



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:05 AM UTC

PDB ID : 4QLB / pdb_00004qlb
Title : Structural Basis for the Recruitment of Glycogen Synthase by Glycogenin
Authors : Zeqiraj, E.; Judd, A.; Sicheri, F.
Deposited on : 2014-06-11
Resolution : 2.60 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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

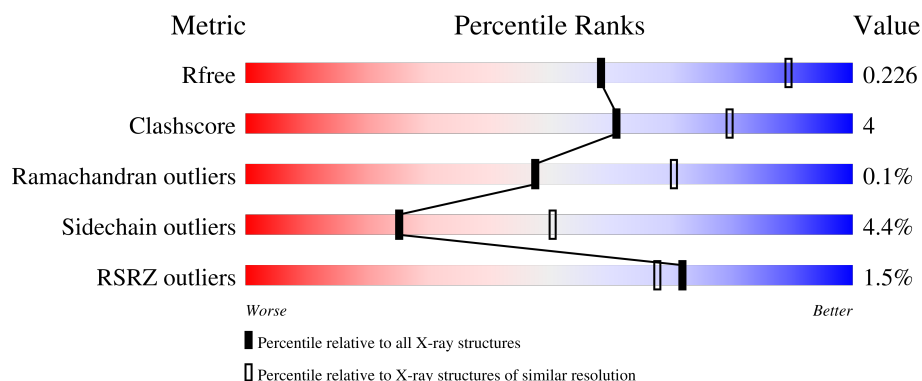
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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

Mol	Chain	Length	Quality of chain
1	A	674	% 82% 13% • •
1	B	674	2% 79% 16% • 5%
1	C	674	% 84% 11% • •
1	D	674	% 82% 13% • •
2	E	36	6% 78% 14% • 6%

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Mol	Chain	Length	Quality of chain
2	F	36	6% 78% 19%
2	G	36	92% 6%
2	H	36	3% 78% 14% 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 22070 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 Probable glycogen [starch] synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	650	Total	C	N	O	S	0	0	0
			5209	3306	912	957	34			
1	C	646	Total	C	N	O	S	2	0	0
			5191	3296	908	953	34			
1	D	651	Total	C	N	O	S	9	0	0
			5226	3319	915	959	33			
1	B	642	Total	C	N	O	S	12	1	0
			5170	3287	906	943	34			

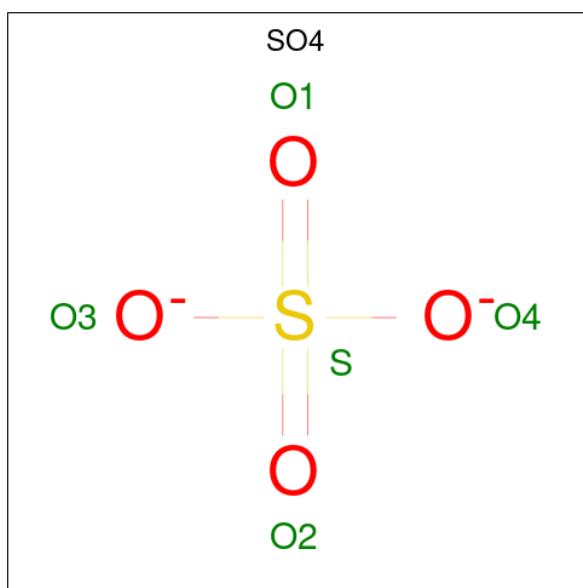
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9U2D9
A	0	ALA	-	expression tag	UNP Q9U2D9
C	-1	GLY	-	expression tag	UNP Q9U2D9
C	0	ALA	-	expression tag	UNP Q9U2D9
D	-1	GLY	-	expression tag	UNP Q9U2D9
D	0	ALA	-	expression tag	UNP Q9U2D9
B	-1	GLY	-	expression tag	UNP Q9U2D9
B	0	ALA	-	expression tag	UNP Q9U2D9

- Molecule 2 is a protein called Protein GYG-1, isoform b.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	34	Total	C	N	O	0	0	0
			273	169	52	52			
2	E	34	Total	C	N	O	0	0	0
			273	169	52	52			
2	H	33	Total	C	N	O	1	0	0
			266	164	51	51			
2	F	35	Total	C	N	O	0	0	0
			281	173	54	54			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	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 GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

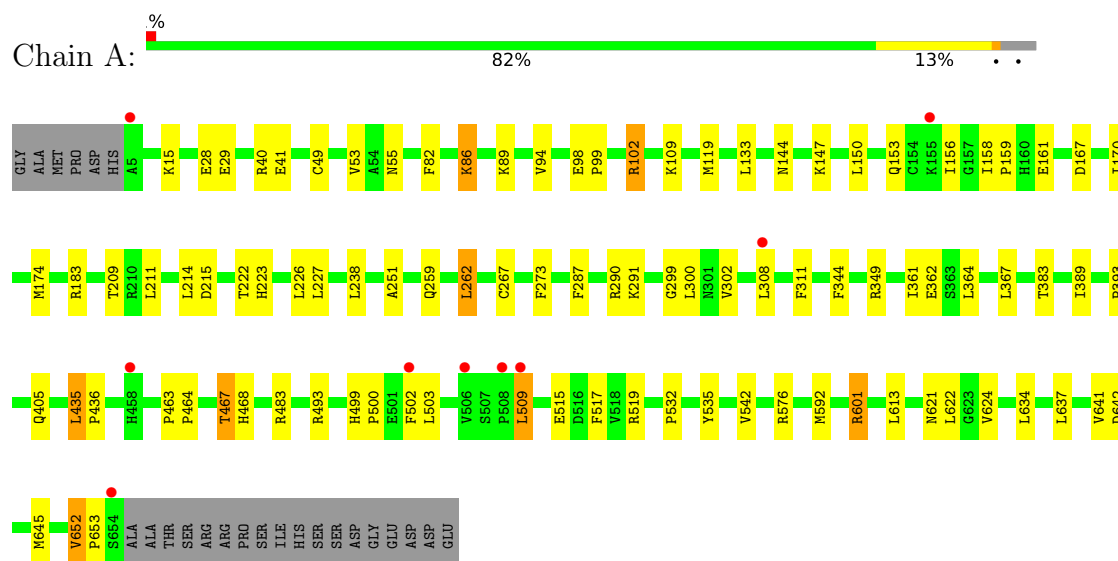
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	29	Total	O	0	0
			29	29		
5	C	34	Total	O	0	0
			34	34		
5	D	17	Total	O	0	0
			17	17		
5	B	30	Total	O	0	0
			30	30		
5	G	2	Total	O	0	0
			2	2		
5	H	1	Total	O	0	0
			1	1		

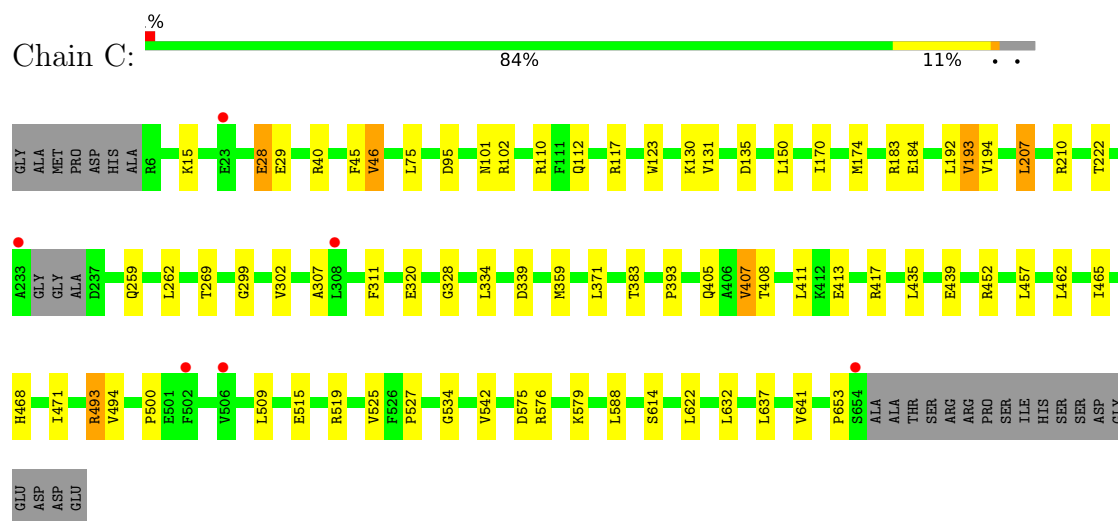
3 Residue-property plots [i](#)

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.

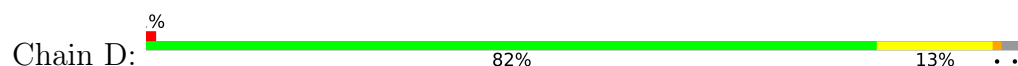
- Molecule 1: Probable glycogen [starch] synthase

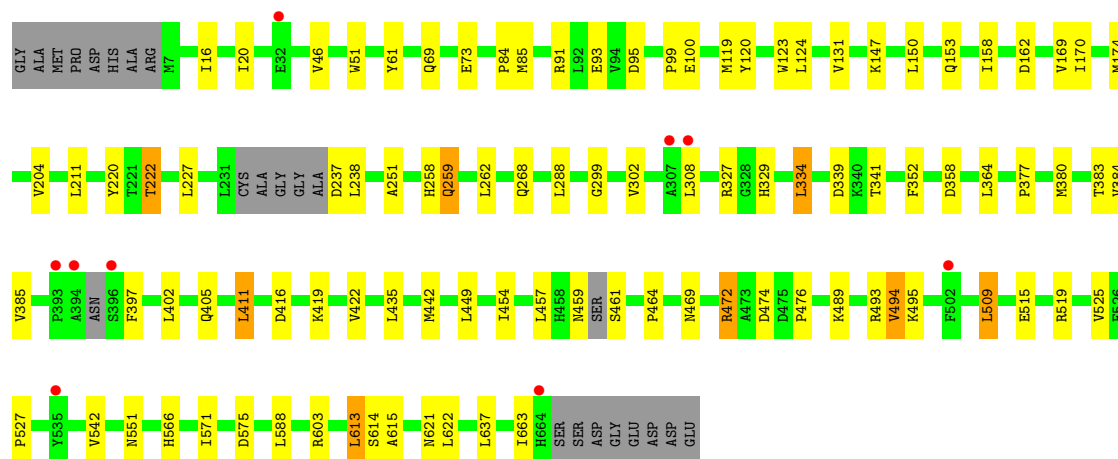


- Molecule 1: Probable glycogen [starch] synthase

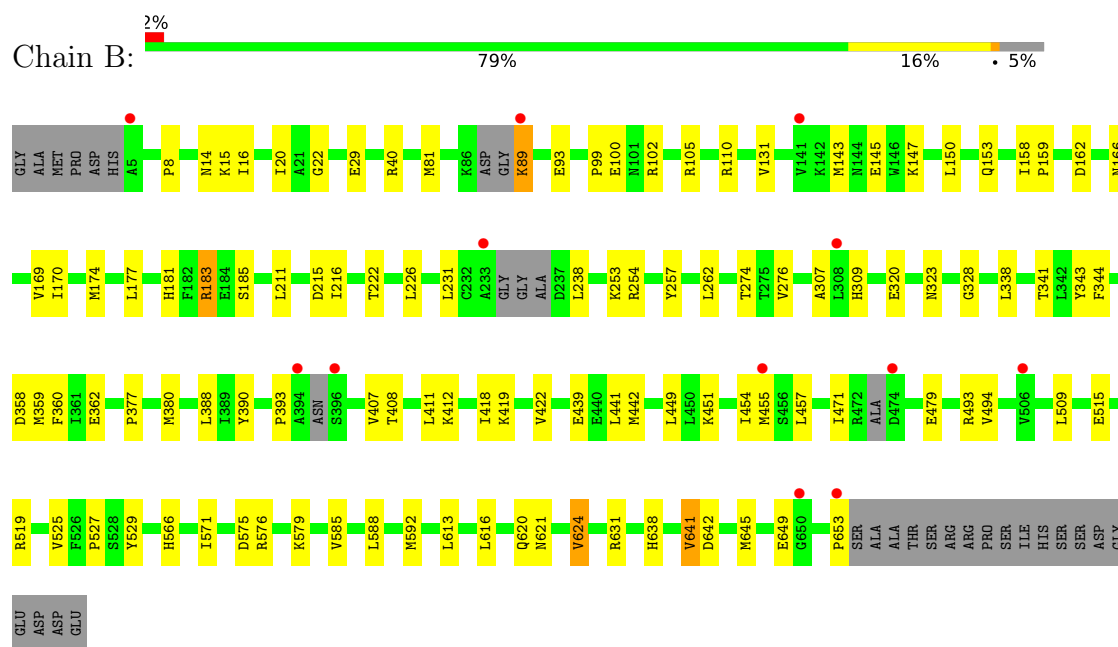


- Molecule 1: Probable glycogen [starch] synthase

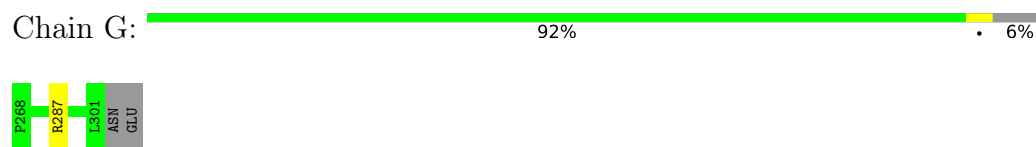




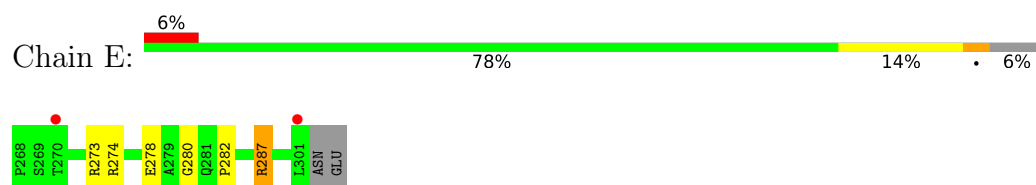
- Molecule 1: Probable glycogen [starch] synthase



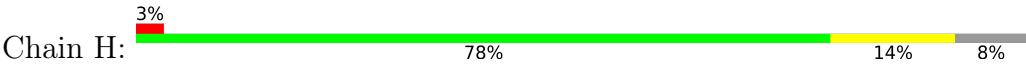
- Molecule 2: Protein GYG-1, isoform b



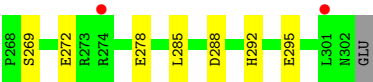
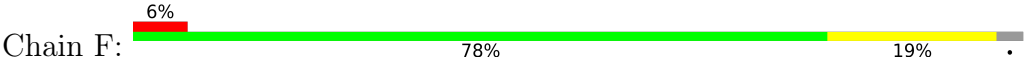
- Molecule 2: Protein GYG-1, isoform b



- Molecule 2: Protein GYG-1, isoform b



● Molecule 2: Protein GYG-1, isoform b



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	94.59Å 162.88Å 115.79Å 90.00° 95.78° 90.00°	Depositor
Resolution (Å)	49.11 – 2.60 49.11 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.11-2.60) 99.6 (49.11-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1683)	Depositor
R, R_{free}	0.179 , 0.224 0.183 , 0.226	Depositor DCC
R_{free} test set	2654 reflections (2.48%)	wwPDB-VP
Wilson B-factor (Å ²)	50.8	Xtriage
Anisotropy	0.422	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22070	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% 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	0.27	0/5332	0.69	0/7206
1	B	0.27	0/5292	0.69	0/7145
1	C	0.28	0/5313	0.69	0/7179
1	D	0.26	0/5347	0.67	0/7223
2	E	0.26	0/279	0.64	0/377
2	F	0.27	0/287	0.68	0/388
2	G	0.27	0/279	0.66	0/377
2	H	0.27	0/271	0.65	0/366
All	All	0.27	0/22400	0.69	0/30261

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 [i](#)

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	5209	0	5108	45	0
1	B	5170	0	5081	57	0
1	C	5191	0	5091	32	0
1	D	5226	0	5128	50	0
2	E	273	0	256	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	281	0	262	4	0
2	G	273	0	256	0	0
2	H	266	0	248	1	0
3	A	10	0	0	0	0
3	B	10	0	0	1	0
3	C	15	0	0	0	0
3	D	15	0	0	1	0
4	C	6	0	8	1	0
4	D	6	0	8	0	0
4	G	6	0	8	0	0
5	A	29	0	0	0	0
5	B	30	0	0	0	0
5	C	34	0	0	0	0
5	D	17	0	0	0	0
5	G	2	0	0	0	0
5	H	1	0	0	0	0
All	All	22070	0	21454	184	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 4.

All (184) 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:C:46:VAL:HG11	1:C:75:LEU:HD13	1.69	0.73
1:B:359:MET:HE3	1:B:527:PRO:HB2	1.71	0.72
1:C:101:ASN:OD1	1:C:130:LYS:NZ	2.24	0.70
1:B:575:ASP:HB3	1:B:579:LYS:HE2	1.75	0.68
1:D:170:ILE:HG22	1:D:174:MET:HE2	1.76	0.68
1:C:407:VAL:HG13	1:C:457:LEU:HD23	1.74	0.68
2:E:273:ARG:HH22	2:E:287:ARG:HB2	1.57	0.68
1:A:147:LYS:HE2	1:A:158:ILE:HB	1.75	0.68
1:B:525:VAL:HG21	1:B:592:MET:HE3	1.77	0.67
1:B:170:ILE:HG22	1:B:174:MET:HE2	1.79	0.65
1:B:359:MET:HG3	1:B:585:VAL:HG22	1.80	0.64
1:A:86:LYS:NZ	1:A:167:ASP:OD2	2.31	0.63
1:C:170:ILE:HG22	1:C:174:MET:HE2	1.80	0.63
1:A:170:ILE:HG22	1:A:174:MET:HE2	1.79	0.63
1:B:110:ARG:NH1	1:B:185:SER:OG	2.32	0.63
1:A:41:GLU:HA	1:A:652:VAL:HG11	1.82	0.62
1:B:89:LYS:NZ	1:B:93:GLU:OE2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:MET:HG2	1:B:147:LYS:HE3	1.81	0.61
1:B:20:ILE:HD12	1:B:613:LEU:HA	1.82	0.61
1:B:159:PRO:HA	2:F:278:GLU:HA	1.83	0.60
1:A:227:LEU:HD21	1:A:251:ALA:HB2	1.83	0.59
1:B:360:PHE:HE1	1:B:592:MET:HE1	1.68	0.59
1:D:341:THR:HG22	1:D:383:THR:HB	1.85	0.58
1:C:210:ARG:NH1	1:C:269:THR:O	2.37	0.58
1:D:227:LEU:HD21	1:D:251:ALA:HB2	1.86	0.58
1:B:183:ARG:HD3	1:B:215:ASP:HB3	1.84	0.58
1:D:566:HIS:HB2	1:D:571:ILE:HB	1.87	0.57
1:D:147:LYS:HE2	1:D:158:ILE:HB	1.85	0.57
1:A:435:LEU:HD22	1:A:436:PRO:HD2	1.86	0.57
1:A:144:ASN:OD1	2:E:274:ARG:NH2	2.36	0.56
1:D:405:GLN:HG3	1:D:509:LEU:HA	1.88	0.55
1:C:575:ASP:HB3	1:C:579:LYS:HE2	1.86	0.55
1:B:525:VAL:HG12	1:B:527:PRO:HD3	1.88	0.55
1:D:85:MET:HE2	1:D:119:MET:HG2	1.89	0.55
1:D:329:HIS:CE1	1:D:464:PRO:HG2	2.42	0.55
2:F:269:SER:HB3	2:F:272:GLU:HG3	1.89	0.55
1:B:153:GLN:HB3	1:B:211:LEU:HD13	1.89	0.54
1:A:634:LEU:HB3	1:A:641:VAL:HG11	1.89	0.54
1:B:393:PRO:HB2	1:B:471:ILE:HD12	1.88	0.54
1:A:15:LYS:HE3	1:A:29:GLU:HB3	1.91	0.53
1:A:153:GLN:HB3	1:A:211:LEU:HD13	1.90	0.53
1:A:383:THR:OG1	1:A:493:ARG:NH1	2.42	0.53
1:D:422:VAL:HG11	1:B:422:VAL:HG11	1.90	0.53
1:D:615:ALA:O	1:D:621:ASN:ND2	2.42	0.53
1:C:299:GLY:HA2	1:C:622:LEU:HD12	1.91	0.53
1:C:40:ARG:NH1	1:C:653:PRO:O	2.28	0.53
1:C:123:TRP:HB2	1:C:131:VAL:HG21	1.91	0.53
1:A:468:HIS:HB2	1:A:500:PRO:HG2	1.89	0.52
1:D:454:ILE:HA	1:D:457:LEU:HD12	1.91	0.52
1:A:222:THR:HG23	1:A:273:PHE:HE1	1.74	0.52
1:B:177:LEU:O	1:B:181:HIS:ND1	2.34	0.52
1:D:20:ILE:HD12	1:D:613:LEU:HA	1.91	0.52
1:A:362:GLU:OE1	1:A:483:ARG:NH1	2.44	0.51
1:B:81:MET:HB2	1:B:131:VAL:HG12	1.91	0.51
1:B:102:ARG:HH22	1:B:653:PRO:HB2	1.75	0.51
1:B:102:ARG:NH2	1:B:653:PRO:HB2	2.26	0.51
1:B:183:ARG:NH1	1:B:215:ASP:OD2	2.41	0.51
1:B:529:TYR:HB2	1:B:576:ARG:NH2	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:638:HIS:O	1:B:641:VAL:HG22	2.11	0.51
1:A:209:THR:HG23	1:A:214:LEU:HD12	1.93	0.50
1:C:525:VAL:HG12	1:C:527:PRO:HD3	1.94	0.50
1:B:418:ILE:HG21	1:B:442:MET:HE3	1.93	0.50
1:D:551:ASN:ND2	1:D:575:ASP:OD1	2.42	0.50
1:B:145:GLU:OE1	1:B:145:GLU:N	2.43	0.50
1:B:323:ASN:OD1	1:B:343:TYR:OH	2.19	0.50
1:D:459:ASN:O	1:D:461:SER:N	2.44	0.49
1:C:383:THR:OG1	1:C:493:ARG:NH1	2.43	0.49
1:A:94:VAL:HG21	1:A:133:LEU:HD11	1.94	0.49
1:A:159:PRO:HA	2:E:278:GLU:HA	1.94	0.49
1:D:416:ASP:N	1:D:416:ASP:OD1	2.40	0.49
1:B:621:ASN:O	1:B:624:VAL:HG22	2.12	0.49
1:C:393:PRO:HB2	1:C:471:ILE:HD12	1.95	0.49
1:B:344:PHE:CD2	1:B:592:MET:HE2	2.48	0.49
1:B:344:PHE:HD2	1:B:592:MET:HE2	1.78	0.49
1:B:454:ILE:HA	1:B:457:LEU:HD12	1.95	0.49
1:C:328:GLY:HA2	1:C:408:THR:HG21	1.94	0.48
1:D:411:LEU:HG	1:D:457:LEU:HD11	1.95	0.48
1:D:515:GLU:O	1:D:519:ARG:HG3	2.14	0.48
1:B:162:ASP:O	1:B:166:ASN:ND2	2.47	0.48
1:C:371:LEU:HB3	1:C:493:ARG:HG2	1.95	0.48
1:B:566:HIS:HB2	1:B:571:ILE:HB	1.96	0.48
1:C:302:VAL:HG13	1:C:542:VAL:HG13	1.96	0.48
1:A:515:GLU:O	1:A:519:ARG:HG3	2.14	0.48
1:A:642:ASP:HA	1:A:645:MET:HE2	1.96	0.47
1:A:405:GLN:HG3	1:A:509:LEU:HA	1.95	0.47
1:B:631[B]:ARG:NH2	1:B:642:ASP:OD1	2.48	0.47
1:D:268:GLN:NE2	1:D:288:LEU:O	2.47	0.47
1:D:364:LEU:HD22	1:D:494:VAL:HG21	1.96	0.47
1:D:397:PHE:O	1:D:469:ASN:ND2	2.47	0.47
1:D:95:ASP:HB2	1:D:124:LEU:HD21	1.97	0.47
1:B:328:GLY:HA2	1:B:408:THR:HG21	1.97	0.47
1:C:112:GLN:HG2	1:C:117:ARG:HA	1.96	0.47
1:B:362:GLU:HG3	1:B:585:VAL:HG11	1.96	0.46
1:C:95:ASP:OD2	1:B:451:LYS:NZ	2.34	0.46
1:B:407:VAL:HG12	1:B:457:LEU:HD23	1.98	0.46
1:D:384:VAL:O	1:D:495:LYS:N	2.48	0.46
1:A:601:ARG:HB3	1:B:22:GLY:HA3	1.96	0.46
1:C:515:GLU:O	1:C:519:ARG:HG3	2.14	0.46
1:D:327:ARG:HA	1:D:334:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:ILE:HG21	1:A:262:LEU:HD13	1.97	0.46
1:D:299:GLY:HA2	1:D:622:LEU:HD12	1.98	0.45
1:D:416:ASP:HA	1:D:419:LYS:HE3	1.96	0.45
1:B:158:ILE:HG13	1:B:169:VAL:HG21	1.98	0.45
1:B:253:LYS:HG3	1:B:254:ARG:HG3	1.98	0.45
1:D:419:LYS:HG2	1:B:419:LYS:HG2	1.99	0.45
1:D:302:VAL:HG13	1:D:542:VAL:HG13	1.98	0.45
1:D:459:ASN:OD1	1:D:461:SER:N	2.49	0.45
1:A:223:HIS:O	1:A:532:PRO:HB3	2.16	0.45
1:B:642:ASP:HA	1:B:645:MET:HE3	1.99	0.45
1:D:603:ARG:HD2	3:D:702:SO4:O2	2.17	0.45
1:D:153:GLN:HB3	1:D:211:LEU:HD13	1.99	0.45
1:D:385:VAL:HG22	1:D:495:LYS:HB2	1.98	0.44
1:A:238:LEU:HD11	1:A:287:PHE:HZ	1.81	0.44
1:A:267:CYS:O	1:A:290:ARG:NH1	2.49	0.44
1:A:302:VAL:HG13	1:A:542:VAL:HG13	1.99	0.44
1:A:621:ASN:O	1:A:624:VAL:HG23	2.17	0.44
1:A:367:LEU:HD22	1:A:592:MET:HE2	1.99	0.44
1:B:40:ARG:NH2	1:B:653:PRO:O	2.48	0.44
1:D:237:ASP:OD1	1:D:238:LEU:N	2.51	0.44
2:H:292:HIS:HA	2:H:295:GLU:HG2	2.00	0.44
1:A:463:PRO:HA	1:A:464:PRO:HD3	1.90	0.43
1:B:16:ILE:O	1:B:20:ILE:HG12	2.18	0.43
1:D:442:MET:HE2	1:B:441:LEU:HD11	2.00	0.43
1:D:99:PRO:HA	1:D:120:TYR:CE1	2.54	0.43
1:D:220:TYR:CE2	1:D:222:THR:HG23	2.53	0.43
1:D:377:PRO:HA	1:D:380:MET:HE2	1.99	0.43
1:B:358:ASP:OD1	1:B:359:MET:N	2.50	0.43
1:A:183:ARG:HE	1:A:215:ASP:HB3	1.84	0.43
1:C:45:PHE:HB2	1:C:193:VAL:HB	2.01	0.43
1:D:525:VAL:HG12	1:D:527:PRO:HD3	2.00	0.43
1:B:338:LEU:HA	1:B:341:THR:HG22	2.00	0.43
1:A:344:PHE:HD2	1:A:592:MET:HE3	1.83	0.43
1:A:40:ARG:NH2	1:A:653:PRO:O	2.46	0.42
1:D:162:ASP:OD2	1:D:258:HIS:NE2	2.45	0.42
1:A:467:THR:HG21	1:A:499:HIS:CD2	2.54	0.42
1:C:28:GLU:H	1:C:28:GLU:HG2	1.53	0.42
1:D:169:VAL:HA	1:D:204:VAL:HG11	2.01	0.42
1:D:352:PHE:CD2	1:D:476:PRO:HB2	2.53	0.42
1:D:472:ARG:HB3	1:D:474:ASP:OD1	2.19	0.42
1:B:257:TYR:OH	2:F:288:ASP:O	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:MET:HE3	1:A:119:MET:HB2	1.93	0.42
1:D:358:ASP:OD1	1:D:358:ASP:N	2.53	0.42
1:B:388:LEU:HD12	1:B:390:TYR:HE2	1.83	0.42
1:D:61:TYR:OH	1:D:93:GLU:OE1	2.20	0.42
1:D:489:LYS:O	1:D:495:LYS:NZ	2.53	0.42
1:B:8:PRO:O	1:B:624:VAL:HG11	2.19	0.42
1:C:405:GLN:HG3	1:C:509:LEU:HA	2.02	0.42
1:D:51:TRP:CE3	1:D:84:PRO:HG3	2.55	0.42
1:B:515:GLU:O	1:B:519:ARG:HG3	2.18	0.42
1:C:15:LYS:HE3	1:C:29:GLU:HB3	2.02	0.42
1:C:110:ARG:NH1	1:C:184:GLU:OE1	2.42	0.42
1:D:69:GLN:O	1:D:73:GLU:HB2	2.20	0.42
1:B:99:PRO:HG2	1:B:105:ARG:HG2	2.01	0.42
1:B:377:PRO:HA	1:B:380:MET:HE2	2.01	0.42
1:A:389:ILE:HD11	1:A:517:PHE:CE2	2.55	0.41
1:B:15:LYS:HE3	1:B:29:GLU:HB3	2.02	0.41
1:A:55:ASN:OD1	1:A:89:LYS:HD2	2.19	0.41
2:F:292:HIS:HA	2:F:295:GLU:HG2	2.02	0.41
1:A:98:GLU:HA	1:A:99:PRO:HD3	1.92	0.41
1:A:102:ARG:CD	1:A:102:ARG:H	2.33	0.41
1:D:16:ILE:O	1:D:20:ILE:HG12	2.20	0.41
1:D:123:TRP:HB2	1:D:131:VAL:HG21	2.01	0.41
1:A:49:CYS:HB2	1:A:82:PHE:HB2	2.03	0.41
1:C:307:ALA:O	1:C:311:PHE:HB3	2.21	0.41
1:A:349:ARG:H	1:A:349:ARG:HG3	1.49	0.41
1:C:117:ARG:HG3	1:C:135:ASP:HB3	2.02	0.41
1:A:28:GLU:OE1	1:A:28:GLU:N	2.52	0.41
1:C:468:HIS:CD2	1:C:500:PRO:HD2	2.56	0.41
1:A:299:GLY:HA2	1:A:622:LEU:HD12	2.02	0.41
1:C:192:LEU:HD13	1:C:641:VAL:HG23	2.02	0.41
1:B:307:ALA:O	1:B:309:HIS:N	2.54	0.41
2:E:280:GLY:C	2:E:282:PRO:HD3	2.46	0.41
1:A:361:ILE:HA	1:A:364:LEU:HD12	2.03	0.40
1:C:465:ILE:H	1:C:465:ILE:HG13	1.67	0.40
1:C:534:GLY:HA2	4:C:704:GOL:H11	2.04	0.40
1:B:14:ASN:ND2	3:B:701:SO4:O4	2.50	0.40
1:A:262:LEU:HA	1:A:262:LEU:HD12	1.85	0.40
1:B:231:LEU:HB3	1:B:238:LEU:HD13	2.03	0.40
1:A:291:LYS:HE3	1:A:291:LYS:HB2	1.90	0.40
1:C:207:LEU:HD12	1:C:207:LEU:HA	1.92	0.40
1:C:359:MET:HE2	1:C:527:PRO:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:542:VAL:HA	1:C:614:SER:CB	2.52	0.40
1:D:259:GLN:HE21	1:D:259:GLN:HB3	1.50	0.40
1:D:542:VAL:HA	1:D:614:SER:HB3	2.02	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	648/674 (96%)	624 (96%)	23 (4%)	1 (0%)	43	66
1	B	633/674 (94%)	610 (96%)	22 (4%)	1 (0%)	43	66
1	C	642/674 (95%)	622 (97%)	20 (3%)	0	100	100
1	D	643/674 (95%)	619 (96%)	24 (4%)	0	100	100
2	E	32/36 (89%)	32 (100%)	0	0	100	100
2	F	33/36 (92%)	33 (100%)	0	0	100	100
2	G	32/36 (89%)	32 (100%)	0	0	100	100
2	H	31/36 (86%)	30 (97%)	1 (3%)	0	100	100
All	All	2694/2840 (95%)	2602 (97%)	90 (3%)	2 (0%)	48	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	509	LEU
1	A	393	PRO

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	562/581 (97%)	539 (96%)	23 (4%)	27	54
1	B	559/581 (96%)	534 (96%)	25 (4%)	24	50
1	C	562/581 (97%)	534 (95%)	28 (5%)	22	46
1	D	565/581 (97%)	543 (96%)	22 (4%)	28	55
2	E	26/28 (93%)	25 (96%)	1 (4%)	29	56
2	F	27/28 (96%)	26 (96%)	1 (4%)	30	57
2	G	26/28 (93%)	25 (96%)	1 (4%)	29	56
2	H	25/28 (89%)	22 (88%)	3 (12%)	5	10
All	All	2352/2436 (97%)	2248 (96%)	104 (4%)	25	50

All (104) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	VAL
1	A	86	LYS
1	A	102	ARG
1	A	109	LYS
1	A	150	LEU
1	A	161	GLU
1	A	226	LEU
1	A	259	GLN
1	A	262	LEU
1	A	300	LEU
1	A	308	LEU
1	A	311	PHE
1	A	435	LEU
1	A	467	THR
1	A	502	PHE
1	A	503	LEU
1	A	509	LEU
1	A	535	TYR
1	A	576	ARG

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Mol	Chain	Res	Type
1	A	601	ARG
1	A	613	LEU
1	A	637	LEU
1	A	652	VAL
1	C	28	GLU
1	C	46	VAL
1	C	102	ARG
1	C	150	LEU
1	C	183	ARG
1	C	193	VAL
1	C	194	VAL
1	C	207	LEU
1	C	222	THR
1	C	259	GLN
1	C	262	LEU
1	C	320	GLU
1	C	334	LEU
1	C	339	ASP
1	C	407	VAL
1	C	411	LEU
1	C	413	GLU
1	C	417	ARG
1	C	435	LEU
1	C	439	GLU
1	C	452	ARG
1	C	462	LEU
1	C	493	ARG
1	C	494	VAL
1	C	576	ARG
1	C	588	LEU
1	C	632	LEU
1	C	637	LEU
1	D	46	VAL
1	D	91	ARG
1	D	100	GLU
1	D	150	LEU
1	D	222	THR
1	D	259	GLN
1	D	262	LEU
1	D	308	LEU
1	D	334	LEU
1	D	339	ASP

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Mol	Chain	Res	Type
1	D	402	LEU
1	D	411	LEU
1	D	435	LEU
1	D	449	LEU
1	D	472	ARG
1	D	493	ARG
1	D	494	VAL
1	D	509	LEU
1	D	588	LEU
1	D	613	LEU
1	D	637	LEU
1	D	663	ILE
1	B	89	LYS
1	B	100	GLU
1	B	150	LEU
1	B	183	ARG
1	B	216	ILE
1	B	222	THR
1	B	226	LEU
1	B	262	LEU
1	B	274	THR
1	B	276	VAL
1	B	320	GLU
1	B	411	LEU
1	B	412	LYS
1	B	439	GLU
1	B	449	LEU
1	B	455	MET
1	B	479	GLU
1	B	493	ARG
1	B	494	VAL
1	B	588	LEU
1	B	616	LEU
1	B	620	GLN
1	B	624	VAL
1	B	641	VAL
1	B	649	GLU
2	G	287	ARG
2	E	287	ARG
2	H	270	THR
2	H	271	GLU
2	H	274	ARG

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Mol	Chain	Res	Type
2	F	285	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	HIS
1	A	268	GLN
1	A	301	ASN
1	A	578	HIS
1	A	598	GLN
1	A	620	GLN
1	C	424	GLN
1	C	468	HIS
1	C	499	HIS
1	D	434	HIS
1	B	301	ASN
1	B	405	GLN
1	B	432	GLN
1	B	469	ASN
1	B	620	GLN
1	B	621	ASN
2	F	302	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

13 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	$\# Z > 2$
3	SO4	C	701	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	D	701	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	A	701	-	4,4,4	0.23	0	6,6,6	0.07	0
4	GOL	D	704	-	5,5,5	0.38	0	5,5,5	0.28	0
3	SO4	D	703	-	4,4,4	0.24	0	6,6,6	0.11	0
3	SO4	A	702	-	4,4,4	0.23	0	6,6,6	0.10	0
3	SO4	D	702	-	4,4,4	0.22	0	6,6,6	0.09	0
4	GOL	C	704	-	5,5,5	0.38	0	5,5,5	0.26	0
4	GOL	G	401	-	5,5,5	0.38	0	5,5,5	0.35	0
3	SO4	C	703	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	C	702	-	4,4,4	0.22	0	6,6,6	0.06	0
3	SO4	B	701	-	4,4,4	0.25	0	6,6,6	0.08	0
3	SO4	B	702	-	4,4,4	0.24	0	6,6,6	0.09	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
4	GOL	C	704	-	-	2/4/4/4	-
4	GOL	D	704	-	-	2/4/4/4	-
4	GOL	G	401	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	704	GOL	O1-C1-C2-C3
4	D	704	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
4	G	401	GOL	O1-C1-C2-C3
4	C	704	GOL	O1-C1-C2-O2
4	D	704	GOL	O1-C1-C2-O2
4	G	401	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	702	SO4	1	0
4	C	704	GOL	1	0
3	B	701	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	650/674 (96%)	-0.18	9 (1%) 73 69	29, 53, 86, 123	0
1	B	642/674 (95%)	-0.15	12 (1%) 66 61	25, 58, 89, 117	4 (0%)
1	C	646/674 (95%)	-0.35	6 (0%) 81 78	31, 48, 80, 116	2 (0%)
1	D	651/674 (96%)	-0.12	9 (1%) 73 69	31, 59, 90, 111	9 (1%)
2	E	34/36 (94%)	0.49	2 (5%) 28 23	59, 84, 125, 134	0
2	F	35/36 (97%)	0.78	2 (5%) 29 24	69, 84, 113, 129	0
2	G	34/36 (94%)	-0.35	0 100 100	38, 50, 76, 82	0
2	H	33/36 (91%)	0.44	1 (3%) 52 47	70, 88, 103, 108	1 (3%)
All	All	2725/2840 (95%)	-0.17	41 (1%) 72 68	25, 55, 90, 134	16 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	502	PHE	4.6
1	A	506	VAL	3.7
1	A	502	PHE	3.7
1	C	233	ALA	3.7
1	B	233	ALA	3.6
1	C	308	LEU	3.5
1	D	394	ALA	3.4
1	D	308	LEU	3.2
1	B	396	SER	3.1
1	B	653	PRO	3.0
1	A	5	ALA	3.0
1	D	664	HIS	2.9
2	F	301	LEU	2.8
1	C	654	SER	2.7
1	A	308	LEU	2.7
1	B	394	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	307	ALA	2.6
1	B	5	ALA	2.5
2	E	270	THR	2.4
1	B	474	ASP	2.4
1	A	508	PRO	2.4
1	B	506	VAL	2.4
1	B	650	GLY	2.4
1	B	89	LYS	2.3
1	D	393	PRO	2.3
1	B	308	LEU	2.3
2	F	274	ARG	2.3
2	H	269	SER	2.3
1	C	506	VAL	2.2
2	E	301	LEU	2.2
1	A	155	LYS	2.2
1	A	654	SER	2.2
1	C	502	PHE	2.2
1	D	32	GLU	2.1
1	B	455	MET	2.1
1	B	141	VAL	2.1
1	D	396	SER	2.1
1	A	458	HIS	2.0
1	D	535	TYR	2.0
1	C	23	GLU	2.0
1	A	509	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	C	703	5/5	0.75	0.11	116,116,118,120	0
4	GOL	C	704	6/6	0.82	0.19	71,76,80,82	0
4	GOL	D	704	6/6	0.82	0.20	84,87,90,93	0
3	SO4	D	701	5/5	0.84	0.10	93,101,105,105	0
3	SO4	C	701	5/5	0.88	0.11	88,92,93,94	0
3	SO4	A	701	5/5	0.89	0.09	87,89,90,92	0
3	SO4	D	703	5/5	0.93	0.07	66,67,68,70	0
4	GOL	G	401	6/6	0.93	0.09	52,57,58,59	0
3	SO4	B	701	5/5	0.95	0.09	54,55,66,69	0
3	SO4	D	702	5/5	0.98	0.05	43,46,47,52	0
3	SO4	C	702	5/5	0.99	0.04	34,44,45,52	0
3	SO4	A	702	5/5	0.99	0.04	35,36,39,45	0
3	SO4	B	702	5/5	0.99	0.04	35,42,43,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.