



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 24, 2018 – 08:03 AM EST

PDB ID : 1FA9
Title : HUMAN LIVER GLYCOGEN PHOSPHORYLASE A COMPLEXED WITH AMP
Authors : Rath, V.L.; Ammirati, M.; LeMotte, P.K.; Fennell, K.F.; Mansour, M.N.; Danley, D.E.; Hynes, T.R.; Schulte, G.K.; Wasilko, D.J.; Pandit, J.
Deposited on : 2000-07-12
Resolution : 2.40 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	:	rb-20030736
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)	:	rb-20030736

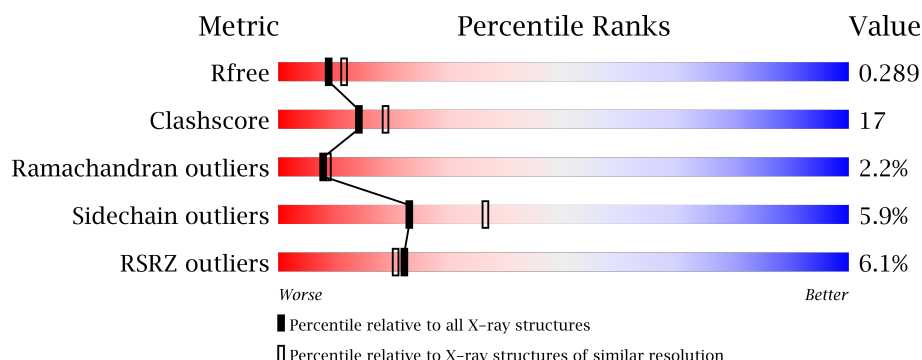
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.40 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	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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	846	

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	GLC	A	998	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7042 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 GLYCOGEN PHOSPHORYLASE, LIVER FORM.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	834	6750	4325	1154	1241	1	29	0	0	0

There is a discrepancy between the modelled and reference sequences:

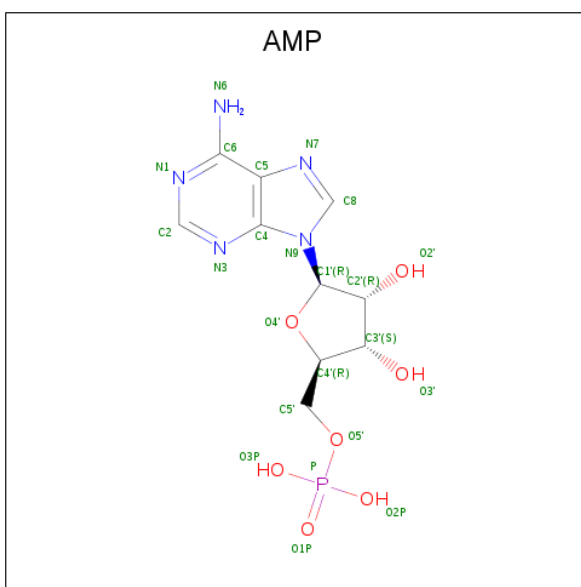
Chain	Residue	Modelled	Actual	Comment	Reference
A	14	SEP	SER	MODIFIED RESIDUE	UNP P06737

- Molecule 2 is ALPHA-D-GLUCOSE (three-letter code: GLC) (formula: $C_6H_{12}O_6$).



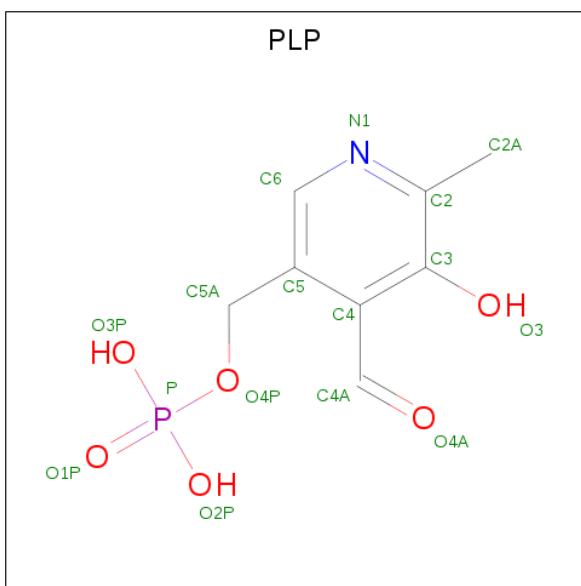
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	12	6	6	0	0

- Molecule 3 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 4 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

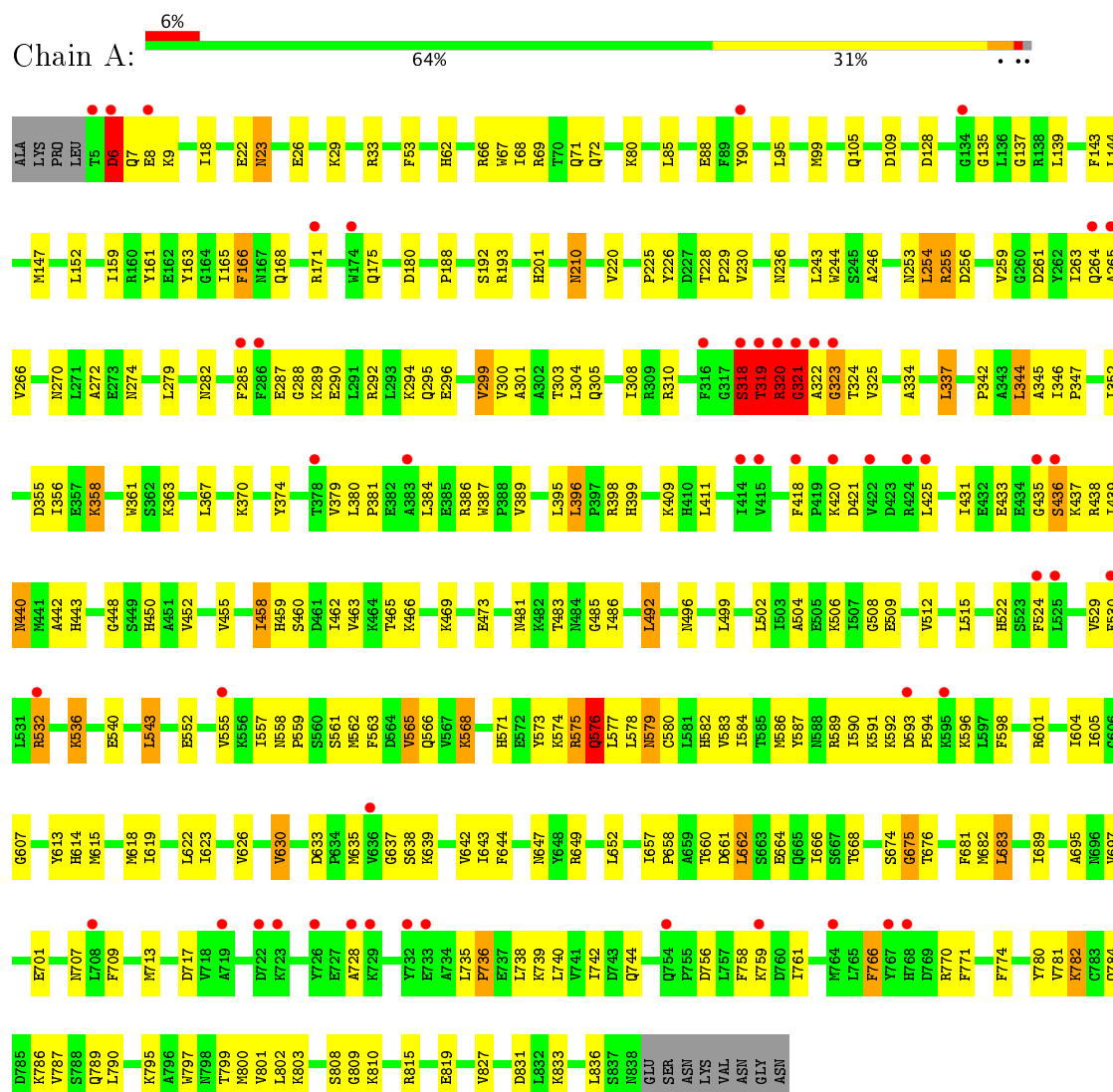
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	242	Total 242	O 242	0	0

3 Residue-property plots

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: GLYCOGEN PHOSPHORYLASE, LIVER FORM



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	123.91Å 123.91Å 127.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.40 41.07 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.40) 90.6 (41.07-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 2.20Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.235 , 0.295 0.211 , 0.289	Depositor DCC
R_{free} test set	4103 reflections (10.35%)	DCC
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 75.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7042	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% 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: AMP, GLC, PLP, SEP

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	0.53	5/6887 (0.1%)	0.83	10/9311 (0.1%)

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	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	321	GLY	C-N	-25.47	0.75	1.34
1	A	318	SER	C-N	16.64	1.72	1.34
1	A	319	THR	C-N	-7.53	1.16	1.34
1	A	320	ARG	C-N	-7.49	1.19	1.33
1	A	321	GLY	N-CA	-6.75	1.35	1.46

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	318	SER	O-C-N	-42.91	54.04	122.70
1	A	321	GLY	O-C-N	15.21	147.03	122.70
1	A	318	SER	CA-C-N	-14.42	85.47	117.20
1	A	321	GLY	CA-C-N	-13.74	86.98	117.20
1	A	320	ARG	O-C-N	10.84	141.63	123.20
1	A	321	GLY	N-CA-C	-10.30	87.35	113.10
1	A	319	THR	O-C-N	9.56	138.00	122.70
1	A	320	ARG	CA-C-N	-9.50	97.21	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	319	THR	CA-C-N	-7.54	100.61	117.20
1	A	320	ARG	C-N-CA	6.06	135.03	122.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	320	ARG	Mainchain

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	6750	0	6733	235	1
2	A	12	0	12	5	0
3	A	23	0	12	1	0
4	A	15	0	7	2	0
5	A	242	0	0	9	0
All	All	7042	0	6764	237	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 17.

All (237) 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:320:ARG:NH1	1:A:323:GLY:HA2	1.33	1.36
1:A:318:SER:O	1:A:319:THR:OG1	1.56	1.18
1:A:320:ARG:NH1	1:A:323:GLY:CA	2.15	1.08
1:A:486:ILE:HD11	1:A:676:THR:HG23	1.38	1.03
1:A:320:ARG:HH11	1:A:323:GLY:HA2	1.13	0.96
1:A:320:ARG:HH11	1:A:323:GLY:CA	1.81	0.90
1:A:320:ARG:CZ	1:A:323:GLY:HA2	2.04	0.87
1:A:69:ARG:HH11	1:A:72:GLN:HE22	1.19	0.84
1:A:23:ASN:H	1:A:23:ASN:HD22	1.28	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:VAL:H	1:A:459:HIS:HD2	1.27	0.82
1:A:85:LEU:HD21	1:A:303:THR:HG21	1.63	0.81
1:A:319:THR:O	1:A:322:ALA:HB3	1.79	0.81
1:A:440:ASN:HD22	1:A:443:HIS:H	1.32	0.77
1:A:758:PHE:O	1:A:761:ILE:HG22	1.88	0.73
1:A:69:ARG:NH1	1:A:72:GLN:HE22	1.86	0.72
1:A:99:MET:HE3	1:A:105:GLN:HA	1.73	0.71
1:A:384:LEU:HB2	1:A:386:ARG:HH21	1.54	0.71
1:A:80:LYS:HE2	1:A:334:ALA:HB2	1.73	0.70
1:A:168:GLN:HG3	1:A:175:GLN:HG3	1.72	0.70
1:A:22:GLU:HA	5:A:2184:HOH:O	1.90	0.70
1:A:462:ILE:HA	1:A:466:LYS:HD3	1.74	0.70
1:A:455:VAL:H	1:A:459:HIS:CD2	2.10	0.68
1:A:69:ARG:HH11	1:A:72:GLN:NE2	1.91	0.66
1:A:321:GLY:O	1:A:323:GLY:N	2.28	0.66
1:A:668:THR:OG1	1:A:771:PHE:HB3	1.97	0.65
1:A:676:THR:HB	2:A:998:GLC:H62	1.79	0.65
1:A:7:GLN:HG3	1:A:8:GLU:H	1.61	0.65
1:A:571:HIS:H	1:A:576:GLN:HE22	1.43	0.64
1:A:152:LEU:HD22	1:A:827:VAL:CG1	2.29	0.63
1:A:579:ASN:O	1:A:583:VAL:HG23	1.98	0.63
1:A:440:ASN:ND2	1:A:443:HIS:H	1.97	0.63
1:A:529:VAL:O	1:A:532:ARG:HB3	1.99	0.62
1:A:261:ASP:HB3	1:A:264:GLN:HB2	1.79	0.62
1:A:318:SER:C	1:A:319:THR:OG1	2.37	0.62
1:A:676:THR:HG21	5:A:2028:HOH:O	2.00	0.62
1:A:193:ARG:HB2	1:A:225:PRO:HG2	1.82	0.62
1:A:455:VAL:O	1:A:483:THR:HA	1.99	0.62
1:A:575:ARG:C	1:A:577:LEU:H	2.02	0.61
1:A:370:LYS:NZ	1:A:370:LYS:HB3	2.15	0.61
1:A:575:ARG:O	1:A:576:GLN:HG2	2.01	0.61
1:A:358:LYS:HE3	5:A:2053:HOH:O	1.99	0.61
1:A:492:LEU:HG	1:A:683:LEU:HD22	1.82	0.61
1:A:318:SER:HA	1:A:325:VAL:CG1	2.30	0.60
1:A:728:ALA:HB1	1:A:774:PHE:HD1	1.65	0.60
1:A:571:HIS:H	1:A:576:GLN:NE2	2.00	0.60
1:A:455:VAL:N	1:A:459:HIS:HD2	1.99	0.60
1:A:396:LEU:HB3	1:A:399:HIS:HB2	1.83	0.60
1:A:135:GLY:HA3	2:A:998:GLC:O5	2.02	0.60
1:A:7:GLN:HG3	1:A:8:GLU:N	2.17	0.59
1:A:266:VAL:O	1:A:266:VAL:HG12	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:562:MET:O	1:A:563:PHE:HB2	2.03	0.59
1:A:713:MET:HB3	1:A:717:ASP:HB2	1.84	0.59
1:A:210:ASN:N	1:A:210:ASN:HD22	2.00	0.59
1:A:270:ASN:HB2	5:A:2220:HOH:O	2.02	0.59
1:A:411:LEU:HD22	1:A:425:LEU:HD22	1.84	0.59
1:A:562:MET:O	1:A:661:ASP:HB2	2.03	0.59
1:A:568:LYS:NZ	1:A:568:LYS:HB3	2.18	0.58
1:A:152:LEU:HD22	1:A:827:VAL:HG12	1.85	0.58
1:A:728:ALA:HB1	1:A:774:PHE:CD1	2.39	0.58
1:A:450:HIS:HE1	5:A:2092:HOH:O	1.86	0.57
1:A:7:GLN:HG2	1:A:9:LYS:HD3	1.86	0.57
1:A:568:LYS:O	1:A:607:GLY:HA3	2.03	0.57
1:A:352:ILE:HA	1:A:356:ILE:HD12	1.86	0.57
2:A:998:GLC:H61	4:A:999:PLP:P	2.45	0.57
1:A:23:ASN:N	1:A:23:ASN:HD22	1.96	0.57
1:A:318:SER:HA	1:A:325:VAL:HG11	1.85	0.56
1:A:384:LEU:HB2	1:A:386:ARG:NH2	2.19	0.56
1:A:254:LEU:HD13	1:A:255:ARG:HH22	1.71	0.56
1:A:674:SER:HB3	2:A:998:GLC:O4	2.06	0.56
1:A:615:MET:HE2	1:A:761:ILE:HG13	1.87	0.55
1:A:728:ALA:HB3	1:A:766:PHE:HA	1.87	0.55
1:A:799:THR:HB	5:A:2231:HOH:O	2.05	0.55
1:A:790:LEU:HG	1:A:797:TRP:HE3	1.72	0.55
1:A:566:GLN:HB2	1:A:664:GLU:HB2	1.88	0.54
2:A:998:GLC:H61	4:A:999:PLP:O2P	2.08	0.54
1:A:532:ARG:NH1	1:A:536:LYS:HG3	2.21	0.54
1:A:344:LEU:HB2	5:A:2197:HOH:O	2.08	0.54
1:A:558:ASN:HB3	1:A:561:SER:HB2	1.90	0.54
1:A:582:HIS:HD2	1:A:781:VAL:HG13	1.73	0.54
1:A:614:HIS:O	1:A:618:MET:HG2	2.08	0.54
1:A:7:GLN:HG3	1:A:9:LYS:H	1.72	0.54
1:A:292:ARG:O	1:A:296:GLU:HG3	2.08	0.53
1:A:88:GLU:HG2	1:A:137:GLY:HA3	1.91	0.53
1:A:458:ILE:O	1:A:462:ILE:HG13	2.08	0.53
1:A:322:ALA:O	1:A:324:THR:N	2.41	0.53
1:A:68:ILE:O	1:A:72:GLN:HG3	2.08	0.53
1:A:622:LEU:O	1:A:626:VAL:HG23	2.09	0.53
1:A:165:ILE:O	1:A:166:PHE:HB3	2.09	0.53
1:A:346:ILE:HD13	1:A:448:GLY:HA3	1.91	0.53
1:A:355:ASP:OD1	1:A:398:ARG:HD3	2.08	0.53
1:A:586:MET:O	1:A:590:ILE:HG13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:PHE:HE2	1:A:802:LEU:HD13	1.74	0.52
1:A:67:TRP:O	1:A:71:GLN:HG2	2.09	0.52
1:A:662:LEU:HD21	1:A:689:ILE:HB	1.91	0.52
1:A:358:LYS:HB2	1:A:358:LYS:NZ	2.24	0.52
1:A:689:ILE:O	1:A:689:ILE:HG23	2.09	0.52
1:A:263:ILE:N	1:A:263:ILE:HD12	2.24	0.52
1:A:320:ARG:HH11	1:A:323:GLY:C	2.12	0.52
1:A:358:LYS:HB2	1:A:358:LYS:HZ3	1.74	0.52
1:A:707:ASN:ND2	1:A:803:LYS:HD3	2.25	0.52
1:A:321:GLY:C	1:A:323:GLY:N	2.62	0.52
1:A:380:LEU:HD12	1:A:381:PRO:HD2	1.92	0.52
1:A:697:VAL:O	1:A:701:GLU:HG3	2.10	0.52
1:A:509:GLU:O	1:A:512:VAL:HG22	2.10	0.51
1:A:225:PRO:HB3	1:A:244:TRP:CZ3	2.45	0.51
1:A:370:LYS:HZ3	1:A:370:LYS:HB3	1.76	0.51
1:A:346:ILE:HB	1:A:347:PRO:HD3	1.91	0.51
1:A:53:PHE:CE1	1:A:188:PRO:HD3	2.46	0.51
1:A:626:VAL:O	1:A:630:VAL:HG13	2.11	0.51
1:A:418:PHE:HB3	1:A:421:ASP:CB	2.41	0.51
1:A:22:GLU:HB3	1:A:62:HIS:CE1	2.45	0.50
1:A:469:LYS:O	1:A:473:GLU:HG3	2.11	0.50
1:A:738:LEU:HD11	1:A:774:PHE:CD2	2.46	0.50
1:A:304:LEU:O	1:A:308:ILE:HG12	2.11	0.50
1:A:565:VAL:HG11	1:A:660:THR:HG22	1.93	0.50
1:A:582:HIS:CD2	1:A:781:VAL:HG13	2.46	0.50
1:A:295:GLN:O	1:A:299:VAL:HG23	2.11	0.50
1:A:630:VAL:HG21	1:A:642:VAL:HG23	1.94	0.50
1:A:782:LYS:HE3	1:A:782:LYS:HA	1.94	0.50
1:A:810:LYS:O	1:A:815:ARG:NH1	2.41	0.49
1:A:660:THR:HG21	1:A:681:PHE:HE1	1.76	0.49
1:A:459:HIS:O	1:A:463:VAL:HG23	2.13	0.49
1:A:578:LEU:HG	1:A:780:TYR:CD2	2.48	0.49
1:A:289:LYS:HG2	1:A:387:TRP:HZ3	1.78	0.49
1:A:418:PHE:HB3	1:A:421:ASP:HB3	1.94	0.49
1:A:159:ILE:HD11	1:A:299:VAL:HG22	1.95	0.49
1:A:598:PHE:CD2	1:A:639:LYS:HG2	2.47	0.49
1:A:210:ASN:N	1:A:210:ASN:ND2	2.59	0.49
1:A:433:GLU:HG3	1:A:437:LYS:HE2	1.94	0.49
1:A:6:ASP:O	1:A:7:GLN:HB3	2.13	0.48
1:A:675:GLY:N	1:A:695:ALA:HB2	2.28	0.48
1:A:504:ALA:HA	1:A:508:GLY:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:557:ILE:O	1:A:559:PRO:HD3	2.14	0.48
1:A:431:ILE:HD11	1:A:437:LYS:HD3	1.94	0.48
1:A:522:HIS:C	1:A:524:PHE:H	2.17	0.48
1:A:605:ILE:O	1:A:644:PHE:HA	2.13	0.48
1:A:815:ARG:O	1:A:819:GLU:HG3	2.14	0.48
1:A:23:ASN:HD21	1:A:26:GLU:HG2	1.79	0.48
1:A:485:GLY:O	1:A:486:ILE:HD12	2.14	0.48
1:A:575:ARG:O	1:A:577:LEU:N	2.47	0.48
1:A:255:ARG:O	1:A:259:VAL:HG23	2.14	0.47
1:A:386:ARG:HH11	1:A:386:ARG:HG3	1.78	0.47
1:A:742:ILE:HD11	1:A:774:PHE:HE2	1.79	0.47
1:A:236:ASN:ND2	1:A:833:LYS:HE2	2.29	0.47
1:A:801:VAL:HG11	5:A:2159:HOH:O	2.13	0.47
1:A:573:TYR:CZ	1:A:574:LYS:HE2	2.50	0.47
1:A:492:LEU:HG	1:A:683:LEU:CD2	2.43	0.47
1:A:192:SER:HB3	1:A:226:TYR:CE1	2.50	0.47
1:A:23:ASN:ND2	1:A:23:ASN:H	2.05	0.47
1:A:566:GLN:HE22	1:A:576:GLN:HA	1.80	0.46
1:A:633:ASP:OD2	1:A:635:MET:HB2	2.15	0.46
1:A:279:LEU:HD12	5:A:2080:HOH:O	2.15	0.46
1:A:344:LEU:O	1:A:347:PRO:HD2	2.16	0.46
1:A:168:GLN:O	1:A:647:ASN:HB2	2.16	0.46
1:A:290:GLU:O	1:A:294:LYS:HG3	2.15	0.46
1:A:440:ASN:HD21	1:A:442:ALA:HB3	1.81	0.46
1:A:587:TYR:O	1:A:591:LYS:HG2	2.16	0.46
1:A:555:VAL:HG11	1:A:643:ILE:HD11	1.98	0.46
1:A:515:LEU:HB3	1:A:809:GLY:O	2.16	0.46
1:A:386:ARG:HD3	1:A:440:ASN:HA	1.98	0.46
1:A:282:ASN:O	1:A:288:GLY:HA3	2.16	0.45
1:A:619:ILE:O	1:A:623:ILE:HG13	2.16	0.45
1:A:689:ILE:HA	1:A:709:PHE:HB2	1.97	0.45
1:A:256:ASP:HB3	1:A:261:ASP:HB2	1.98	0.45
1:A:289:LYS:NZ	1:A:289:LYS:HB2	2.32	0.45
1:A:381:PRO:HA	1:A:384:LEU:HG	1.97	0.45
1:A:483:THR:O	1:A:815:ARG:NH2	2.40	0.45
1:A:460:SER:OG	1:A:481:ASN:ND2	2.37	0.45
1:A:486:ILE:CD1	1:A:676:THR:HG23	2.28	0.45
1:A:573:TYR:OH	1:A:574:LYS:HE2	2.16	0.45
1:A:386:ARG:HA	1:A:439:ILE:O	2.17	0.45
1:A:466:LYS:HD2	1:A:466:LYS:N	2.31	0.45
1:A:662:LEU:HD11	1:A:689:ILE:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:657:ILE:HG12	1:A:681:PHE:CE1	2.52	0.44
1:A:165:ILE:HG23	1:A:166:PHE:N	2.32	0.44
1:A:319:THR:O	1:A:325:VAL:HG13	2.15	0.44
1:A:589:ARG:O	1:A:592:LYS:HB2	2.17	0.44
1:A:300:VAL:HG13	1:A:345:ALA:HA	1.98	0.44
1:A:675:GLY:CA	1:A:695:ALA:HB2	2.48	0.44
1:A:310:ARG:HD3	3:A:997:AMP:O3P	2.17	0.44
1:A:163:TYR:O	1:A:180:ASP:HB3	2.16	0.44
1:A:682:MET:HG2	1:A:808:SER:HB3	1.99	0.44
1:A:662:LEU:HG	1:A:787:VAL:HG11	1.99	0.44
1:A:740:LEU:O	1:A:744:GLN:HG3	2.18	0.43
1:A:584:ILE:O	1:A:587:TYR:HB3	2.18	0.43
1:A:318:SER:HA	1:A:325:VAL:HG12	1.98	0.43
1:A:735:LEU:HA	1:A:736:PRO:HD3	1.84	0.43
1:A:592:LYS:HB3	1:A:592:LYS:HE3	1.88	0.43
1:A:29:LYS:HG2	1:A:33:ARG:NH2	2.33	0.43
1:A:465:THR:OG1	1:A:466:LYS:HD2	2.19	0.43
1:A:604:ILE:HA	1:A:643:ILE:O	2.18	0.43
1:A:236:ASN:HD21	1:A:833:LYS:HE2	1.84	0.43
1:A:266:VAL:O	1:A:266:VAL:CG1	2.65	0.43
1:A:319:THR:HG22	1:A:320:ARG:N	2.33	0.43
1:A:143:PHE:O	1:A:147:MET:HG3	2.19	0.43
1:A:637:GLY:C	1:A:639:LYS:H	2.22	0.42
1:A:756:ASP:O	1:A:759:LYS:HB2	2.18	0.42
1:A:795:LYS:O	1:A:799:THR:HG23	2.19	0.42
1:A:568:LYS:HZ3	1:A:568:LYS:HB3	1.83	0.42
1:A:99:MET:CE	1:A:105:GLN:HA	2.46	0.42
1:A:228:THR:HA	1:A:229:PRO:HD3	1.87	0.42
1:A:361:TRP:CZ3	1:A:409:LYS:HD2	2.54	0.42
1:A:800:MET:O	1:A:803:LYS:HB2	2.19	0.42
1:A:321:GLY:C	1:A:323:GLY:H	2.16	0.42
1:A:707:ASN:HD21	1:A:803:LYS:HD3	1.84	0.42
1:A:7:GLN:CG	1:A:8:GLU:H	2.32	0.42
1:A:285:PHE:CD1	1:A:287:GLU:HB2	2.54	0.42
1:A:301:ALA:O	1:A:305:GLN:HG3	2.20	0.42
1:A:389:VAL:HG12	1:A:439:ILE:CG1	2.49	0.42
1:A:66:ARG:HG2	1:A:836:LEU:HD21	2.02	0.42
1:A:363:LYS:O	1:A:367:LEU:HG	2.20	0.42
1:A:515:LEU:HG	1:A:809:GLY:HA2	2.01	0.42
1:A:435:GLY:O	1:A:436:SER:HB3	2.20	0.41
1:A:615:MET:O	1:A:619:ILE:HG13	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ASN:HB3	1:A:265:ALA:HA	2.03	0.41
1:A:201:HIS:CE1	1:A:220:VAL:HG22	2.55	0.41
1:A:270:ASN:ND2	1:A:274:ASN:HD21	2.18	0.41
1:A:379:VAL:HB	1:A:459:HIS:ND1	2.35	0.41
1:A:506:LYS:HB3	1:A:524:PHE:CZ	2.56	0.41
1:A:161:TYR:CE2	1:A:279:LEU:HD13	2.55	0.41
1:A:575:ARG:C	1:A:577:LEU:N	2.72	0.41
1:A:738:LEU:HD11	1:A:774:PHE:CE2	2.55	0.41
1:A:337:LEU:HG	1:A:342:PRO:HG2	2.02	0.41
1:A:536:LYS:O	1:A:540:GLU:HG2	2.21	0.41
1:A:379:VAL:HB	1:A:459:HIS:CE1	2.56	0.41
1:A:601:ARG:HH12	1:A:784:GLN:CD	2.23	0.41
1:A:496:ASN:ND2	1:A:658:PRO:HB3	2.35	0.40
1:A:144:LEU:HB3	1:A:230:VAL:HG11	2.04	0.40
1:A:246:ALA:HB1	1:A:272:ALA:O	2.22	0.40
1:A:580:CYS:SG	1:A:622:LEU:HD13	2.61	0.40
1:A:797:TRP:O	1:A:801:VAL:HG23	2.21	0.40
1:A:395:LEU:O	1:A:396:LEU:HD13	2.21	0.40
1:A:462:ILE:O	1:A:466:LYS:HB2	2.21	0.40
1:A:639:LYS:HB2	1:A:639:LYS:HE3	1.84	0.40
1:A:786:LYS:HA	1:A:789:GLN:HG2	2.03	0.40
1:A:374:TYR:O	1:A:452:VAL:HA	2.22	0.40
1:A:736:PRO:O	1:A:739:LYS:HB3	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)
1:A:319:THR:CG2	1:A:543:LEU:CD2[5_665]	1.53	0.67

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	831/846 (98%)	761 (92%)	52 (6%)	18 (2%)	8 9

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	318	SER
1	A	319	THR
1	A	436	SER
1	A	166	PHE
1	A	321	GLY
1	A	323	GLY
1	A	576	GLN
1	A	575	ARG
1	A	594	PRO
1	A	638	SER
1	A	736	PRO
1	A	766	PHE
1	A	770	ARG
1	A	6	ASP
1	A	593	ASP
1	A	18	ILE
1	A	675	GLY
1	A	666	ILE

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	725/738 (98%)	682 (94%)	43 (6%)	23 36

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASP
1	A	23	ASN
1	A	90	TYR

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Mol	Chain	Res	Type
1	A	95	LEU
1	A	109	ASP
1	A	128	ASP
1	A	139	LEU
1	A	171	ARG
1	A	210	ASN
1	A	243	LEU
1	A	254	LEU
1	A	255	ARG
1	A	299	VAL
1	A	318	SER
1	A	319	THR
1	A	337	LEU
1	A	344	LEU
1	A	358	LYS
1	A	396	LEU
1	A	420	LYS
1	A	438	ARG
1	A	440	ASN
1	A	458	ILE
1	A	492	LEU
1	A	499	LEU
1	A	502	LEU
1	A	532	ARG
1	A	536	LYS
1	A	543	LEU
1	A	552	GLU
1	A	565	VAL
1	A	568	LYS
1	A	576	GLN
1	A	579	ASN
1	A	596	LYS
1	A	613	TYR
1	A	630	VAL
1	A	649	ARG
1	A	652	LEU
1	A	662	LEU
1	A	683	LEU
1	A	782	LYS
1	A	831	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	23	ASN
1	A	32	ASN
1	A	72	GLN
1	A	73	HIS
1	A	114	GLN
1	A	167	ASN
1	A	210	ASN
1	A	219	GLN
1	A	258	ASN
1	A	270	ASN
1	A	282	ASN
1	A	305	GLN
1	A	399	HIS
1	A	408	GLN
1	A	410	HIS
1	A	440	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	484	ASN
1	A	517	GLN
1	A	541	ASN
1	A	547	GLN
1	A	566	GLN
1	A	576	GLN
1	A	579	ASN
1	A	582	HIS
1	A	789	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	SEP	A	14	1	9,9,10	1.29	0	9,12,14	5.92	3 (33%)

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
1	SEP	A	14	1	-	0/5/8/10	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	14	SEP	O3P-P-O1P	-3.23	97.87	110.50
1	A	14	SEP	O2P-P-O1P	6.02	134.07	110.50
1	A	14	SEP	OG-CB-CA	16.07	124.01	108.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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	AMP	A	997	-	22,25,25	1.17	2 (9%)	24,38,38	1.41	2 (8%)
2	GLC	A	998	-	12,12,12	0.25	0	17,17,17	0.53	0
4	PLP	A	999	1	15,15,16	2.52	4 (26%)	20,22,23	1.46	5 (25%)

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	AMP	A	997	-	-	0/6/26/26	0/3/3/3
2	GLC	A	998	-	-	0/2/22/22	0/1/1/1
4	PLP	A	999	1	-	0/6/6/8	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	999	PLP	C4A-C4	-6.66	1.38	1.51
4	A	999	PLP	C3-C2	-4.08	1.37	1.40
4	A	999	PLP	C5-C4	-3.95	1.35	1.40
4	A	999	PLP	C2A-C2	2.13	1.54	1.50
3	A	997	AMP	O4'-C1'	2.26	1.44	1.41
3	A	997	AMP	C2'-C1'	2.79	1.58	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	999	PLP	O2P-P-O4P	-2.80	99.29	106.73
4	A	999	PLP	C5-C6-N1	-2.14	120.24	123.87
3	A	997	AMP	O2P-P-O5'	-2.10	101.13	106.73
4	A	999	PLP	C6-C5-C4	2.16	119.98	118.18
4	A	999	PLP	O3P-P-O2P	2.16	116.33	107.61
4	A	999	PLP	O4P-C5A-C5	2.69	114.72	109.32
3	A	997	AMP	P-O5'-C5'	3.84	128.86	118.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	997	AMP	1	0
2	A	998	GLC	5	0
4	A	999	PLP	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	318:SER	C	319:THR	N	1.72
1	A	320:ARG	C	321:GLY	N	1.19
1	A	319:THR	C	320:ARG	N	1.16
1	A	321:GLY	C	322:ALA	N	0.75

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	833/846 (98%)	0.06	51 (6%) 22 20	24, 51, 90, 110	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	319	THR	10.2
1	A	316	PHE	5.5
1	A	5	THR	5.1
1	A	435	GLY	5.0
1	A	321	GLY	4.9
1	A	320	ARG	4.7
1	A	322	ALA	4.7
1	A	723	LYS	4.3
1	A	719	ALA	3.9
1	A	422	VAL	3.8
1	A	532	ARG	3.8
1	A	415	VAL	3.3
1	A	420	LYS	3.3
1	A	764	MET	3.3
1	A	733	GLU	3.2
1	A	174	TRP	3.2
1	A	171	ARG	3.1
1	A	729	LYS	3.1
1	A	593	ASP	3.0
1	A	767	TYR	3.0
1	A	414	ILE	2.9
1	A	285	PHE	2.9
1	A	286	PHE	2.9
1	A	530	PHE	2.8
1	A	726	TYR	2.7
1	A	595	LYS	2.7
1	A	6	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	318	SER	2.6
1	A	759	LYS	2.5
1	A	134	GLY	2.5
1	A	383	ALA	2.5
1	A	754	GLN	2.5
1	A	418	PHE	2.5
1	A	323	GLY	2.4
1	A	732	TYR	2.4
1	A	378	THR	2.4
1	A	708	LEU	2.4
1	A	264	GLN	2.3
1	A	636	VAL	2.3
1	A	728	ALA	2.3
1	A	768	HIS	2.2
1	A	424	ARG	2.2
1	A	8	GLU	2.2
1	A	425	LEU	2.2
1	A	525	LEU	2.1
1	A	524	PHE	2.1
1	A	722	ASP	2.1
1	A	265	ALA	2.1
1	A	555	VAL	2.1
1	A	436	SER	2.1
1	A	90	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	A	14	10/11	0.99	0.07	-	30,35,38,45	0

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	GLC	A	998	12/12	0.90	0.30	3.44	62,82,98,98	0
4	PLP	A	999	15/16	0.97	0.26	0.94	26,36,58,64	0
3	AMP	A	997	23/23	0.95	0.11	-0.45	30,40,48,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.