



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 10, 2022 – 02:28 PM EST

PDB ID : 6XMM
Title : Human aldolase A I98S
Authors : Meneely, K.M.; Brewer, K.; Lamb, A.L.
Deposited on : 2020-06-30
Resolution : 2.11 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 : 2.25
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) : 2.25

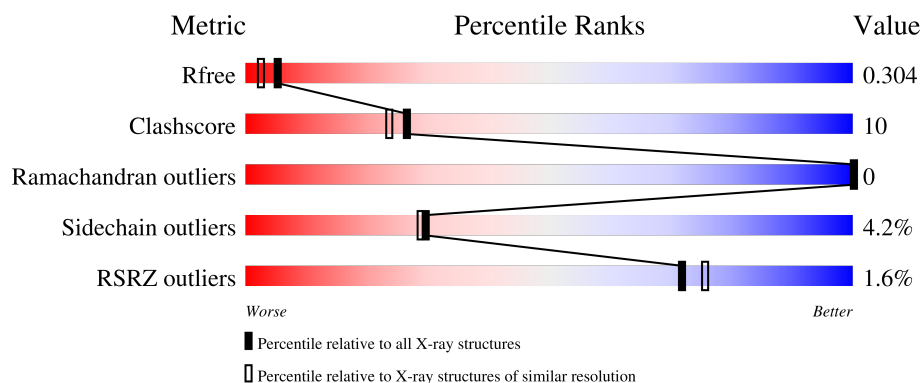
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.11 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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	364	<div> <div>%</div> <div> <div></div> <div>70%</div> <div>26%</div> <div>..</div> </div> </div>
1	B	364	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>21%</div> <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
3	GOL	B	403	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10939 atoms, of which 5462 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.

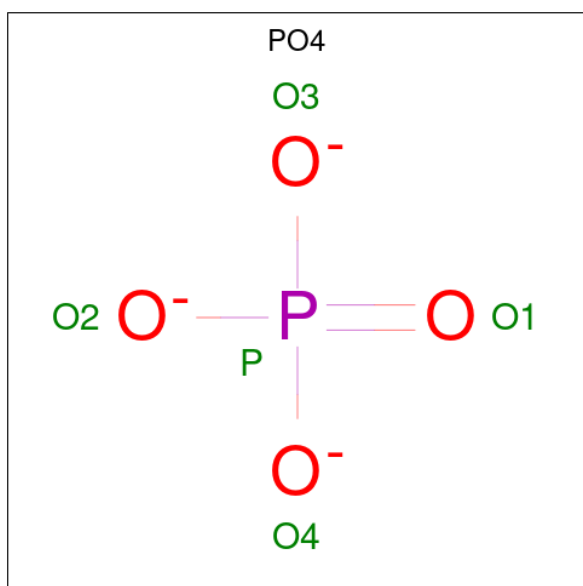
- Molecule 1 is a protein called Fructose-bisphosphate aldolase A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	353	Total	C	H	N	O	S	0	0	0
			5386	1687	2707	471	510	11			
1	B	353	Total	C	H	N	O	S	0	0	0
			5387	1687	2707	471	511	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	98	SER	ILE	engineered mutation	UNP P04075
B	98	SER	ILE	engineered mutation	UNP P04075

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

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

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		

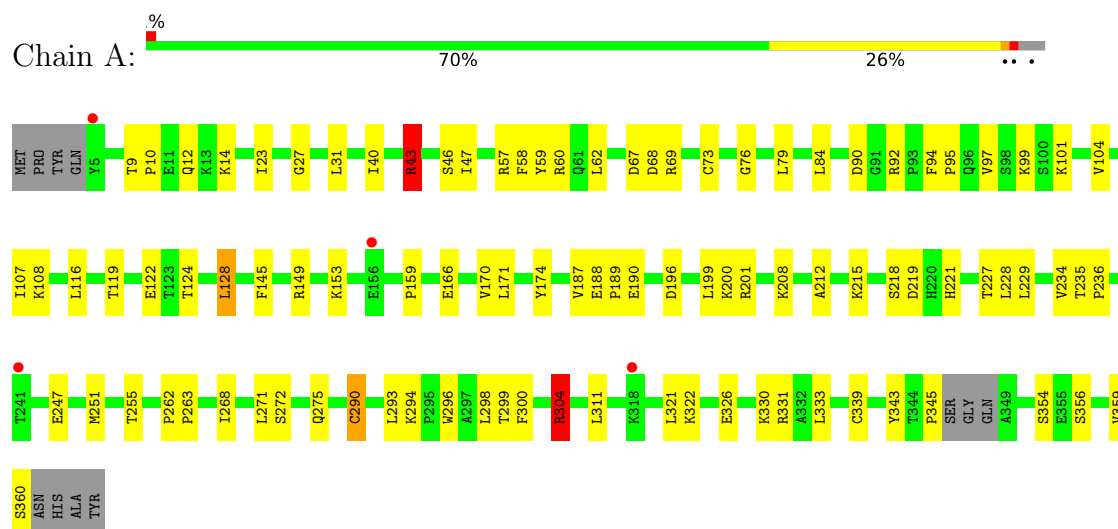
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total 32	O 32	0	0
4	B	30	Total 30	O 30	0	0

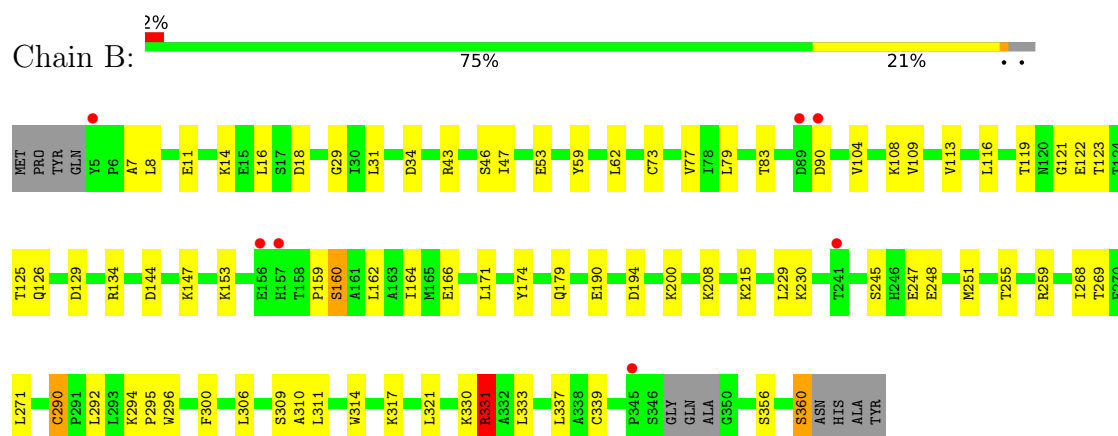
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Fructose-bisphosphate aldolase A



• Molecule 1: Fructose-bisphosphate aldolase A



4 Data and refinement statistics

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, α , β , γ	162.21Å 162.21Å 167.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.06 – 2.11 46.06 – 2.11	Depositor EDS
% Data completeness (in resolution range)	52.2 (46.06-2.11) 52.3 (46.06-2.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 2.10Å)	Xtriage
Refinement program	REFMAC, PHENIX 1.16_3549	Depositor
R, R_{free}	0.234 , 0.295 0.249 , 0.304	Depositor DCC
R_{free} test set	1923 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 29.4	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	0.94	EDS
Total number of atoms	10939	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.57 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4975e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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, PO4

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	0.79	4/2728 (0.1%)	0.93	6/3695 (0.2%)
1	B	0.84	6/2729 (0.2%)	0.92	7/3696 (0.2%)
All	All	0.82	10/5457 (0.2%)	0.93	13/7391 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	290	CYS	CB-SG	12.46	2.03	1.82
1	B	247	GLU	CG-CD	9.33	1.66	1.51
1	B	339	CYS	CB-SG	-7.28	1.69	1.82
1	B	247	GLU	CB-CG	7.23	1.65	1.52
1	A	304	ARG	CZ-NH2	-5.75	1.25	1.33
1	A	304	ARG	CG-CD	5.65	1.66	1.51
1	B	11	GLU	CG-CD	5.48	1.60	1.51
1	B	53	GLU	CB-CG	5.47	1.62	1.52
1	A	166	GLU	CB-CG	5.18	1.62	1.52
1	A	247	GLU	CG-CD	5.13	1.59	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	304	ARG	NE-CZ-NH2	-10.54	115.03	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	360	SER	N-CA-C	7.50	131.24	111.00
1	A	43	ARG	NE-CZ-NH1	-7.37	116.61	120.30
1	A	271	LEU	CB-CG-CD1	7.37	123.53	111.00
1	B	337	LEU	CB-CG-CD1	-6.86	99.33	111.00
1	B	339	CYS	CA-CB-SG	6.79	126.22	114.00
1	A	128	LEU	CB-CG-CD1	-6.39	100.14	111.00
1	B	290	CYS	CA-CB-SG	-5.96	103.26	114.00
1	B	331	ARG	NE-CZ-NH1	-5.92	117.34	120.30
1	A	229	LEU	CB-CG-CD2	-5.44	101.76	111.00
1	A	31	LEU	CB-CG-CD1	5.30	120.01	111.00
1	B	62	LEU	CB-CG-CD1	-5.16	102.22	111.00
1	B	171	LEU	CB-CG-CD2	-5.09	102.35	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	304	ARG	Sidechain
1	A	43	ARG	Sidechain

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	2679	2707	2706	58	0
1	B	2680	2707	2706	55	0
2	A	15	0	0	1	0
2	B	5	0	0	0	0
3	A	6	8	8	1	0
3	B	30	40	40	10	0
4	A	32	0	0	5	1
4	B	30	0	0	2	0
All	All	5477	5462	5460	112	1

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 10.

All (112) 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:B:290:CYS:CB	1:B:290:CYS:SG	2.03	1.44
1:A:43:ARG:NH1	1:A:304:ARG:CZ	2.10	1.15
1:A:43:ARG:HH11	1:A:304:ARG:CZ	1.79	0.93
1:A:43:ARG:HH12	1:A:304:ARG:CZ	1.93	0.81
1:B:7:ALA:O	1:B:8:LEU:HD23	1.85	0.77
1:B:34:ASP:OD1	1:B:147:LYS:NZ	2.14	0.77
1:B:43:ARG:O	1:B:46:SER:HB3	1.86	0.76
1:B:122:GLU:HA	3:B:403:GOL:H11	1.68	0.75
1:A:208:LYS:NZ	4:A:503:HOH:O	2.19	0.73
1:A:251:MET:O	1:A:255:THR:HG23	1.87	0.73
1:A:149:ARG:NH1	1:A:190:GLU:OE2	2.19	0.73
1:A:171:LEU:HD22	1:A:187:VAL:HG13	1.71	0.71
1:B:162:LEU:HD12	1:B:162:LEU:O	1.91	0.70
1:B:290:CYS:SG	1:B:290:CYS:CA	2.79	0.69
1:A:116:LEU:HD11	1:A:124:THR:HB	1.77	0.66
1:A:128:LEU:HD11	1:A:170:VAL:HG23	1.78	0.65
1:B:116:LEU:O	1:B:119:THR:HG22	1.96	0.65
1:B:166:GLU:OE2	3:B:405:GOL:H12	1.98	0.63
1:B:122:GLU:OE2	1:B:160:SER:HB3	1.99	0.63
1:B:121:GLY:O	3:B:403:GOL:H32	1.99	0.62
1:A:43:ARG:HH12	1:A:304:ARG:NH2	1.96	0.62
1:B:360:SER:O	4:B:501:HOH:O	2.16	0.62
1:A:200:LYS:NZ	4:A:505:HOH:O	2.34	0.61
1:A:272:SER:O	1:A:275:GLN:HG3	2.01	0.60
1:A:360:SER:O	4:A:502:HOH:O	2.16	0.60
1:A:67:ASP:OD2	1:A:69:ARG:NH1	2.35	0.59
1:B:122:GLU:HA	3:B:403:GOL:C1	2.32	0.59
1:A:58:PHE:CZ	1:A:321:LEU:HD13	2.38	0.58
1:B:153:LYS:HE3	1:B:194:ASP:HB2	1.85	0.58
1:A:76:GLY:HA2	1:A:104:VAL:O	2.03	0.57
1:A:108:LYS:HD2	4:A:520:HOH:O	2.04	0.56
1:A:187:VAL:HG12	1:A:189:PRO:HD3	1.87	0.56
4:A:521:HOH:O	3:B:406:GOL:H31	2.05	0.56
1:A:272:SER:OG	2:A:401:PO4:O1	2.24	0.56
1:B:31:LEU:HB3	1:B:77:VAL:HG12	1.86	0.56
1:B:43:ARG:NH1	1:B:43:ARG:HG2	2.21	0.55
1:B:108:LYS:NZ	3:B:402:GOL:O2	2.37	0.54
1:A:149:ARG:HG3	1:A:188:GLU:HG2	1.89	0.54
1:A:290:CYS:O	1:A:294:LYS:NZ	2.41	0.54
1:B:47:ILE:HD13	1:B:311:LEU:HG	1.89	0.54
1:A:359:VAL:HG12	1:A:360:SER:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:PRO:O	1:A:14:LYS:HE2	2.09	0.53
1:A:27:GLY:HA2	1:A:339:CYS:SG	2.50	0.51
1:B:123:THR:N	3:B:403:GOL:H12	2.26	0.51
1:A:343:TYR:CE2	1:A:345:PRO:HG3	2.45	0.51
1:A:43:ARG:HH11	1:A:304:ARG:NH1	2.07	0.51
1:B:122:GLU:OE1	1:B:159:PRO:HA	2.11	0.51
1:A:43:ARG:NH1	1:A:304:ARG:NE	2.58	0.50
1:B:79:LEU:HB3	1:B:83:THR:HB	1.92	0.50
1:B:119:THR:HG23	1:B:122:GLU:H	1.76	0.50
1:A:196:ASP:OD1	1:A:196:ASP:N	2.45	0.49
1:B:164:ILE:CD1	1:B:208:LYS:HE2	2.42	0.49
1:A:294:LYS:HD2	1:A:298:LEU:HD12	1.94	0.49
1:A:326:GLU:O	1:A:330:LYS:HG3	2.12	0.49
1:A:221:HIS:ND1	3:A:404:GOL:H31	2.28	0.49
1:B:190:GLU:OE1	4:B:502:HOH:O	2.20	0.49
1:A:299:THR:HG23	1:A:300:PHE:N	2.28	0.49
1:B:306:LEU:HD23	1:B:331:ARG:HB3	1.94	0.49
1:B:153:LYS:HE3	1:B:194:ASP:CB	2.43	0.48
1:B:43:ARG:HG2	1:B:43:ARG:HH11	1.78	0.47
1:B:16:LEU:HD13	1:B:179:GLN:HG2	1.96	0.47
1:A:73:CYS:SG	1:A:333:LEU:HD23	2.55	0.47
1:A:215:LYS:NZ	1:A:219:ASP:OD1	2.44	0.47
1:A:268:ILE:HB	1:A:298:LEU:HD23	1.96	0.47
1:B:166:GLU:OE2	3:B:405:GOL:C1	2.61	0.47
1:B:271:LEU:HD12	1:B:271:LEU:O	2.15	0.47
1:B:292:LEU:O	1:B:294:LYS:HG3	2.15	0.47
1:A:47:ILE:HD13	1:A:311:LEU:HG	1.96	0.47
1:B:251:MET:O	1:B:255:THR:HG23	2.14	0.46
1:A:294:LYS:HD2	1:A:298:LEU:CD1	2.44	0.46
1:A:153:LYS:O	1:A:159:PRO:HD3	2.16	0.46
1:A:227:THR:O	1:A:228:LEU:HD23	2.16	0.46
1:B:14:LYS:HE3	1:B:18:ASP:OD2	2.16	0.46
1:B:29:GLY:HA3	1:B:300:PHE:CZ	2.51	0.46
1:B:123:THR:H	3:B:403:GOL:H12	1.81	0.46
1:B:255:THR:O	1:B:259:ARG:HG3	2.16	0.45
1:A:293:LEU:HD23	1:A:294:LYS:N	2.31	0.45
1:A:212:ALA:HA	1:B:215:LYS:HE2	1.99	0.45
1:B:73:CYS:SG	1:B:333:LEU:HD12	2.57	0.44
1:A:119:THR:HB	1:A:122:GLU:OE2	2.16	0.44
1:A:23:ILE:HD11	1:A:145:PHE:CD1	2.53	0.44
1:B:116:LEU:O	1:B:119:THR:CG2	2.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:ASP:OD2	1:A:92:ARG:NE	2.49	0.44
1:B:230:LYS:HA	1:B:269:THR:O	2.18	0.44
1:A:84:LEU:HD22	1:A:107:ILE:HD13	2.00	0.43
1:B:59:TYR:CZ	1:B:311:LEU:HD13	2.53	0.43
1:A:199:LEU:HD11	1:A:234:VAL:HG12	1.99	0.43
1:B:229:LEU:HB3	1:B:268:ILE:HD13	2.01	0.43
1:B:309:SER:O	1:B:310:ALA:C	2.56	0.43
1:B:113:VAL:HB	1:B:123:THR:HB	2.00	0.43
1:B:317:LYS:HE2	1:B:317:LYS:HB3	1.84	0.43
1:A:326:GLU:O	1:A:326:GLU:HG3	2.19	0.43
1:B:360:SER:HA	3:B:404:GOL:O1	2.19	0.43
1:B:125:THR:HG22	1:B:126:GLN:N	2.35	0.42
1:A:293:LEU:HD22	1:B:295:PRO:HB3	2.02	0.42
1:B:14:LYS:CE	1:B:18:ASP:OD2	2.68	0.42
1:B:245:SER:OG	1:B:248:GLU:HG3	2.20	0.42
1:B:104:VAL:CG1	1:B:144:ASP:HB2	2.50	0.41
1:B:290:CYS:O	1:B:294:LYS:NZ	2.46	0.41
1:A:9:THR:OG1	1:A:12:GLN:HG3	2.20	0.41
1:A:116:LEU:CD1	1:A:124:THR:HB	2.46	0.41
1:A:94:PHE:N	1:A:95:PRO:CD	2.83	0.41
1:A:40:ILE:O	1:A:40:ILE:HG13	2.20	0.41
1:B:200:LYS:HD3	1:B:200:LYS:HA	1.89	0.41
1:A:59:TYR:O	1:A:62:LEU:HB3	2.21	0.41
1:A:97:VAL:O	1:A:101:LYS:HG3	2.21	0.40
1:A:262:PRO:HA	1:A:263:PRO:HD3	1.89	0.40
1:A:235:THR:HB	1:A:236:PRO:HD2	2.02	0.40
1:B:109:VAL:O	1:B:134:ARG:NH2	2.51	0.40
1:A:79:LEU:HD12	1:A:84:LEU:HD12	2.02	0.40
1:A:9:THR:HG23	1:A:12:GLN:OE1	2.20	0.40
1:B:314:TRP:O	1:B:317:LYS:HG2	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:529:HOH:O	4:A:529:HOH:O[4_545]	1.93	0.27

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	349/364 (96%)	326 (93%)	23 (7%)	0	100	100
1	B	349/364 (96%)	327 (94%)	22 (6%)	0	100	100
All	All	698/728 (96%)	653 (94%)	45 (6%)	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	283/292 (97%)	268 (95%)	15 (5%)	22	20
1	B	284/292 (97%)	275 (97%)	9 (3%)	39	40
All	All	567/584 (97%)	543 (96%)	24 (4%)	30	29

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	SER
1	A	57	ARG
1	A	60	ARG
1	A	68	ASP
1	A	99	LYS
1	A	174	TYR
1	A	201	ARG
1	A	218	SER

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Mol	Chain	Res	Type
1	A	290	CYS
1	A	296	TRP
1	A	304	ARG
1	A	322	LYS
1	A	331	ARG
1	A	354	SER
1	A	356	SER
1	B	90	ASP
1	B	129	ASP
1	B	160	SER
1	B	174	TYR
1	B	296	TRP
1	B	321	LEU
1	B	330	LYS
1	B	331	ARG
1	B	356	SER

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

10 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	GOL	B	403	-	5,5,5	1.23	0	5,5,5	1.08	0
3	GOL	B	406	-	5,5,5	1.42	1 (20%)	5,5,5	0.63	0
2	PO4	B	401	-	4,4,4	0.91	0	6,6,6	0.99	0
2	PO4	A	403	-	4,4,4	0.97	0	6,6,6	0.51	0
3	GOL	B	402	-	5,5,5	1.03	0	5,5,5	0.54	0
2	PO4	A	401	-	4,4,4	0.43	0	6,6,6	1.17	0
3	GOL	B	405	-	5,5,5	1.67	2 (40%)	5,5,5	1.08	0
3	GOL	B	404	-	5,5,5	1.21	1 (20%)	5,5,5	0.88	0
3	GOL	A	404	-	5,5,5	0.92	0	5,5,5	0.98	0
2	PO4	A	402	-	4,4,4	0.72	0	6,6,6	1.03	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	403	-	-	3/4/4/4	-
3	GOL	B	406	-	-	3/4/4/4	-
3	GOL	B	402	-	-	0/4/4/4	-
3	GOL	B	405	-	-	2/4/4/4	-
3	GOL	B	404	-	-	4/4/4/4	-
3	GOL	A	404	-	-	0/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	406	GOL	C3-C2	2.75	1.63	1.51
3	B	405	GOL	C1-C2	2.71	1.62	1.51
3	B	405	GOL	C3-C2	2.52	1.62	1.51
3	B	404	GOL	C1-C2	2.17	1.60	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	404	GOL	O1-C1-C2-C3
3	B	404	GOL	C1-C2-C3-O3
3	B	405	GOL	O1-C1-C2-C3
3	B	406	GOL	O1-C1-C2-C3
3	B	404	GOL	O1-C1-C2-O2
3	B	404	GOL	O2-C2-C3-O3
3	B	405	GOL	O1-C1-C2-O2
3	B	403	GOL	O1-C1-C2-O2
3	B	403	GOL	O2-C2-C3-O3
3	B	403	GOL	O1-C1-C2-C3
3	B	406	GOL	O1-C1-C2-O2
3	B	406	GOL	O2-C2-C3-O3

There are no ring outliers.

7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	403	GOL	5	0
3	B	406	GOL	1	0
3	B	402	GOL	1	0
2	A	401	PO4	1	0
3	B	405	GOL	2	0
3	B	404	GOL	1	0
3	A	404	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	353/364 (96%)	0.17	4 (1%) 80 84	23, 44, 62, 76	0
1	B	353/364 (96%)	0.24	7 (1%) 65 69	25, 44, 62, 79	0
All	All	706/728 (96%)	0.20	11 (1%) 72 76	23, 44, 62, 79	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	5	TYR	4.4
1	A	5	TYR	4.2
1	B	156	GLU	4.0
1	B	345	PRO	3.2
1	B	157	HIS	3.1
1	B	90	ASP	2.9
1	A	318	LYS	2.5
1	B	89	ASP	2.4
1	A	156	GLU	2.2
1	B	241	THR	2.2
1	A	241	THR	2.1

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(Å ²)	Q<0.9
3	GOL	B	402	6/6	0.82	0.15	52,64,80,80	0
3	GOL	B	405	6/6	0.82	0.26	45,65,82,82	0
3	GOL	B	406	6/6	0.86	0.31	54,66,74,74	0
3	GOL	B	404	6/6	0.88	0.15	60,72,82,82	0
3	GOL	B	403	6/6	0.89	0.27	40,55,71,71	0
3	GOL	A	404	6/6	0.90	0.19	46,61,83,83	0
2	PO4	A	401	5/5	0.92	0.12	57,57,73,79	0
2	PO4	B	401	5/5	0.95	0.12	52,53,66,68	0
2	PO4	A	403	5/5	0.96	0.10	46,61,69,70	0
2	PO4	A	402	5/5	0.97	0.08	43,56,64,68	0

6.5 Other polymers [i](#)

There are no such residues in this entry.