



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:26 pm GMT

PDB ID : 1U0E
Title : Crystal structure of mouse phosphoglucose isomerase
Authors : Solomons, J.T.G.; Zimmerly, E.M.; Burns, S.; Krishnamurthy, N.; Swan, M.K.;
Krings, S.; Muirhead, H.; Chirgwin, J.; Davies, C.
Deposited on : 2004-07-13
Resolution : 1.60 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

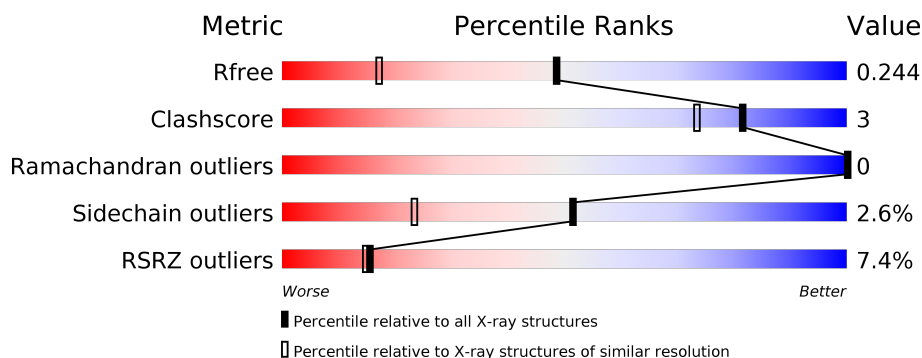
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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}	100719	2696 (1.60-1.60)
Clashscore	112137	2967 (1.60-1.60)
Ramachandran outliers	110173	2887 (1.60-1.60)
Sidechain outliers	110143	2886 (1.60-1.60)
RSRZ outliers	101464	2714 (1.60-1.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	564	<div> <div>9%</div> <div>89%</div> <div>9%</div> <div>..</div> </div>
1	B	564	<div> <div>5%</div> <div>89%</div> <div>9%</div> <div>.</div> </div>

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	SO4	A	1207	-	-	-	X
2	SO4	B	1204	-	-	-	X
2	SO4	B	1205	-	-	-	X
2	SO4	B	1208	-	-	-	X
2	SO4	B	1209	-	-	-	X
3	BME	A	1212	-	-	-	X
3	BME	A	1215	-	-	-	X
4	GOL	A	1221	-	-	-	X
4	GOL	A	1223	-	-	-	X
4	GOL	A	1227	-	-	X	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9970 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 Glucose-6-phosphate isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	0	6	0
			4419	2824	765	812	18			
1	B	556	Total	C	N	O	S	0	5	0
			4422	2826	768	810	18			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	263	LEU	PHE	SEE REMARK 999	UNP P06745
A	558	HIS	-	EXPRESSION TAG	UNP P06745
A	559	HIS	-	EXPRESSION TAG	UNP P06745
A	560	HIS	-	EXPRESSION TAG	UNP P06745
A	561	HIS	-	EXPRESSION TAG	UNP P06745
A	562	HIS	-	EXPRESSION TAG	UNP P06745
A	563	HIS	-	EXPRESSION TAG	UNP P06745
B	263	LEU	PHE	SEE REMARK 999	UNP P06745
B	558	HIS	-	EXPRESSION TAG	UNP P06745
B	559	HIS	-	EXPRESSION TAG	UNP P06745
B	560	HIS	-	EXPRESSION TAG	UNP P06745
B	561	HIS	-	EXPRESSION TAG	UNP P06745
B	562	HIS	-	EXPRESSION TAG	UNP P06745
B	563	HIS	-	EXPRESSION TAG	UNP P06745

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



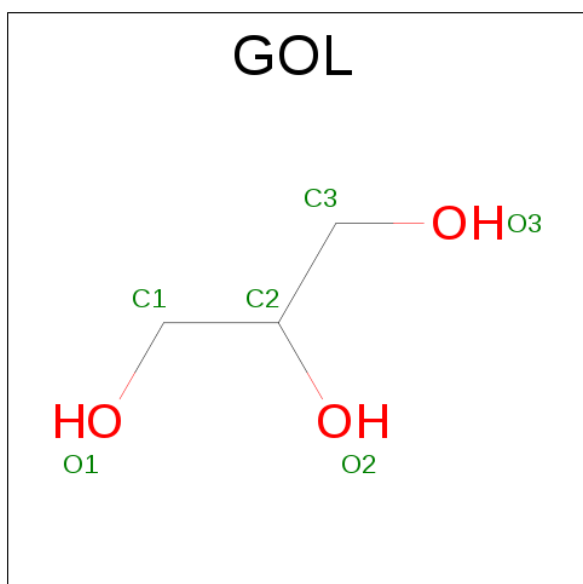
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total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

- Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

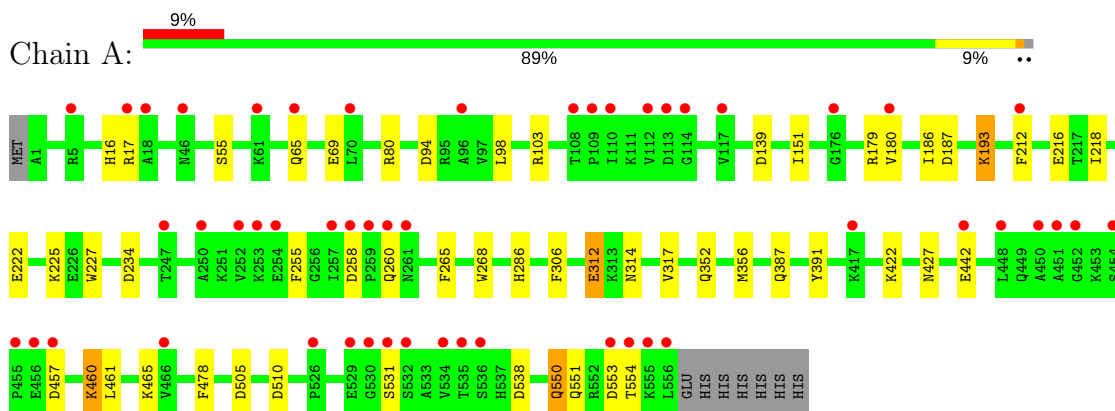
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	525	Total 525	O 525	0	0
5	B	492	Total 492	O 492	0	0

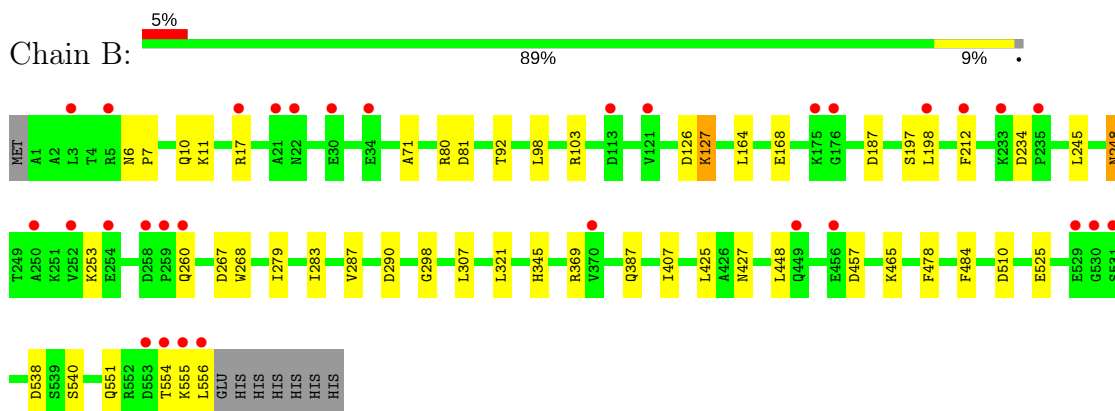
3 Residue-property plots [i](#)

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: Glucose-6-phosphate isomerase



• Molecule 1: Glucose-6-phosphate isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.20Å 116.10Å 73.10Å 90.00° 101.30° 90.00°	Depositor
Resolution (Å)	14.96 – 1.60 14.96 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.9 (14.96-1.60) 98.3 (14.96-1.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.211 , 0.246 0.212 , 0.244	Depositor DCC
R_{free} test set	7322 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	26.8	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9970	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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: GOL, SO4, BME

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	0.49	0/4558	0.69	9/6170 (0.1%)
1	B	0.46	0/4556	0.71	10/6166 (0.2%)
All	All	0.48	0/9114	0.70	19/12336 (0.2%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	290	ASP	CB-CG-OD2	8.48	125.93	118.30
1	B	457	ASP	CB-CG-OD2	6.91	124.52	118.30
1	B	187	ASP	CB-CG-OD2	6.81	124.43	118.30
1	B	267[A]	ASP	CB-CG-OD2	6.67	124.30	118.30
1	B	267[B]	ASP	CB-CG-OD2	6.67	124.30	118.30
1	A	457	ASP	CB-CG-OD2	6.61	124.25	118.30
1	B	234	ASP	CB-CG-OD2	6.46	124.11	118.30
1	A	187	ASP	CB-CG-OD2	6.25	123.92	118.30
1	B	126	ASP	CB-CG-OD2	6.21	123.89	118.30
1	A	234	ASP	CB-CG-OD2	5.88	123.59	118.30
1	B	510	ASP	CB-CG-OD2	5.69	123.42	118.30
1	A	139	ASP	CB-CG-OD2	5.50	123.25	118.30
1	B	81	ASP	CB-CG-OD2	5.36	123.12	118.30
1	A	538	ASP	CB-CG-OD2	5.36	123.12	118.30
1	A	510	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	94	ASP	CB-CG-OD2	5.27	123.04	118.30
1	A	553	ASP	CB-CG-OD2	5.24	123.02	118.30
1	A	505	ASP	CB-CG-OD2	5.17	122.95	118.30
1	B	538	ASP	CB-CG-OD2	5.14	122.93	118.30

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	4419	0	4402	31	0
1	B	4422	0	4406	21	0
2	A	20	0	0	0	0
2	B	30	0	0	0	0
3	A	20	0	30	4	0
4	A	30	0	40	7	0
4	B	12	0	16	0	0
5	A	525	0	0	6	0
5	B	492	0	0	4	0
All	All	9970	0	8894	53	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 (53) 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:65:GLN:O	1:A:69:GLU:HG2	1.76	0.86
1:A:179:ARG:HG2	4:A:1227:GOL:H11	1.62	0.80
1:A:227:TRP:HE1	3:A:1215:BME:H22	1.60	0.66
1:A:186:ILE:HB	1:A:216:GLU:HG3	1.80	0.63
1:A:225:LYS:NZ	5:A:1746:HOH:O	2.33	0.62
3:A:1213:BME:H22	1:B:551:GLN:HE22	1.65	0.61
1:B:345:HIS:HD2	5:B:1352:HOH:O	1.85	0.59
4:A:1227:GOL:H2	5:A:1581:HOH:O	2.03	0.59
1:A:460:LYS:HE3	1:B:92:THR:HA	1.85	0.58
1:B:168:GLU:OE2	1:B:345:HIS:HE1	1.88	0.57
1:A:227:TRP:HE1	3:A:1215:BME:C2	2.18	0.56
1:A:554:THR:HG21	5:A:1590:HOH:O	2.06	0.54
1:B:554:THR:HG21	5:B:1543:HOH:O	2.09	0.53
1:A:16:HIS:HD2	5:A:1586:HOH:O	1.91	0.53
1:A:179:ARG:HA	4:A:1227:GOL:H32	1.91	0.52
1:B:245:LEU:HD13	1:B:279:ILE:HA	1.91	0.52
1:A:180[B]:VAL:HG21	1:A:286:HIS:HB2	1.91	0.52
1:A:227:TRP:NE1	3:A:1215:BME:H22	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1227:GOL:H12	5:A:1608:HOH:O	2.10	0.51
1:A:550:GLN:NE2	1:A:551:GLN:OE1	2.44	0.50
1:B:80:ARG:HD2	1:B:307:LEU:HA	1.92	0.50
1:A:387:GLN:HE22	1:A:427:ASN:HB3	1.77	0.49
1:B:407:ILE:HD13	1:B:425:LEU:HD23	1.94	0.49
1:A:80:ARG:HG3	1:A:306:PHE:CE2	2.47	0.49
1:A:222:GLU:HG2	1:A:255:PHE:HE1	1.79	0.48
1:B:248:ASN:C	1:B:248:ASN:HD22	2.17	0.48
1:A:17:ARG:HG2	5:A:1586:HOH:O	2.13	0.47
1:A:151:ILE:HB	1:A:180[A]:VAL:HG12	1.97	0.47
1:A:186:ILE:HB	1:A:216:GLU:CG	2.45	0.46
1:A:193:LYS:HD2	1:A:193:LYS:HA	1.70	0.46
1:B:387:GLN:HE22	1:B:427:ASN:HB3	1.79	0.46
1:B:10:GLN:HG2	5:B:1445:HOH:O	2.15	0.46
1:B:369[B]:ARG:NH2	5:B:1604:HOH:O	2.39	0.46
1:A:352:GLN:O	1:A:356:MET:HB2	2.16	0.44
1:A:312:GLU:CD	1:A:312:GLU:H	2.21	0.44
1:A:218:ILE:O	1:A:222:GLU:HG3	2.17	0.43
1:B:98:LEU:HB2	1:B:268:TRP:CE3	2.54	0.43
1:B:71:ALA:HB2	1:B:321:LEU:HD21	2.00	0.43
1:B:6:ASN:HA	1:B:7:PRO:HD3	1.93	0.42
1:B:127:LYS:CE	1:B:260:GLN:O	2.68	0.42
1:B:298:GLY:HA3	1:B:484:PHE:O	2.20	0.42
1:A:258:ASP:OD2	1:A:260:GLN:HG2	2.20	0.42
1:B:283:ILE:O	1:B:287:VAL:HG22	2.19	0.42
1:B:448:LEU:HD21	1:B:465:LYS:HE3	2.02	0.42
1:A:422:LYS:HE3	1:B:525:GLU:HG2	2.01	0.41
1:A:387:GLN:HA	1:A:391:TYR:CD1	2.55	0.41
1:A:98:LEU:HB2	1:A:268:TRP:CE3	2.56	0.41
1:A:55:SER:OG	1:B:540:SER:HB2	2.21	0.41
1:A:314:ASN:HB3	1:A:317:VAL:HB	2.03	0.41
1:A:222:GLU:HG2	1:A:255:PHE:CE1	2.56	0.40
1:A:286:HIS:CE1	4:A:1227:GOL:H31	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	560/564 (99%)	543 (97%)	17 (3%)	0	100	100
1	B	559/564 (99%)	544 (97%)	15 (3%)	0	100	100
All	All	1119/1128 (99%)	1087 (97%)	32 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	480/482 (100%)	468 (98%)	12 (2%)	53	25
1	B	479/482 (99%)	466 (97%)	13 (3%)	50	22
All	All	959/964 (100%)	934 (97%)	25 (3%)	51	23

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	ARG
1	A	193	LYS
1	A	212	PHE
1	A	265	PHE
1	A	312	GLU
1	A	442	GLU
1	A	460	LYS
1	A	461	LEU

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Mol	Chain	Res	Type
1	A	465	LYS
1	A	478	PHE
1	A	531	SER
1	A	550	GLN
1	B	11	LYS
1	B	17	ARG
1	B	103	ARG
1	B	127	LYS
1	B	164	LEU
1	B	197	SER
1	B	198	LEU
1	B	212	PHE
1	B	248	ASN
1	B	253	LYS
1	B	478	PHE
1	B	555	LYS
1	B	556	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	16	HIS
1	A	37	ASN
1	A	38	ASN
1	A	65	GLN
1	A	82	ASN
1	A	104	ASN
1	A	260	GLN
1	A	387	GLN
1	A	449	GLN
1	A	550	GLN
1	A	551	GLN
1	B	8	GLN
1	B	16	HIS
1	B	22	ASN
1	B	65	GLN
1	B	82	ASN
1	B	248	ASN
1	B	345	HIS
1	B	387	GLN
1	B	449	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

22 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	SO4	A	1201	-	4,4,4	0.17	0	6,6,6	0.33	0
2	SO4	A	1202	-	4,4,4	0.21	0	6,6,6	0.39	0
2	SO4	A	1206	-	4,4,4	0.15	0	6,6,6	0.16	0
2	SO4	A	1207	-	4,4,4	0.18	0	6,6,6	0.23	0
3	BME	A	1211	-	3,3,3	0.25	0	2,2,2	0.33	0
3	BME	A	1212	-	3,3,3	0.21	0	2,2,2	0.36	0
3	BME	A	1213	-	3,3,3	0.35	0	2,2,2	0.30	0
3	BME	A	1214	-	3,3,3	0.23	0	2,2,2	0.40	0
3	BME	A	1215	-	3,3,3	0.23	0	2,2,2	0.12	0
4	GOL	A	1221	-	5,5,5	0.34	0	5,5,5	0.54	0
4	GOL	A	1223	-	5,5,5	0.33	0	5,5,5	0.26	0
4	GOL	A	1225	-	5,5,5	0.31	0	5,5,5	0.44	0
4	GOL	A	1226	-	5,5,5	0.36	0	5,5,5	0.44	0
4	GOL	A	1227	-	5,5,5	0.36	0	5,5,5	0.21	0
2	SO4	B	1203	-	4,4,4	0.21	0	6,6,6	0.15	0
2	SO4	B	1204	-	4,4,4	0.15	0	6,6,6	0.24	0
2	SO4	B	1205	-	4,4,4	0.16	0	6,6,6	0.11	0
2	SO4	B	1208	-	4,4,4	0.18	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	B	1209	-	4,4,4	0.18	0	6,6,6	0.23	0
2	SO4	B	1210	-	4,4,4	0.18	0	6,6,6	0.11	0
4	GOL	B	1222	-	5,5,5	0.46	0	5,5,5	0.44	0
4	GOL	B	1224	-	5,5,5	0.35	0	5,5,5	0.35	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	SO4	A	1201	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1202	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1206	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1207	-	-	0/0/0/0	0/0/0/0
3	BME	A	1211	-	-	0/1/1/1	0/0/0/0
3	BME	A	1212	-	-	0/1/1/1	0/0/0/0
3	BME	A	1213	-	-	0/1/1/1	0/0/0/0
3	BME	A	1214	-	-	0/1/1/1	0/0/0/0
3	BME	A	1215	-	-	0/1/1/1	0/0/0/0
4	GOL	A	1221	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1223	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1225	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1226	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1227	-	-	0/4/4/4	0/0/0/0
2	SO4	B	1203	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1204	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1205	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1208	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1209	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1210	-	-	0/0/0/0	0/0/0/0
4	GOL	B	1222	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1224	-	-	0/4/4/4	0/0/0/0

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.

3 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1213	BME	1	0
3	A	1215	BME	3	0
4	A	1227	GOL	7	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	556/564 (98%)	0.54	51 (9%) 10 9	14, 21, 35, 45	1 (0%)
1	B	556/564 (98%)	0.50	31 (5%) 25 24	15, 23, 33, 43	1 (0%)
All	All	1112/1128 (98%)	0.52	82 (7%) 15 15	14, 22, 34, 45	2 (0%)

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	555	LYS	8.0
1	A	451	ALA	7.2
1	A	553	ASP	5.8
1	B	556	LEU	5.5
1	B	555	LYS	5.0
1	A	554	THR	4.8
1	B	553	ASP	4.8
1	A	531	SER	4.5
1	A	556	LEU	4.5
1	B	529	GLU	4.5
1	A	456	GLU	4.5
1	A	252	VAL	4.3
1	B	21	ALA	4.2
1	B	456	GLU	4.1
1	A	529	GLU	4.0
1	B	22	ASN	4.0
1	A	114	GLY	4.0
1	A	442	GLU	4.0
1	A	108	THR	3.8
1	A	5	ARG	3.7
1	A	452	GLY	3.7
1	A	448	LEU	3.7
1	B	30	GLU	3.6
1	B	250	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	252	VAL	3.5
1	A	254	GLU	3.4
1	A	455	PRO	3.3
1	A	530	GLY	3.3
1	A	457	ASP	3.3
1	A	450	ALA	3.3
1	B	370	VAL	3.1
1	A	260	GLN	3.1
1	A	454	SER	3.0
1	A	534	VAL	3.0
1	B	254	GLU	2.9
1	A	417	LYS	2.9
1	B	449	GLN	2.9
1	A	113	ASP	2.9
1	B	176	GLY	2.9
1	A	109	PRO	2.8
1	A	258	ASP	2.8
1	B	554	THR	2.8
1	A	261	ASN	2.8
1	A	61	LYS	2.7
1	A	70	LEU	2.7
1	B	531	SER	2.6
1	B	175	LYS	2.6
1	B	260	GLN	2.6
1	A	532	SER	2.6
1	A	526	PRO	2.6
1	B	17	ARG	2.5
1	A	176	GLY	2.5
1	B	34	GLU	2.5
1	A	17	ARG	2.4
1	A	535	THR	2.4
1	A	96	ALA	2.4
1	A	259	PRO	2.3
1	A	212	PHE	2.3
1	B	235	PRO	2.3
1	A	18	ALA	2.3
1	B	212	PHE	2.3
1	A	250	ALA	2.2
1	A	46	ASN	2.2
1	B	259	PRO	2.2
1	B	121	VAL	2.2
1	B	233	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	112	VAL	2.2
1	A	536	SER	2.1
1	B	258	ASP	2.1
1	A	65	GLN	2.1
1	A	110	ILE	2.1
1	A	117	VAL	2.1
1	B	113	ASP	2.1
1	A	247	THR	2.1
1	B	3	LEU	2.1
1	A	253	LYS	2.0
1	B	530	GLY	2.0
1	A	180[A]	VAL	2.0
1	A	466	VAL	2.0
1	B	5	ARG	2.0
1	A	257	ILE	2.0
1	B	198	LEU	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	A	1207	5/5	0.74	0.41	32.89	45,46,46,46	5
2	SO4	B	1208	5/5	0.91	0.39	14.18	45,46,46,46	0
2	SO4	B	1205	5/5	0.88	0.28	10.28	47,47,48,48	0
2	SO4	B	1209	5/5	0.86	0.28	7.43	33,35,37,37	5
4	GOL	A	1227	6/6	0.62	0.32	6.05	38,40,42,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	BME	A	1212	4/4	0.69	0.20	5.28	51,52,53,57	0
3	BME	A	1215	4/4	0.67	0.21	3.81	40,42,43,48	0
2	SO4	B	1204	5/5	0.88	0.32	3.66	41,42,43,43	5
4	GOL	A	1223	6/6	0.78	0.13	3.53	44,45,45,46	0
4	GOL	A	1221	6/6	0.74	0.19	2.42	30,31,33,34	0
2	SO4	A	1201	5/5	0.95	0.17	1.91	33,34,35,35	0
4	GOL	A	1225	6/6	0.76	0.16	1.00	47,48,48,49	0
2	SO4	A	1202	5/5	0.91	0.17	0.47	37,37,39,39	0
4	GOL	B	1224	6/6	0.81	0.14	0.30	35,38,39,41	0
3	BME	A	1211	4/4	0.80	0.12	0.02	40,42,42,47	0
4	GOL	A	1226	6/6	0.85	0.11	-0.49	39,39,39,40	0
4	GOL	B	1222	6/6	0.91	0.09	-0.83	24,25,27,28	0
2	SO4	B	1210	5/5	0.89	0.44	-	45,45,45,46	5
3	BME	A	1213	4/4	0.64	0.20	-	48,48,49,52	0
3	BME	A	1214	4/4	0.78	0.30	-	47,47,48,50	0
2	SO4	B	1203	5/5	0.92	0.24	-	43,44,44,45	0
2	SO4	A	1206	5/5	0.89	0.43	-	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.