



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 11:52 PM BST

PDB ID : 3ZW8
Title : Crystal Structure Of Rat Peroxisomal Multifunctional Enzyme Type 1 (rpMFE1) In Apo Form
Authors : Kasaragod, P.; Schmitz, W.; Hiltunen, J.K.; Wierenga, R.K.
Deposited on : 2011-07-28
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.13.1
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) : 2.13.1

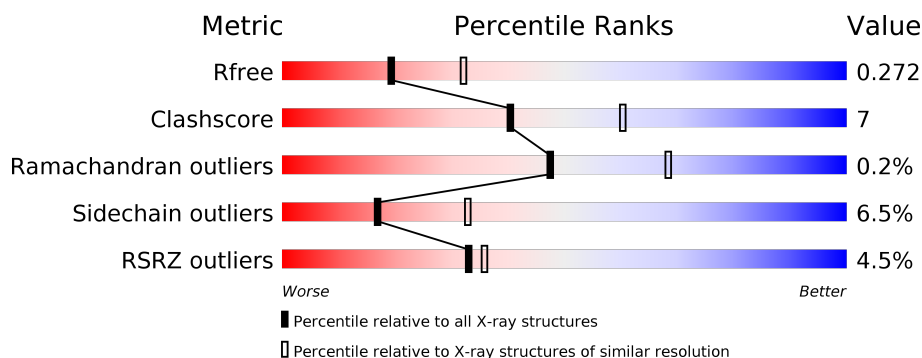
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 $\leq 5\%$. 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	742	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>• •</div> </div> </div>
1	B	742	<div> <div>5%</div> <div> <div></div> <div>77%</div> <div>18%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11373 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 PEROXISOMAL BIFUNCTIONAL ENZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	725	Total	C	N	O	S	0	0	0
			5562	3553	976	1010	23			
1	B	720	Total	C	N	O	S	0	0	0
			5530	3535	968	1004	23			

There are 40 discrepancies between the modelled and reference sequences:

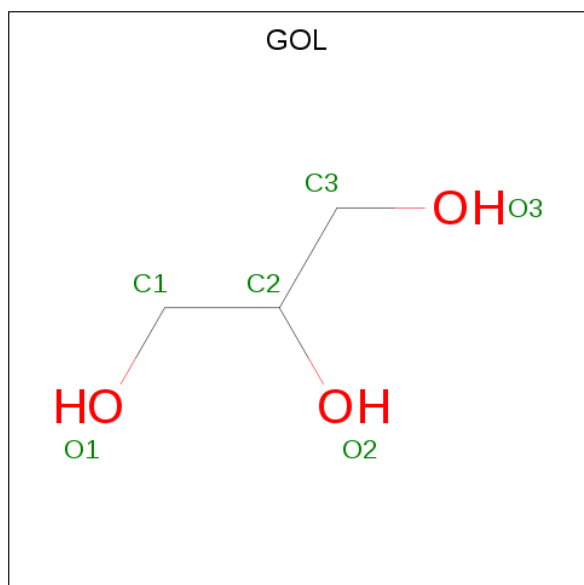
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P07896
A	-18	GLY	-	expression tag	UNP P07896
A	-17	SER	-	expression tag	UNP P07896
A	-16	SER	-	expression tag	UNP P07896
A	-15	HIS	-	expression tag	UNP P07896
A	-14	HIS	-	expression tag	UNP P07896
A	-13	HIS	-	expression tag	UNP P07896
A	-12	HIS	-	expression tag	UNP P07896
A	-11	HIS	-	expression tag	UNP P07896
A	-10	HIS	-	expression tag	UNP P07896
A	-9	SER	-	expression tag	UNP P07896
A	-8	SER	-	expression tag	UNP P07896
A	-7	GLY	-	expression tag	UNP P07896
A	-6	LEU	-	expression tag	UNP P07896
A	-5	VAL	-	expression tag	UNP P07896
A	-4	PRO	-	expression tag	UNP P07896
A	-3	ARG	-	expression tag	UNP P07896
A	-2	GLY	-	expression tag	UNP P07896
A	-1	SER	-	expression tag	UNP P07896
A	0	HIS	-	expression tag	UNP P07896
B	-19	MET	-	expression tag	UNP P07896
B	-18	GLY	-	expression tag	UNP P07896
B	-17	SER	-	expression tag	UNP P07896
B	-16	SER	-	expression tag	UNP P07896
B	-15	HIS	-	expression tag	UNP P07896

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP P07896
B	-13	HIS	-	expression tag	UNP P07896
B	-12	HIS	-	expression tag	UNP P07896
B	-11	HIS	-	expression tag	UNP P07896
B	-10	HIS	-	expression tag	UNP P07896
B	-9	SER	-	expression tag	UNP P07896
B	-8	SER	-	expression tag	UNP P07896
B	-7	GLY	-	expression tag	UNP P07896
B	-6	LEU	-	expression tag	UNP P07896
B	-5	VAL	-	expression tag	UNP P07896
B	-4	PRO	-	expression tag	UNP P07896
B	-3	ARG	-	expression tag	UNP P07896
B	-2	GLY	-	expression tag	UNP P07896
B	-1	SER	-	expression tag	UNP P07896
B	0	HIS	-	expression tag	UNP P07896

- 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	0	0
			6	3	3		

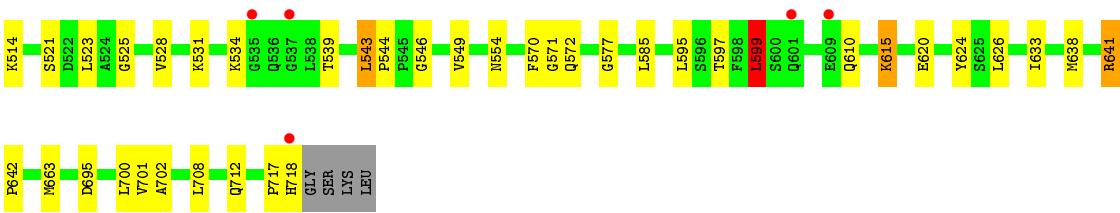
- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	148	Total	O	0	0
			148	148		
4	B	97	Total	O	0	0
			97	97		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.22Å 125.68Å 226.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.50 42.02 – 2.50	Depositor EDS
% Data completeness (in resolution range)	86.2 (100.00-2.50) 86.2 (42.02-2.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.03 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.230 , 0.277 0.226 , 0.272	Depositor DCC
R_{free} test set	2872 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.582	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	11373	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4

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	0.78	0/5691	0.79	4/7709 (0.1%)
1	B	0.77	1/5658 (0.0%)	0.79	6/7666 (0.1%)
All	All	0.77	1/11349 (0.0%)	0.79	10/15375 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	487	TYR	CD1-CE1	5.59	1.47	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	234	ARG	NE-CZ-NH2	-10.96	114.82	120.30
1	A	234	ARG	NE-CZ-NH1	8.30	124.45	120.30
1	B	234	ARG	NE-CZ-NH1	8.21	124.40	120.30
1	B	234	ARG	NE-CZ-NH2	-7.55	116.52	120.30
1	A	657	ARG	NE-CZ-NH2	5.81	123.21	120.30
1	A	657	ARG	NE-CZ-NH1	-5.57	117.52	120.30
1	B	24	VAL	CB-CA-C	-5.30	101.33	111.40
1	B	599	LEU	CB-CG-CD1	5.23	119.89	111.00
1	B	508	LEU	CA-CB-CG	-5.13	103.51	115.30
1	B	626	LEU	CA-CB-CG	5.12	127.07	115.30

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	5562	0	5667	67	0
1	B	5530	0	5636	95	0
2	A	6	0	8	2	0
3	A	15	0	0	0	0
3	B	15	0	0	2	0
4	A	148	0	0	12	0
4	B	97	0	0	25	0
All	All	11373	0	11311	161	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 (161) 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:635:GLU:HG2	4:A:2115:HOH:O	1.71	0.90
1:B:136:GLN:HG3	1:B:248:ILE:HD12	1.58	0.83
1:B:554:ASN:HB2	4:B:2077:HOH:O	1.77	0.82
1:A:589:HIS:HE1	4:A:2108:HOH:O	1.63	0.80
1:A:135:THR:HG21	1:A:235:SER:OG	1.82	0.80
1:A:136:GLN:HG3	1:A:248:ILE:HD12	1.63	0.79
1:B:219:VAL:HG22	1:B:229:PRO:HB2	1.64	0.79
1:B:145:PRO:HD2	4:B:2025:HOH:O	1.84	0.77
1:B:122:PRO:O	1:B:125:THR:HB	1.85	0.77
1:A:603:ARG:HD3	4:A:2112:HOH:O	1.85	0.76
1:A:71:PRO:HD2	1:A:259:ARG:HD2	1.67	0.75
1:B:135:THR:HG21	1:B:235:SER:OG	1.85	0.74
1:A:122:PRO:O	1:A:125:THR:HB	1.87	0.74
1:A:62:ASP:HB3	4:A:2008:HOH:O	1.89	0.73
1:B:162:ALA:C	4:B:2027:HOH:O	2.27	0.72
1:A:382:PHE:CE1	1:A:531:LYS:NZ	2.60	0.69
1:B:135:THR:HB	1:B:251:GLU:OE2	1.92	0.69
1:A:382:PHE:HE1	1:A:531:LYS:NZ	1.94	0.66
1:B:160:ASP:OD1	1:B:164:ARG:NH2	2.28	0.66
1:B:168:LEU:HG	4:B:2027:HOH:O	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:554:ASN:CB	4:B:2077:HOH:O	2.40	0.64
1:B:348:SER:O	1:B:352:GLN:HG3	1.96	0.64
1:B:250:GLU:HB2	4:B:2034:HOH:O	1.99	0.63
1:B:440:ARG:O	1:B:467:LYS:HB3	1.98	0.63
1:B:158:SER:HB3	1:B:355:GLN:HG2	1.82	0.61
1:B:717:PRO:HA	4:B:2084:HOH:O	2.00	0.60
1:B:219:VAL:CG2	1:B:229:PRO:HB2	2.32	0.59
1:B:68:ALA:HB2	1:B:260:ALA:HA	1.84	0.59
1:A:135:THR:HB	1:A:251:GLU:OE1	2.04	0.58
1:A:160:ASP:OD1	1:A:164:ARG:NH2	2.37	0.58
1:A:675:LEU:HD12	1:A:701:VAL:HG11	1.87	0.57
1:A:96:VAL:HG13	1:A:98:LEU:HG	1.87	0.57
1:B:168:LEU:N	4:B:2027:HOH:O	2.38	0.56
1:B:615:LYS:HE3	4:B:2067:HOH:O	2.06	0.56
1:A:294:GLN:HB3	4:A:2053:HOH:O	2.05	0.55
1:B:245:GLU:HG3	4:B:2037:HOH:O	2.06	0.55
1:B:424:PRO:HD2	4:B:2057:HOH:O	2.05	0.55
1:A:428:ILE:HG13	1:A:446:PRO:HA	1.90	0.54
1:B:33:ARG:NH1	1:B:81:GLU:OE1	2.35	0.54
1:B:425:GLN:HA	1:B:449:TYR:O	2.08	0.54
1:B:641:ARG:HB2	1:B:642:PRO:HD2	1.91	0.53
1:A:525:GLY:O	1:A:528:VAL:HG12	2.08	0.53
1:A:497:GLU:OE1	1:A:611:ARG:NH1	2.42	0.53
1:B:162:ALA:CB	4:B:2027:HOH:O	2.57	0.53
1:B:525:GLY:O	1:B:528:VAL:HG12	2.09	0.53
1:B:97:ALA:HB3	1:B:119:VAL:HG12	1.91	0.52
1:B:162:ALA:HB1	4:B:2027:HOH:O	2.09	0.52
1:B:633:ILE:HG23	1:B:638:MET:HB2	1.92	0.52
1:B:125:THR:HG21	4:B:2021:HOH:O	2.10	0.52
1:B:349:ARG:O	1:B:353:ASN:HB2	2.08	0.52
1:A:-1:SER:N	1:A:31:GLU:OE2	2.43	0.52
1:A:219:VAL:HG22	1:A:229:PRO:HB2	1.92	0.52
1:A:131:GLY:H	2:A:1721:GOL:H32	1.76	0.51
1:B:110:TYR:CE2	1:B:187:ILE:HD13	2.45	0.51
1:B:108:CYS:O	1:B:111:ARG:NH1	2.42	0.51
1:B:3:GLU:HA	1:B:3:GLU:OE1	2.10	0.51
1:B:620:GLU:HG2	1:B:624:TYR:CE2	2.46	0.51
1:B:133:ARG:HD2	1:B:248:ILE:CG1	2.41	0.50
1:B:425:GLN:CD	4:B:2057:HOH:O	2.50	0.50
1:A:-2:GLY:HA2	1:A:31:GLU:OE2	2.12	0.50
1:A:183:PHE:O	1:A:186:LYS:HG2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:571:GLY:HA2	1:B:577:GLY:HA3	1.93	0.50
1:B:708:LEU:C	1:B:708:LEU:HD23	2.32	0.49
1:B:712:GLN:OE1	1:B:712:GLN:HA	2.12	0.49
1:B:137:LEU:O	1:B:140:ARG:HB2	2.13	0.49
1:B:717:PRO:CA	4:B:2084:HOH:O	2.60	0.49
1:B:129:LEU:C	1:B:129:LEU:HD12	2.33	0.49
1:B:223:TYR:O	1:B:226:VAL:HG13	2.13	0.48
1:B:283:PRO:HA	1:B:718:HIS:HE1	1.77	0.48
1:A:601:GLN:HG3	4:B:2052:HOH:O	2.13	0.48
1:A:543:LEU:HD11	1:A:547:THR:HG21	1.95	0.48
1:A:571:GLY:HA2	1:A:577:GLY:HA3	1.94	0.48
1:B:379:GLU:OE1	1:B:388:LYS:HD3	2.14	0.48
1:A:433:PHE:CE1	1:A:441:LEU:HD13	2.49	0.48
1:A:362:LEU:O	1:A:362:LEU:HD12	2.14	0.47
1:B:6:ARG:HH12	1:B:10:SER:HA	1.78	0.47
1:A:565:CYS:O	1:B:570:PHE:CE2	2.67	0.47
1:A:348:SER:HB2	4:A:2057:HOH:O	2.13	0.47
1:B:137:LEU:O	1:B:138:LEU:C	2.53	0.47
1:B:479:VAL:HG22	1:B:633:ILE:HG21	1.96	0.47
1:B:428:ILE:HG13	1:B:446:PRO:HA	1.97	0.47
1:B:151:ILE:HD12	1:B:236:ILE:HD11	1.97	0.47
1:B:136:GLN:NE2	4:B:2024:HOH:O	2.45	0.46
1:A:382:PHE:HE1	1:A:531:LYS:HZ3	1.63	0.46
1:A:440:ARG:O	1:A:467:LYS:HB3	2.15	0.46
1:B:37:GLN:HB3	4:B:2003:HOH:O	2.15	0.46
1:B:700:LEU:O	1:B:701:VAL:C	2.52	0.46
1:A:133:ARG:HD2	1:A:248:ILE:HD11	1.98	0.46
1:B:219:VAL:HG11	1:B:230:GLU:HA	1.97	0.46
1:B:18:ASN:O	1:B:22:ASN:HA	2.15	0.46
1:A:6:ARG:HH12	1:A:10:SER:HA	1.81	0.46
1:A:110:TYR:CE2	1:A:187:ILE:HD13	2.51	0.45
1:B:135:THR:HG22	1:B:136:GLN:OE1	2.17	0.45
1:B:138:LEU:HB3	1:B:139:PRO:HD3	1.97	0.45
1:A:-4:PRO:N	4:A:2003:HOH:O	2.49	0.45
1:B:663:MET:CE	1:B:663:MET:HA	2.46	0.45
1:A:274:GLU:OE2	1:A:651:HIS:NE2	2.41	0.45
1:A:135:THR:HG22	1:A:136:GLN:OE1	2.15	0.45
1:B:252:GLU:O	1:B:256:MET:HG3	2.17	0.44
1:B:304:LEU:HD11	1:B:324:ALA:HB1	2.00	0.44
1:B:24:VAL:HG11	1:B:75:LEU:HD13	1.98	0.44
1:A:671:LEU:O	1:A:672:PRO:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:ARG:HD2	1:A:248:ILE:CG1	2.47	0.44
1:B:157:LEU:HG	1:B:161:GLU:HG2	1.99	0.44
1:B:595:LEU:HG	1:B:599:LEU:HD22	2.00	0.43
1:B:145:PRO:CD	4:B:2025:HOH:O	2.57	0.43
1:A:121:LEU:O	1:A:154:GLY:HA2	2.18	0.43
1:A:599:LEU:O	1:A:603:ARG:HG3	2.18	0.43
1:B:97:ALA:O	1:B:119:VAL:HA	2.18	0.43
1:A:123:GLU:HB3	1:A:128:ILE:HG13	2.01	0.43
1:A:689:PRO:HD2	4:A:2105:HOH:O	2.18	0.43
1:B:68:ALA:CB	1:B:260:ALA:HA	2.48	0.43
1:B:280:TRP:O	1:B:288:TRP:HD1	2.02	0.43
1:B:140:ARG:HD3	1:B:197:ILE:O	2.19	0.43
1:B:315:PHE:HE1	1:B:461:LEU:HD11	1.83	0.43
1:A:304:LEU:HD11	1:A:324:ALA:HB1	2.01	0.42
1:B:430:THR:HB	1:B:442:LEU:HD11	2.01	0.42
1:A:572:GLN:HB3	1:A:572:GLN:HE21	1.56	0.42
1:B:546:GLY:HA2	4:B:2075:HOH:O	2.20	0.42
1:A:422:ASP:HB2	4:A:2069:HOH:O	2.18	0.42
1:A:473:GLY:HA2	4:A:2076:HOH:O	2.18	0.42
1:B:462:SER:HA	1:B:465:ILE:HG12	2.01	0.42
1:A:379:GLU:OE1	1:A:388:LYS:HD3	2.19	0.42
1:B:135:THR:HG21	1:B:235:SER:HG	1.84	0.42
1:B:168:LEU:CG	4:B:2027:HOH:O	2.62	0.42
1:B:543:LEU:HD22	1:B:544:PRO:HD2	2.00	0.42
1:A:578:TRP:O	1:A:595:LEU:HD22	2.19	0.42
1:B:166:GLY:HA2	4:B:2028:HOH:O	2.19	0.42
1:A:441:LEU:HD12	1:A:652:GLY:HA3	2.02	0.42
1:A:131:GLY:H	2:A:1721:GOL:C3	2.31	0.42
1:A:243:PRO:HB2	1:A:245:GLU:OE2	2.20	0.42
1:B:263:GLN:HG3	4:B:2044:HOH:O	2.19	0.42
1:B:362:LEU:O	1:B:362:LEU:HD12	2.20	0.42
1:B:534:LYS:HG3	1:B:539:THR:HG23	2.02	0.42
1:B:196:ARG:NH1	3:B:3001:SO4:O1	2.53	0.41
1:A:51:CYS:HB3	1:A:92:ALA:HB3	2.02	0.41
1:B:60:GLY:HA3	3:B:1719:SO4:O4	2.20	0.41
1:A:708:LEU:HA	1:A:711:TRP:CE2	2.55	0.41
1:A:67:SER:HB2	1:A:70:THR:OG1	2.20	0.41
1:B:212:PHE:CZ	1:B:237:GLN:HA	2.54	0.41
1:B:473:GLY:HA3	1:B:638:MET:SD	2.60	0.41
1:B:137:LEU:O	1:B:140:ARG:N	2.50	0.41
1:B:140:ARG:NE	1:B:200:LYS:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:359:LYS:HA	1:B:360:PRO:HD3	1.94	0.41
1:B:148:LEU:HD13	1:B:215:ALA:HB2	2.02	0.41
1:A:462:SER:HA	1:A:465:ILE:HG12	2.03	0.41
1:B:465:ILE:HG13	1:B:467:LYS:HG3	2.01	0.41
1:B:702:ALA:O	4:B:2094:HOH:O	2.22	0.41
1:A:635:GLU:CG	4:A:2115:HOH:O	2.49	0.41
1:A:299:VAL:HA	1:A:376:LEU:O	2.21	0.40
1:A:641:ARG:HD3	1:A:643:GLU:OE1	2.21	0.40
1:A:441:LEU:HD11	1:A:648:ILE:HG23	2.03	0.40
1:A:219:VAL:HG11	1:A:230:GLU:HA	2.03	0.40
1:A:118:ARG:HD2	4:A:2019:HOH:O	2.20	0.40
1:A:33:ARG:NH1	1:A:81:GLU:OE1	2.42	0.40
1:A:582:ASP:OD1	1:A:586:GLY:HA3	2.22	0.40
1:A:592:ASP:HA	1:A:593:PRO:HD3	1.86	0.40
1:B:110:TYR:HA	1:B:169:ASP:OD2	2.22	0.40
1:B:52:GLY:HA3	1:B:56:ASN:O	2.22	0.40
1:A:359:LYS:HA	1:A:360:PRO:HD3	1.99	0.40
1:B:129:LEU:HD11	1:B:255:PHE:HB2	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	723/742 (97%)	681 (94%)	40 (6%)	2 (0%)	41	61
1	B	718/742 (97%)	675 (94%)	42 (6%)	1 (0%)	51	73
All	All	1441/1484 (97%)	1356 (94%)	82 (6%)	3 (0%)	47	68

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	-1	SER
1	A	70	THR
1	B	65	GLY

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	594/609 (98%)	555 (93%)	39 (7%)	16	32
1	B	591/609 (97%)	553 (94%)	38 (6%)	17	33
All	All	1185/1218 (97%)	1108 (94%)	77 (6%)	17	33

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	24	VAL
1	A	63	ILE
1	A	69	PHE
1	A	70	THR
1	A	77	SER
1	A	125	THR
1	A	135	THR
1	A	157	LEU
1	A	165	LEU
1	A	172	VAL
1	A	188	ILE
1	A	210	SER
1	A	219	VAL
1	A	226	VAL
1	A	234	ARG
1	A	245	GLU
1	A	248	ILE
1	A	258	LEU
1	A	352	GLN
1	A	353	ASN

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Mol	Chain	Res	Type
1	A	359	LYS
1	A	362	LEU
1	A	371	LEU
1	A	390	LYS
1	A	441	LEU
1	A	449	TYR
1	A	514	LYS
1	A	521	SER
1	A	523	LEU
1	A	572	GLN
1	A	585	LEU
1	A	597	THR
1	A	609	GLU
1	A	610	GLN
1	A	641	ARG
1	A	675	LEU
1	A	676	GLU
1	A	695	ASP
1	B	0	HIS
1	B	3	GLU
1	B	63	ILE
1	B	70	THR
1	B	77	SER
1	B	125	THR
1	B	135	THR
1	B	157	LEU
1	B	165	LEU
1	B	186	LYS
1	B	188	ILE
1	B	210	SER
1	B	214	GLU
1	B	219	VAL
1	B	226	VAL
1	B	245	GLU
1	B	248	ILE
1	B	258	LEU
1	B	279	LYS
1	B	362	LEU
1	B	371	LEU
1	B	382	PHE
1	B	390	LYS
1	B	449	TYR

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Mol	Chain	Res	Type
1	B	514	LYS
1	B	521	SER
1	B	523	LEU
1	B	531	LYS
1	B	543	LEU
1	B	549	VAL
1	B	572	GLN
1	B	585	LEU
1	B	597	THR
1	B	599	LEU
1	B	610	GLN
1	B	615	LYS
1	B	641	ARG
1	B	695	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	GLN
1	A	278	ASN
1	A	352	GLN
1	A	353	ASN
1	A	572	GLN
1	B	185	GLN
1	B	242	HIS
1	B	572	GLN
1	B	606	HIS
1	B	679	GLN
1	B	718	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

7 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	A	1721	-	5,5,5	0.28	0	5,5,5	1.35	1 (20%)
3	SO4	A	1723	-	4,4,4	0.14	0	6,6,6	0.16	0
3	SO4	A	1722	-	4,4,4	0.33	0	6,6,6	0.90	0
3	SO4	B	1719	-	4,4,4	0.27	0	6,6,6	0.55	0
3	SO4	B	1720	-	4,4,4	0.12	0	6,6,6	0.26	0
3	SO4	A	3001	-	4,4,4	0.17	0	6,6,6	0.50	0
3	SO4	B	3001	-	4,4,4	0.27	0	6,6,6	0.60	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	A	1721	-	-	1/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1721	GOL	C3-C2-C1	-2.54	101.81	111.70

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1721	GOL	C1-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1721	GOL	2	0
3	B	1719	SO4	1	0
3	B	3001	SO4	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, 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	725/742 (97%)	0.09	30 (4%) 37 40	2, 26, 60, 104	0
1	B	720/742 (97%)	-0.02	35 (4%) 29 31	3, 27, 60, 104	0
All	All	1445/1484 (97%)	0.03	65 (4%) 33 36	2, 27, 60, 104	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	356	ALA	8.0
1	A	348	SER	7.6
1	B	-1	SER	5.9
1	B	356	ALA	5.8
1	A	69	PHE	4.9
1	B	355	GLN	4.6
1	B	718	HIS	4.2
1	B	5	LEU	4.1
1	B	44	THR	4.1
1	A	340	THR	3.9
1	B	609	GLU	3.8
1	A	350	ALA	3.8
1	B	357	SER	3.7
1	A	70	THR	3.6
1	A	-3	ARG	3.4
1	B	535	GLY	3.2
1	A	353	ASN	3.2
1	A	347	ALA	3.1
1	A	337	LYS	3.1
1	B	185	GLN	3.1
1	A	351	HIS	3.1
1	A	355	GLN	3.1
1	B	0	HIS	3.1
1	A	342	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	188	ILE	3.0
1	B	182	LYS	3.0
1	B	9	HIS	3.0
1	A	357	SER	2.9
1	B	178	GLU	2.9
1	A	354	GLY	2.9
1	A	359	LYS	2.8
1	B	181	ILE	2.8
1	B	8	PRO	2.8
1	B	43	HIS	2.8
1	A	331	GLN	2.8
1	A	341	PHE	2.7
1	B	6	ARG	2.7
1	A	422	ASP	2.7
1	A	358	ALA	2.7
1	A	397	ALA	2.7
1	B	449	TYR	2.7
1	A	334	ALA	2.6
1	B	4	TYR	2.6
1	A	546	GLY	2.6
1	A	338	ILE	2.6
1	B	7	LEU	2.5
1	B	358	ALA	2.5
1	B	351	HIS	2.5
1	B	11	LEU	2.5
1	B	537	GLY	2.5
1	A	352	GLN	2.4
1	A	344	GLU	2.4
1	B	207	ASN	2.4
1	B	448	ARG	2.3
1	A	360	PRO	2.3
1	B	41	SER	2.3
1	B	13	MET	2.2
1	B	337	LYS	2.1
1	A	587	ARG	2.1
1	B	64	HIS	2.1
1	A	386	ASN	2.1
1	B	601	GLN	2.1
1	A	346	GLU	2.1
1	B	359	LYS	2.1
1	B	177	VAL	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, 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(\AA^2)	Q<0.9
3	SO4	B	1720	5/5	0.84	0.21	90,90,90,91	0
3	SO4	A	1723	5/5	0.89	0.27	97,98,99,99	0
3	SO4	B	3001	5/5	0.91	0.14	61,62,63,63	0
3	SO4	B	1719	5/5	0.92	0.17	72,72,73,73	0
3	SO4	A	1722	5/5	0.94	0.12	46,47,49,50	0
2	GOL	A	1721	6/6	0.96	0.15	12,15,16,17	0
3	SO4	A	3001	5/5	0.98	0.11	19,20,23,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.