Full wwPDB X-ray Structure Validation Report

May 24, 2020 – 07:03 am BST

PDB ID	:	6HRS
Title	:	Structure of the TRPML2 ELD at pH 4.5
Authors	:	Bader, N.; Viet, K.K.; Wagner, A.; Hellmich, U.A.; Schindelin, H.
Deposited on	:	2018-09-28
Resolution	:	2.95 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 following versions of software and data (see references (1)) were used in the production of this report:

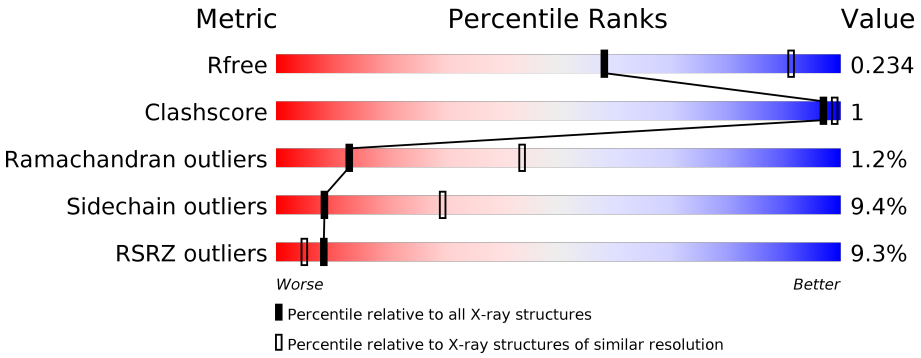
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 on 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	199	8% 81% 11% • 7%
1	B	199	7% 85% 11% •
1	C	199	11% 83% 10% • 6%
1	D	199	9% 85% 10% 5%
1	E	199	8% 81% 13% 6%
1	F	199	9% 82% 9% • 9%

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Mol	Chain	Length	Quality of chain
1	G	199	11% 83% 10% • 6%
1	H	199	8% 82% 10% 8%

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
2	GOL	C	301	-	-	-	X

2 Entry composition (i)

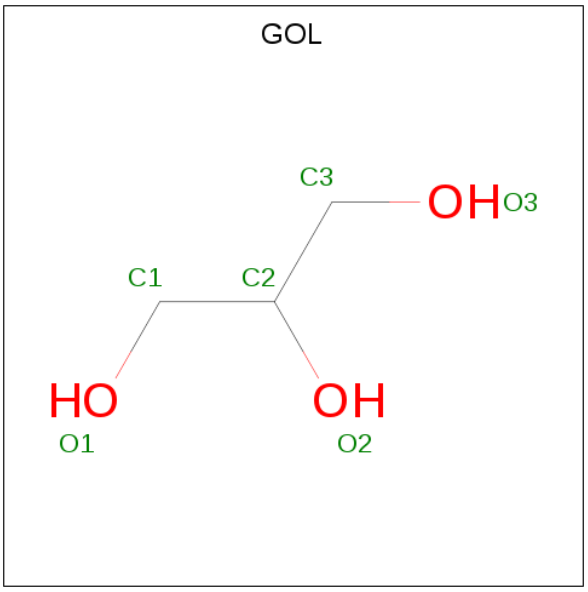
There are 3 unique types of molecules in this entry. The entry contains 23994 atoms, of which 11749 are hydrogens and 0 are deuteriums.

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 Mucolipin-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	185	Total	C	H	N	O	S	1455	0	0
			2972	969	1455	247	296	5			
1	B	191	Total	C	H	N	O	S	1500	0	0
			3065	999	1500	254	306	6			
1	C	187	Total	C	H	N	O	S	1474	0	0
			3004	979	1474	247	298	6			
1	D	189	Total	C	H	N	O	S	1490	0	0
			3035	988	1490	250	302	5			
1	E	187	Total	C	H	N	O	S	1481	0	0
			3017	983	1481	249	299	5			
1	F	182	Total	C	H	N	O	S	1432	0	0
			2923	954	1432	240	292	5			
1	G	187	Total	C	H	N	O	S	1476	0	0
			3007	980	1476	248	298	5			
1	H	183	Total	C	H	N	O	S	1441	0	0
			2941	960	1441	243	292	5			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is water.

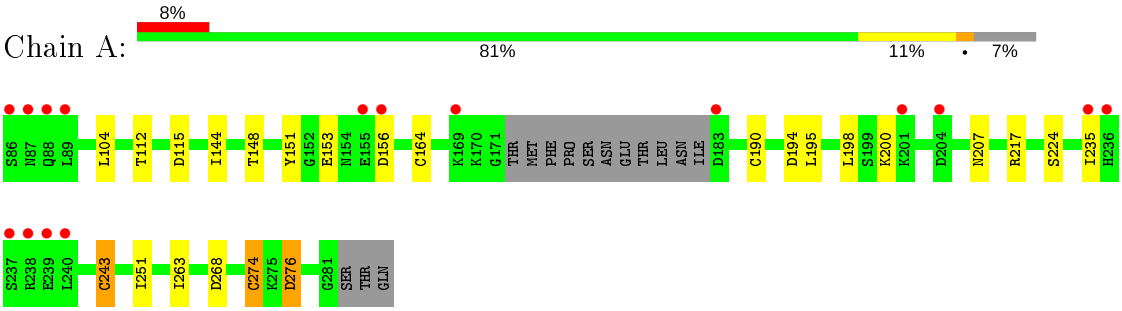
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	6	Total O 6 6	0	0
3	C	1	Total O 1 1	0	0
3	D	3	Total O 3 3	0	0
3	E	7	Total O 7 7	0	0
3	F	1	Total O 1 1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

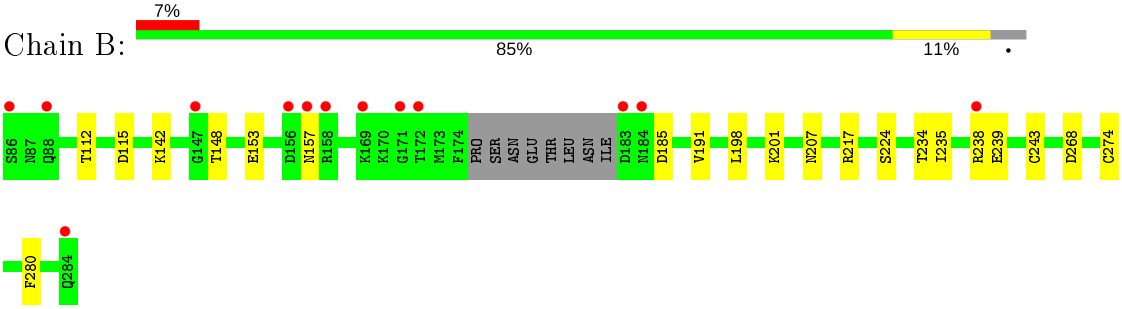
- Molecule 1: Mucolipin-2

Chain A:



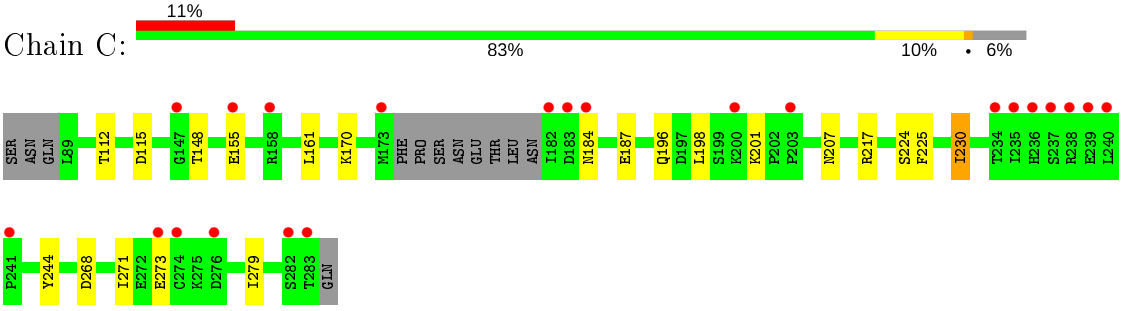
- Molecule 1: Mucolipin-2

Chain B:



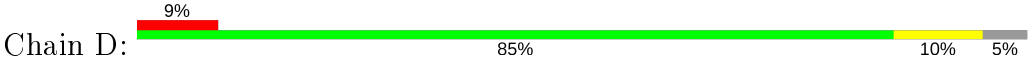
- Molecule 1: Mucolipin-2

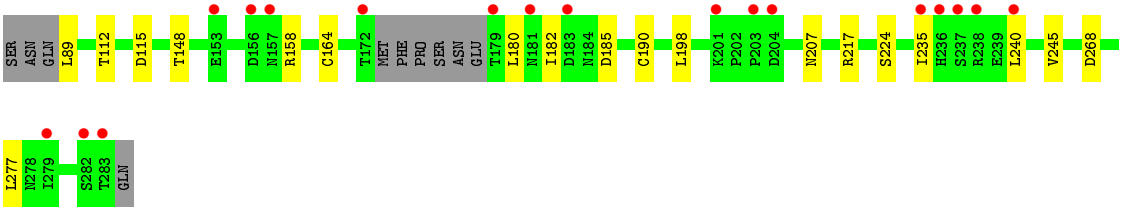
Chain C:



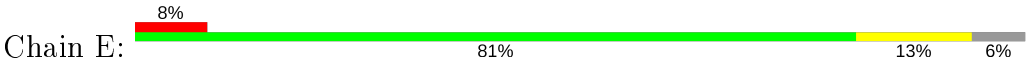
- Molecule 1: Mucolipin-2

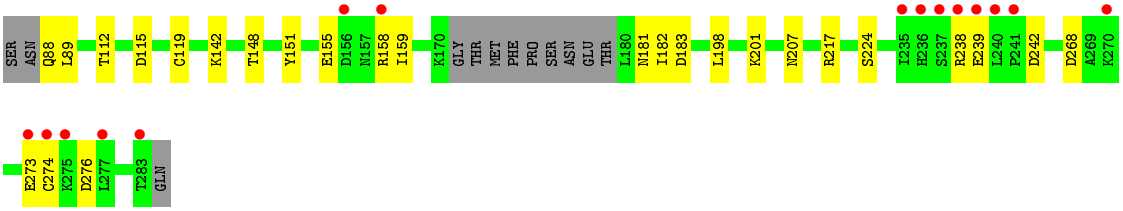
Chain D:



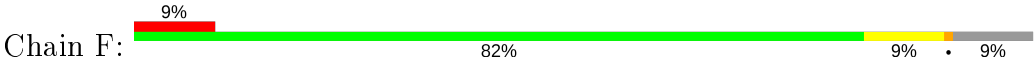


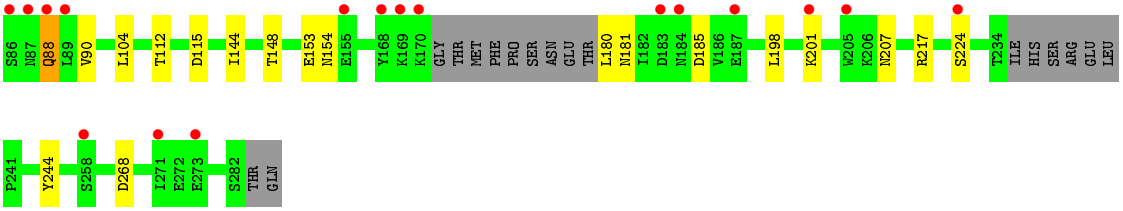
• Molecule 1: Mucolipin-2



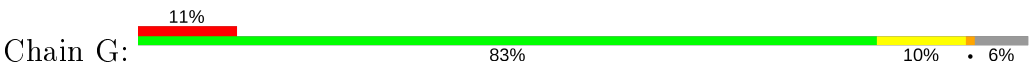


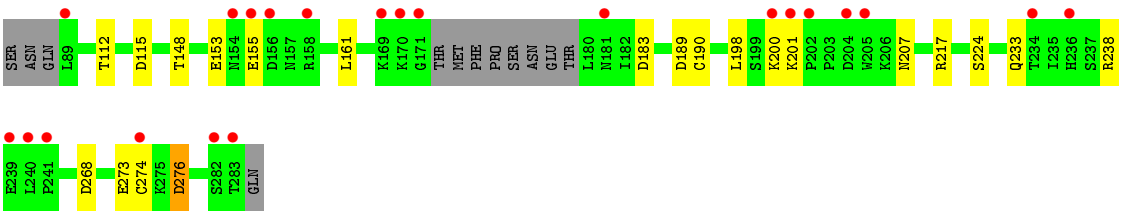
• Molecule 1: Mucolipin-2



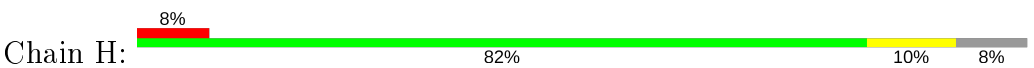


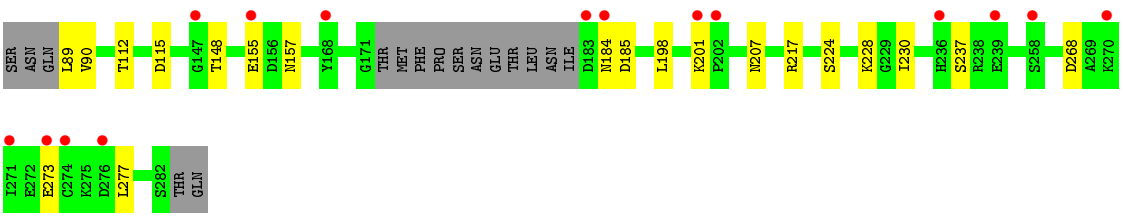
• Molecule 1: Mucolipin-2





• Molecule 1: Mucolipin-2





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	74.52Å 142.47Å 85.19Å 90.00° 104.49° 90.00°	Depositor
Resolution (Å)	28.13 – 2.95 27.94 – 2.95	Depositor EDS
% Data completeness (in resolution range)	98.8 (28.13-2.95) 98.8 (27.94-2.95)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.33 (at 2.95Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.182 , 0.216 0.195 , 0.234	Depositor DCC
R_{free} test set	1868 reflections (5.22%)	wwPDB-VP
Wilson B-factor (Å^2)	88.5	Xtriage
Anisotropy	0.233	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 86.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	23994	wwPDB-VP
Average B, all atoms (Å^2)	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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	0.54	0/1549	0.69	0/2086
1	B	0.54	0/1598	0.68	0/2152
1	C	0.50	0/1562	0.64	0/2104
1	D	0.51	0/1577	0.65	0/2126
1	E	0.48	0/1568	0.64	0/2113
1	F	0.47	0/1521	0.64	0/2047
1	G	0.50	0/1563	0.67	0/2106
1	H	0.48	0/1532	0.66	0/2063
All	All	0.50	0/12470	0.66	0/16797

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	1517	1455	1455	8	0
1	B	1565	1500	1500	2	0
1	C	1530	1474	1475	4	0
1	D	1545	1490	1490	2	0
1	E	1536	1481	1481	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1491	1432	1432	3	0
1	G	1531	1476	1476	0	0
1	H	1500	1441	1441	1	0
2	A	6	0	8	0	0
2	C	6	0	8	0	0
3	A	6	0	0	0	0
3	C	1	0	0	0	0
3	D	3	0	0	0	0
3	E	7	0	0	0	0
3	F	1	0	0	0	0
All	All	12245	11749	11766	21	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 1.

All (21) 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:164:CYS:HG	1:A:190:CYS:HG	1.28	0.78
1:A:164:CYS:CB	1:A:190:CYS:HG	2.06	0.69
1:A:243:CYS:HB3	1:A:274:CYS:SG	2.44	0.57
1:E:151:TYR:HB3	1:E:159:ILE:HD11	1.87	0.56
1:C:230:ILE:HD11	1:C:279:ILE:CD1	2.36	0.55
1:A:151:TYR:CE2	1:A:195:LEU:HD11	2.49	0.47
1:A:104:LEU:HD22	1:A:144:ILE:CG2	2.46	0.45
1:A:251:ILE:O	1:A:263:ILE:HA	2.18	0.44
1:D:164:CYS:SG	1:D:190:CYS:SG	3.00	0.43
1:F:104:LEU:HD22	1:F:144:ILE:CG2	2.48	0.43
1:A:164:CYS:CB	1:A:190:CYS:SG	3.05	0.43
1:B:142:LYS:HA	1:B:280:PHE:CD1	2.54	0.43
1:A:164:CYS:HB3	1:A:190:CYS:SG	2.59	0.42
1:B:243:CYS:HB3	1:B:274:CYS:SG	2.59	0.42
1:H:228:LYS:HD3	1:H:277:LEU:HD13	2.01	0.42
1:C:230:ILE:HD11	1:C:279:ILE:HD12	2.02	0.42
1:F:90:VAL:HB	1:F:244:TYR:OH	2.20	0.42
1:D:180:LEU:HD11	1:D:182:ILE:HD12	2.01	0.41
1:C:244:TYR:CE2	1:C:271:ILE:CD1	3.04	0.41
1:F:104:LEU:HD22	1:F:144:ILE:HG22	2.03	0.41
1:C:161:LEU:HB3	1:C:225:PHE:HB3	2.02	0.41

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	181/199 (91%)	170 (94%)	9 (5%)	2 (1%)	14	46
1	B	187/199 (94%)	179 (96%)	7 (4%)	1 (0%)	29	64
1	C	183/199 (92%)	173 (94%)	8 (4%)	2 (1%)	14	46
1	D	185/199 (93%)	177 (96%)	7 (4%)	1 (0%)	29	64
1	E	183/199 (92%)	172 (94%)	7 (4%)	4 (2%)	6	28
1	F	176/199 (88%)	168 (96%)	6 (3%)	2 (1%)	14	46
1	G	183/199 (92%)	171 (93%)	10 (6%)	2 (1%)	14	46
1	H	179/199 (90%)	172 (96%)	4 (2%)	3 (2%)	9	34
All	All	1457/1592 (92%)	1382 (95%)	58 (4%)	17 (1%)	13	43

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	276	ASP
1	H	155	GLU
1	C	170	LYS
1	E	181	ASN
1	E	242	ASP
1	H	185	ASP
1	A	115	ASP
1	B	115	ASP
1	C	115	ASP
1	D	115	ASP
1	E	115	ASP
1	E	155	GLU
1	F	115	ASP
1	G	115	ASP
1	H	115	ASP
1	G	276	ASP
1	F	88	GLN

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	169/183 (92%)	154 (91%)	15 (9%)	9 32
1	B	175/183 (96%)	159 (91%)	16 (9%)	9 31
1	C	171/183 (93%)	157 (92%)	14 (8%)	11 36
1	D	173/183 (94%)	159 (92%)	14 (8%)	11 36
1	E	172/183 (94%)	152 (88%)	20 (12%)	5 20
1	F	167/183 (91%)	153 (92%)	14 (8%)	11 35
1	G	171/183 (93%)	151 (88%)	20 (12%)	5 20
1	H	167/183 (91%)	152 (91%)	15 (9%)	9 32
All	All	1365/1464 (93%)	1237 (91%)	128 (9%)	8 29

All (128) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	THR
1	A	148	THR
1	A	153	GLU
1	A	156	ASP
1	A	194	ASP
1	A	198	LEU
1	A	200	LYS
1	A	207	ASN
1	A	217	ARG
1	A	224	SER
1	A	235	ILE
1	A	243	CYS
1	A	268	ASP
1	A	274	CYS
1	A	276	ASP
1	B	112	THR
1	B	148	THR
1	B	153	GLU
1	B	157	ASN

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Mol	Chain	Res	Type
1	B	185	ASP
1	B	191	VAL
1	B	198	LEU
1	B	201	LYS
1	B	207	ASN
1	B	217	ARG
1	B	224	SER
1	B	234	THR
1	B	235	ILE
1	B	238	ARG
1	B	239	GLU
1	B	268	ASP
1	C	112	THR
1	C	148	THR
1	C	155	GLU
1	C	184	ASN
1	C	187	GLU
1	C	196	GLN
1	C	198	LEU
1	C	201	LYS
1	C	207	ASN
1	C	217	ARG
1	C	224	SER
1	C	230	ILE
1	C	268	ASP
1	C	273	GLU
1	D	89	LEU
1	D	112	THR
1	D	148	THR
1	D	158	ARG
1	D	185	ASP
1	D	198	LEU
1	D	207	ASN
1	D	217	ARG
1	D	224	SER
1	D	235	ILE
1	D	240	LEU
1	D	245	VAL
1	D	268	ASP
1	D	277	LEU
1	E	88	GLN
1	E	89	LEU

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Mol	Chain	Res	Type
1	E	112	THR
1	E	119	CYS
1	E	142	LYS
1	E	148	THR
1	E	158	ARG
1	E	182	ILE
1	E	183	ASP
1	E	198	LEU
1	E	201	LYS
1	E	207	ASN
1	E	217	ARG
1	E	224	SER
1	E	238	ARG
1	E	239	GLU
1	E	268	ASP
1	E	273	GLU
1	E	274	CYS
1	E	276	ASP
1	F	88	GLN
1	F	112	THR
1	F	148	THR
1	F	153	GLU
1	F	154	ASN
1	F	180	LEU
1	F	181	ASN
1	F	185	ASP
1	F	198	LEU
1	F	201	LYS
1	F	207	ASN
1	F	217	ARG
1	F	224	SER
1	F	268	ASP
1	G	112	THR
1	G	148	THR
1	G	153	GLU
1	G	155	GLU
1	G	161	LEU
1	G	183	ASP
1	G	189	ASP
1	G	190	CYS
1	G	198	LEU
1	G	200	LYS

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Mol	Chain	Res	Type
1	G	201	LYS
1	G	207	ASN
1	G	217	ARG
1	G	224	SER
1	G	233	GLN
1	G	238	ARG
1	G	268	ASP
1	G	273	GLU
1	G	274	CYS
1	G	276	ASP
1	H	89	LEU
1	H	90	VAL
1	H	112	THR
1	H	148	THR
1	H	157	ASN
1	H	184	ASN
1	H	198	LEU
1	H	201	LYS
1	H	207	ASN
1	H	217	ARG
1	H	224	SER
1	H	230	ILE
1	H	237	SER
1	H	268	ASP
1	H	273	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	157	ASN
1	F	157	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 ligands are 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	$\#\|Z\| > 2$
2	GOL	C	301	-	5,5,5	0.22	0	5,5,5	0.78	0
2	GOL	A	401	-	5,5,5	0.10	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
2	GOL	C	301	-	-	2/4/4/4	-
2	GOL	A	401	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	GOL	C1-C2-C3-O3
2	C	301	GOL	O1-C1-C2-C3
2	C	301	GOL	C1-C2-C3-O3
2	A	401	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	185/199 (92%)	0.27	16 (8%) 10 6	56, 102, 188, 279	0
1	B	191/199 (95%)	0.06	13 (6%) 17 10	57, 95, 166, 268	0
1	C	187/199 (93%)	0.48	22 (11%) 4 2	66, 114, 211, 277	0
1	D	189/199 (94%)	0.29	18 (9%) 8 5	57, 98, 169, 230	0
1	E	187/199 (93%)	0.17	15 (8%) 12 7	66, 112, 197, 254	0
1	F	182/199 (91%)	0.43	17 (9%) 8 5	65, 111, 181, 258	0
1	G	187/199 (93%)	0.53	22 (11%) 4 2	66, 111, 202, 248	0
1	H	183/199 (91%)	0.27	15 (8%) 11 6	65, 117, 201, 239	0
All	All	1491/1592 (93%)	0.31	138 (9%) 8 5	56, 108, 194, 279	0

All (138) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	155	GLU	8.3
1	A	183	ASP	7.9
1	C	236	HIS	7.6
1	G	283	THR	7.6
1	C	237	SER	7.2
1	C	240	LEU	6.4
1	C	283	THR	6.3
1	A	240	LEU	6.0
1	B	284	GLN	5.7
1	G	241	PRO	5.4
1	C	276	ASP	5.4
1	H	184	ASN	5.4
1	F	86	SER	5.4
1	D	236	HIS	5.3
1	D	153	GLU	5.2
1	A	237	SER	5.1

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Mol	Chain	Res	Type	RSRZ
1	F	88	GLN	4.8
1	C	183	ASP	4.7
1	A	236	HIS	4.7
1	D	204	ASP	4.6
1	E	240	LEU	4.5
1	D	237	SER	4.5
1	A	87	ASN	4.5
1	B	184	ASN	4.4
1	C	241	PRO	4.4
1	A	89	LEU	4.4
1	G	239	GLU	4.3
1	H	183	ASP	4.3
1	E	236	HIS	4.3
1	F	169	LYS	4.2
1	D	172	THR	4.2
1	C	155	GLU	4.1
1	E	238	ARG	4.1
1	A	86	SER	4.0
1	F	155	GLU	4.0
1	C	238	ARG	3.8
1	F	183	ASP	3.7
1	G	171	GLY	3.7
1	D	203	PRO	3.7
1	E	235	ILE	3.7
1	G	282	SER	3.7
1	B	156	ASP	3.6
1	D	235	ILE	3.6
1	B	183	ASP	3.6
1	F	187	GLU	3.5
1	G	204	ASP	3.5
1	H	155	GLU	3.4
1	G	158	ARG	3.4
1	F	184	ASN	3.3
1	F	87	ASN	3.3
1	H	201	LYS	3.2
1	A	88	GLN	3.2
1	A	238	ARG	3.2
1	C	173	MET	3.2
1	G	234	THR	3.2
1	H	236	HIS	3.2
1	A	156	ASP	3.2
1	B	172	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	184	ASN	3.1
1	B	238	ARG	3.1
1	D	240	LEU	3.1
1	B	86	SER	3.1
1	C	282	SER	3.0
1	E	283	THR	3.0
1	G	181	ASN	3.0
1	G	274	CYS	3.0
1	D	283	THR	3.0
1	F	273	GLU	3.0
1	B	157	ASN	2.9
1	B	88	GLN	2.9
1	F	258	SER	2.9
1	C	235	ILE	2.9
1	H	270	LYS	2.9
1	D	279	ILE	2.8
1	F	271	ILE	2.8
1	H	274	CYS	2.8
1	E	237	SER	2.8
1	H	276	ASP	2.8
1	F	170	LYS	2.8
1	D	183	ASP	2.8
1	F	168	TYR	2.7
1	C	182	ILE	2.7
1	E	158	ARG	2.7
1	E	241	PRO	2.7
1	D	201	LYS	2.7
1	A	239	GLU	2.7
1	H	271	ILE	2.7
1	A	169	LYS	2.6
1	D	238	ARG	2.5
1	A	155	GLU	2.5
1	G	202	PRO	2.5
1	A	201	LYS	2.5
1	A	235	ILE	2.5
1	F	201	LYS	2.5
1	C	273	GLU	2.4
1	E	275	LYS	2.4
1	G	169	LYS	2.4
1	G	201	LYS	2.4
1	H	202	PRO	2.4
1	E	156	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	H	168	TYR	2.3
1	C	239	GLU	2.3
1	C	158	ARG	2.3
1	D	179	THR	2.3
1	C	200	LYS	2.3
1	D	282	SER	2.3
1	B	158	ARG	2.3
1	F	89	LEU	2.3
1	E	239	GLU	2.2
1	G	200	LYS	2.2
1	H	258	SER	2.2
1	F	205	TRP	2.2
1	D	157	ASN	2.2
1	H	273	GLU	2.2
1	G	205	TRP	2.2
1	E	277	LEU	2.2
1	G	89	LEU	2.2
1	C	147	GLY	2.2
1	A	204	ASP	2.2
1	H	147	GLY	2.1
1	B	147	GLY	2.1
1	B	171	GLY	2.1
1	F	224	SER	2.1
1	B	169	LYS	2.1
1	D	156	ASP	2.1
1	H	239	GLU	2.1
1	G	236	HIS	2.1
1	G	156	ASP	2.1
1	D	181	ASN	2.1
1	E	270	LYS	2.1
1	C	203	PRO	2.1
1	E	274	CYS	2.0
1	G	240	LEU	2.0
1	C	234	THR	2.0
1	E	273	GLU	2.0
1	C	274	CYS	2.0
1	G	154	ASN	2.0
1	G	170	LYS	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 carbohydrates 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
2	GOL	C	301	6/6	0.66	0.50	117,119,122,122	0
2	GOL	A	401	6/6	0.81	0.13	153,153,157,160	0

6.5 Other polymers (i)

There are no such residues in this entry.