 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 Protein SSO2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	0	0
			1445	888	253	298	6			
1	C	181	Total	C	N	O	S	0	0	0
			1476	904	261	305	6			
1	E	181	Total	C	N	O	S	0	0	0
			1476	907	258	305	6			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	GLY	-	expression tag	UNP P39926
A	33	SER	-	expression tag	UNP P39926
A	34	HIS	-	expression tag	UNP P39926
A	35	MET	-	expression tag	UNP P39926
A	228	LEU	-	expression tag	UNP P39926
A	229	THR	-	expression tag	UNP P39926
A	230	GLN	-	expression tag	UNP P39926
A	231	LEU	-	expression tag	UNP P39926
A	232	PHE	-	expression tag	UNP P39926
A	233	ASN	-	expression tag	UNP P39926
A	234	ASP	-	expression tag	UNP P39926
A	235	MET	-	expression tag	UNP P39926
A	236	GLU	-	expression tag	UNP P39926
A	237	GLU	-	expression tag	UNP P39926
A	238	LEU	-	expression tag	UNP P39926
A	239	VAL	-	expression tag	UNP P39926
A	240	ILE	-	expression tag	UNP P39926
A	241	GLU	-	expression tag	UNP P39926
C	32	GLY	-	expression tag	UNP P39926
C	33	SER	-	expression tag	UNP P39926
C	34	HIS	-	expression tag	UNP P39926
C	35	MET	-	expression tag	UNP P39926
C	228	LEU	-	expression tag	UNP P39926

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Chain	Residue	Modelled	Actual	Comment	Reference
C	229	THR	-	expression tag	UNP P39926
C	230	GLN	-	expression tag	UNP P39926
C	231	LEU	-	expression tag	UNP P39926
C	232	PHE	-	expression tag	UNP P39926
C	233	ASN	-	expression tag	UNP P39926
C	234	ASP	-	expression tag	UNP P39926
C	235	MET	-	expression tag	UNP P39926
C	236	GLU	-	expression tag	UNP P39926
C	237	GLU	-	expression tag	UNP P39926
C	238	LEU	-	expression tag	UNP P39926
C	239	VAL	-	expression tag	UNP P39926
C	240	ILE	-	expression tag	UNP P39926
C	241	GLU	-	expression tag	UNP P39926
E	32	GLY	-	expression tag	UNP P39926
E	33	SER	-	expression tag	UNP P39926
E	34	HIS	-	expression tag	UNP P39926
E	35	MET	-	expression tag	UNP P39926
E	228	LEU	-	expression tag	UNP P39926
E	229	THR	-	expression tag	UNP P39926
E	230	GLN	-	expression tag	UNP P39926
E	231	LEU	-	expression tag	UNP P39926
E	232	PHE	-	expression tag	UNP P39926
E	233	ASN	-	expression tag	UNP P39926
E	234	ASP	-	expression tag	UNP P39926
E	235	MET	-	expression tag	UNP P39926
E	236	GLU	-	expression tag	UNP P39926
E	237	GLU	-	expression tag	UNP P39926
E	238	LEU	-	expression tag	UNP P39926
E	239	VAL	-	expression tag	UNP P39926
E	240	ILE	-	expression tag	UNP P39926
E	241	GLU	-	expression tag	UNP P39926

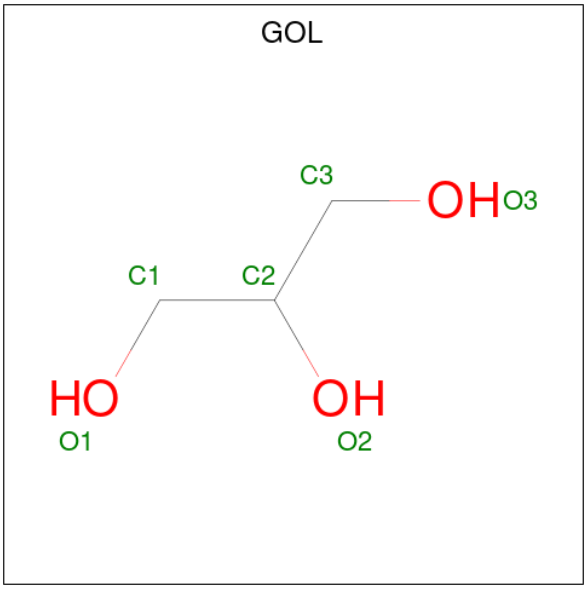
- Molecule 2 is a protein called Exocyst complex component SEC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1433	914	250	266	3			
2	D	173	Total	C	N	O	S	0	0	0
			1433	914	250	266	3			
2	F	171	Total	C	N	O	S	0	0	0
			1416	904	246	263	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	71	GLN	-	expression tag	UNP P33332
B	72	GLY	-	expression tag	UNP P33332
B	73	HIS	-	expression tag	UNP P33332
B	74	MET	-	expression tag	UNP P33332
D	71	GLN	-	expression tag	UNP P33332
D	72	GLY	-	expression tag	UNP P33332
D	73	HIS	-	expression tag	UNP P33332
D	74	MET	-	expression tag	UNP P33332
F	71	GLN	-	expression tag	UNP P33332
F	72	GLY	-	expression tag	UNP P33332
F	73	HIS	-	expression tag	UNP P33332
F	74	MET	-	expression tag	UNP P33332

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	42	Total O 42 42	0	0
4	B	80	Total O 80 80	0	0
4	C	29	Total O 29 29	0	0

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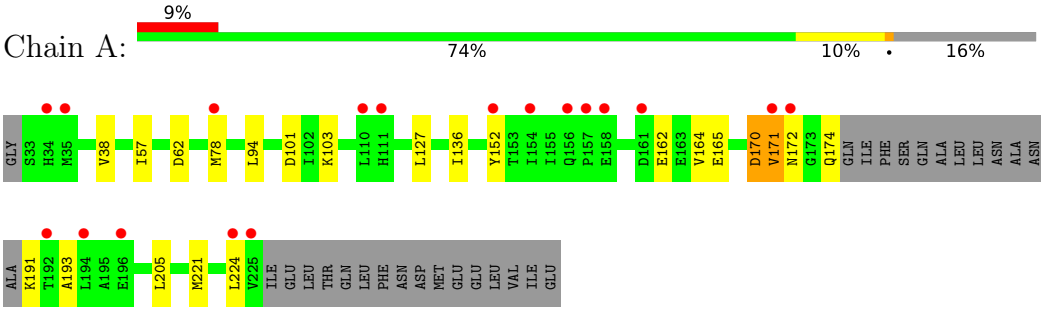
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	76	Total O 76 76	0	0
4	E	20	Total O 20 20	0	0
4	F	78	Total O 78 78	0	0

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.

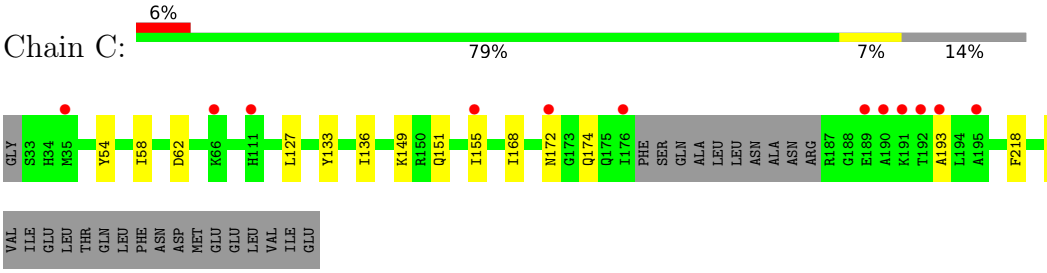
• Molecule 1: Protein SSO2

Chain A:



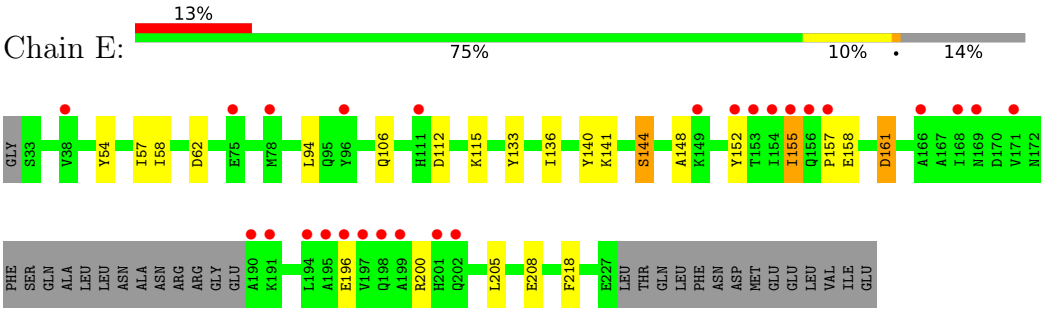
• Molecule 1: Protein SSO2

Chain C:



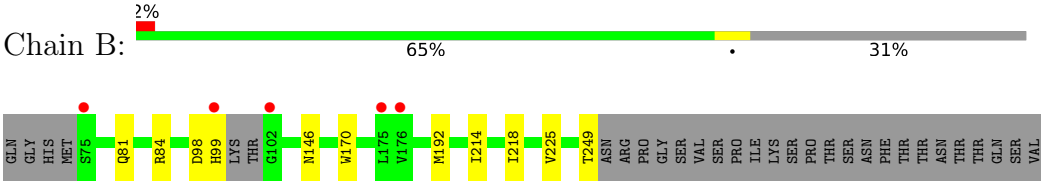
• Molecule 1: Protein SSO2

Chain E:



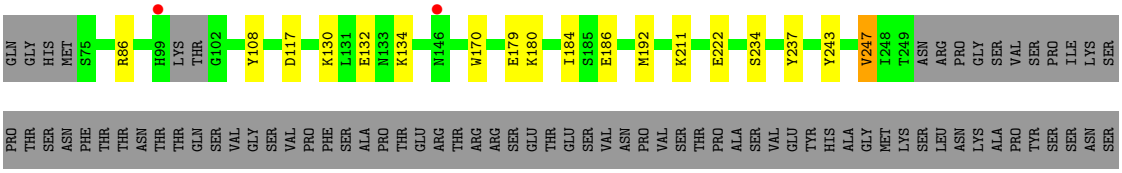
• Molecule 2: Exocyst complex component SEC3

Chain B:



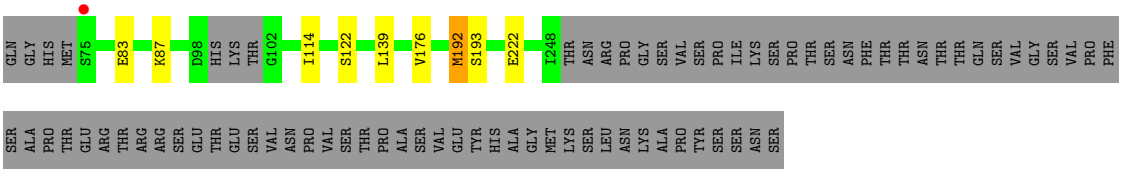
• Molecule 2: Exocyst complex component SEC3

Chain D:



• Molecule 2: Exocyst complex component SEC3

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	101.14Å 135.80Å 185.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 2.20 49.22 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.98-2.20) 99.7 (49.22-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.96 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.229 , 0.264 0.232 , 0.268	Depositor DCC
R_{free} test set	2000 reflections (2.68%)	wwPDB-VP
Wilson B-factor (Å^2)	50.3	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 39.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9010	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.24% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: GOL

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	0.23	0/1458	0.33	0/1958
1	C	0.22	0/1489	0.33	0/1998
1	E	0.23	0/1489	0.35	0/2000
2	B	0.24	0/1465	0.42	0/1978
2	D	0.24	0/1465	0.42	0/1978
2	F	0.24	0/1447	0.41	0/1953
All	All	0.23	0/8813	0.38	0/11865

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1445	0	1408	10	0
1	C	1476	0	1434	7	0
1	E	1476	0	1438	11	0
2	B	1433	0	1433	7	0
2	D	1433	0	1433	13	0
2	F	1416	0	1419	5	0
3	D	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	42	0	0	1	0
4	B	80	0	0	2	0
4	C	29	0	0	0	0
4	D	76	0	0	3	0
4	E	20	0	0	1	0
4	F	78	0	0	2	0
All	All	9010	0	8573	51	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 3.

All (51) 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:A:170:ASP:HB2	1:A:171:VAL:HG13	1.67	0.76
2:F:193:SER:OG	4:F:401:HOH:O	2.06	0.74
2:D:179:GLU:OE1	4:D:501:HOH:O	2.06	0.73
2:B:146:ASN:OD1	4:B:401:HOH:O	2.06	0.73
2:D:211:LYS:NZ	4:D:503:HOH:O	2.23	0.71
1:E:106:GLN:O	4:E:301:HOH:O	2.09	0.70
1:C:62:ASP:HB2	1:C:136:ILE:HD13	1.75	0.67
2:B:218:ILE:HG12	2:B:225:VAL:HG12	1.80	0.62
1:E:152:TYR:HA	1:E:155:ILE:HG22	1.82	0.62
1:E:62:ASP:HB2	1:E:136:ILE:HD13	1.83	0.60
1:A:191:LYS:HG3	1:A:193:ALA:H	1.67	0.58
2:B:81:GLN:OE1	2:B:84:ARG:NH1	2.36	0.58
1:E:161:ASP:OD2	1:E:161:ASP:N	2.42	0.53
1:A:103:LYS:HZ3	1:A:224:LEU:HD21	1.75	0.52
1:A:62:ASP:HB2	1:A:136:ILE:HD13	1.91	0.52
1:A:152:TYR:HD2	1:A:164:VAL:HG22	1.74	0.52
2:B:98:ASP:OD1	2:B:99:HIS:N	2.39	0.52
1:E:148:ALA:HB2	1:E:200:ARG:HG2	1.93	0.50
2:B:214:ILE:O	2:B:218:ILE:HG13	2.11	0.50
1:C:155:ILE:HD11	1:C:193:ALA:HB3	1.94	0.49
1:C:127:LEU:HD21	1:C:221:MET:HB2	1.95	0.48
2:F:83:GLU:HG3	2:F:87:LYS:HE3	1.95	0.48
2:F:122:SER:HB3	4:F:411:HOH:O	2.13	0.48
2:D:243:TYR:O	2:D:247:VAL:HG22	2.14	0.47
2:D:132:GLU:OE1	2:D:132:GLU:N	2.48	0.46
2:D:86:ARG:HG3	2:D:108:TYR:CE1	2.50	0.46
2:B:249:THR:OG1	4:B:402:HOH:O	2.20	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:149:LYS:HG2	1:C:168:ILE:HG13	1.98	0.45
1:C:54:TYR:CZ	1:C:58:ILE:HD11	2.51	0.45
2:D:184:ILE:HG22	2:D:186:GLU:H	1.81	0.45
1:E:112:ASP:HB3	1:E:115:LYS:HB2	1.98	0.45
2:D:192:MET:N	2:D:192:MET:SD	2.91	0.44
2:B:170:TRP:CD1	2:B:192:MET:HG2	2.53	0.44
1:E:157:PRO:HB2	1:E:158:GLU:HG2	2.00	0.43
2:D:170:TRP:CD1	2:D:192:MET:HG2	2.53	0.43
1:E:57:ILE:HD12	1:E:94:LEU:HD12	2.01	0.43
1:E:141:LYS:NZ	1:E:208:GLU:OE1	2.29	0.43
2:F:192:MET:SD	2:F:192:MET:N	2.92	0.43
1:C:151:GLN:HG3	1:C:193:ALA:HB1	2.00	0.43
2:D:130:LYS:HG2	3:D:401:GOL:H11	2.01	0.42
1:E:140:TYR:O	1:E:144:SER:HB2	2.19	0.42
1:E:54:TYR:CZ	1:E:58:ILE:HD11	2.55	0.42
1:C:218:PHE:HZ	2:D:237:TYR:CD2	2.38	0.41
1:A:103:LYS:NZ	1:A:224:LEU:HD21	2.34	0.41
1:A:57:ILE:HD12	1:A:94:LEU:HD12	2.02	0.41
2:F:114:ILE:HD13	2:F:139:LEU:HG	2.01	0.41
1:A:127:LEU:HD21	1:A:221:MET:HB2	2.03	0.41
1:A:162:GLU:OE2	2:D:234:SER:OG	2.23	0.40
1:A:101:ASP:OD2	4:A:301:HOH:O	2.22	0.40
2:D:117:ASP:OD2	2:D:134:LYS:NZ	2.39	0.40
2:D:180:LYS:NZ	4:D:502:HOH:O	2.16	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	173/210 (82%)	169 (98%)	3 (2%)	1 (1%)	25 26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	177/210 (84%)	174 (98%)	3 (2%)	0	100	100
1	E	177/210 (84%)	171 (97%)	6 (3%)	0	100	100
2	B	169/250 (68%)	165 (98%)	4 (2%)	0	100	100
2	D	169/250 (68%)	164 (97%)	5 (3%)	0	100	100
2	F	167/250 (67%)	162 (97%)	4 (2%)	1 (1%)	25	26
All	All	1032/1380 (75%)	1005 (97%)	25 (2%)	2 (0%)	47	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
2	F	222	GLU

5.3.2 Protein sidechains (i)

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	159/187 (85%)	152 (96%)	7 (4%)	28	35
1	C	161/187 (86%)	158 (98%)	3 (2%)	57	71
1	E	162/187 (87%)	155 (96%)	7 (4%)	29	36
2	B	161/230 (70%)	161 (100%)	0	100	100
2	D	161/230 (70%)	159 (99%)	2 (1%)	71	83
2	F	159/230 (69%)	157 (99%)	2 (1%)	69	81
All	All	963/1251 (77%)	942 (98%)	21 (2%)	52	65

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

Mol	Chain	Res	Type
1	A	38	VAL
1	A	78	MET
1	A	165	GLU
1	A	170	ASP

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Mol	Chain	Res	Type
1	A	171	VAL
1	A	174	GLN
1	A	205	LEU
1	C	133	TYR
1	C	172	ASN
1	C	174	GLN
2	D	222	GLU
2	D	247	VAL
1	E	133	TYR
1	E	144	SER
1	E	155	ILE
1	E	161	ASP
1	E	196	GLU
1	E	205	LEU
1	E	218	PHE
2	F	176	VAL
2	F	192	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

There are no monosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	D	401	-	5,5,5	0.36	0	5,5,5	0.22	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	D	401	-	-	0/4/4/4	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	401	GOL	1	0

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, 95^{th} 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	177/210 (84%)	0.53	18 (10%) 6 6	35, 54, 99, 112	0
1	C	181/210 (86%)	0.35	12 (6%) 18 17	34, 52, 99, 112	0
1	E	181/210 (86%)	0.64	28 (15%) 2 1	37, 56, 120, 130	0
2	B	173/250 (69%)	0.12	5 (2%) 51 49	34, 43, 74, 117	0
2	D	173/250 (69%)	-0.07	2 (1%) 79 77	29, 40, 63, 116	0
2	F	171/250 (68%)	-0.10	1 (0%) 89 88	30, 40, 62, 81	0
All	All	1056/1380 (76%)	0.25	66 (6%) 20 19	29, 46, 100, 130	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	197	VAL	5.9
1	A	35	MET	5.6
1	E	191	LYS	5.6
1	E	156	GLN	5.5
1	A	171	VAL	5.3
1	C	172	ASN	5.1
1	A	224	LEU	4.7
1	E	157	PRO	4.4
1	E	190	ALA	4.3
1	E	194	LEU	4.3
1	A	111	HIS	4.3
1	E	38	VAL	4.3
1	A	192	THR	4.3
1	A	196	GLU	4.2
1	E	96	TYR	3.9
2	B	176	VAL	3.7
1	C	192	THR	3.7
1	A	225	VAL	3.6
1	E	168	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	158	GLU	3.5
1	C	111	HIS	3.3
1	E	198	GLN	3.3
2	D	146	ASN	3.2
2	B	99	HIS	3.1
1	E	152	TYR	3.0
1	E	196	GLU	3.0
1	E	111	HIS	2.9
1	E	173	GLY	2.8
1	E	154	ILE	2.8
1	C	195	ALA	2.7
1	E	166	ALA	2.7
1	E	155	ILE	2.7
1	C	189	GLU	2.7
1	E	153	THR	2.7
1	A	110	LEU	2.7
1	A	172	ASN	2.6
1	A	154	ILE	2.6
1	C	190	ALA	2.6
1	C	176	ILE	2.6
1	E	169	ASN	2.6
2	F	75	SER	2.5
1	E	174	GLN	2.5
1	C	193	ALA	2.5
1	E	195	ALA	2.4
1	C	191	LYS	2.4
2	B	175	LEU	2.4
1	C	66	LYS	2.4
1	E	201	HIS	2.4
1	A	157	PRO	2.4
2	B	75	SER	2.4
1	E	171	VAL	2.3
1	A	152	TYR	2.3
1	A	194	LEU	2.3
1	C	35	MET	2.3
1	A	34	HIS	2.2
1	E	75	GLU	2.2
1	A	78	MET	2.1
2	D	99	HIS	2.1
1	E	149	LYS	2.1
1	E	199	ALA	2.1
2	B	102	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	202	GLN	2.1
1	A	161	ASP	2.0
1	E	78	MET	2.0
1	C	155	ILE	2.0
1	A	156	GLN	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

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, 95^{th} 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
3	GOL	D	401	6/6	0.54	0.42	61,64,67,75	0

6.5 Other polymers (i)

There are no such residues in this entry.