



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 09:17 AM GMT

PDB ID : 3DDS
Title : Crystal structure of glycogen phosphorylase complexed with an anthranilimide based inhibitor GSK261
Authors : Nolte, R.T.
Deposited on : 2008-06-06
Resolution : 1.80 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

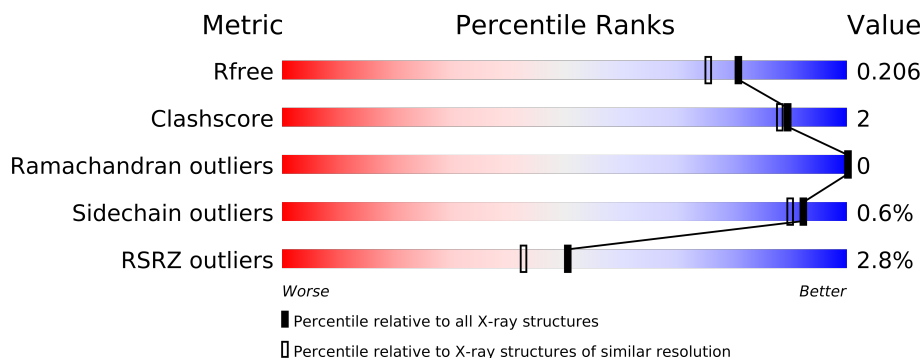
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.80 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}	66092	3513 (1.80-1.80)
Clashscore	79885	4461 (1.80-1.80)
Ramachandran outliers	78287	4404 (1.80-1.80)
Sidechain outliers	78261	4403 (1.80-1.80)
RSRZ outliers	66119	3515 (1.80-1.80)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	848	
1	B	848	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	NBG	B	901	-	X
5	CFF	A	904	-	X
5	CFF	B	903	-	X
6	26B	B	906	-	X
7	MES	B	904	-	X
8	MPD	A	906	-	X

2 Entry composition i

There are 9 unique types of molecules in this entry. The entry contains 14698 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

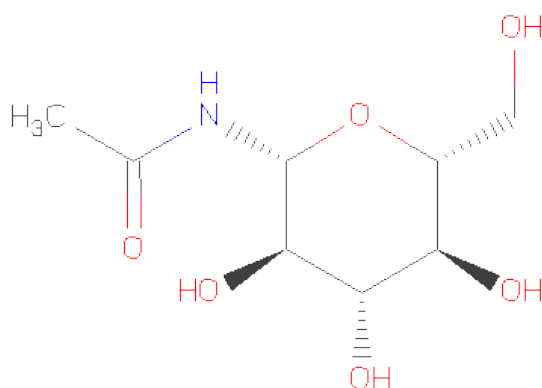
- Molecule 1 is a protein called Glycogen phosphorylase, liver form.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	811	Total	C	N	O	P	S	0	7	0
			6582	4220	1115	1215	1	31			
1	B	802	Total	C	N	O	S		0	9	0
			6539	4196	1105	1207	31				

There are 4 discrepancies between the modelled and reference sequences:

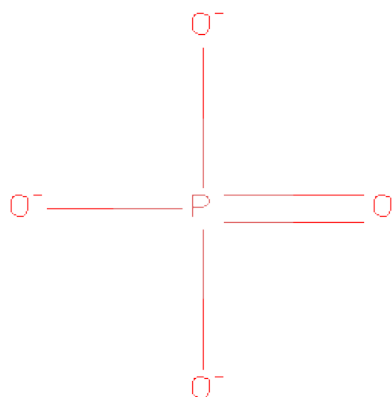
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P06737
A	0	GLY	-	EXPRESSION TAG	UNP P06737
B	-1	GLY	-	EXPRESSION TAG	UNP P06737
B	0	GLY	-	EXPRESSION TAG	UNP P06737

- Molecule 2 is SUGAR (1-N-ACETYL-BETA-D-GLUCOSAMINE) (three-letter code: NBG) (formula: C₈H₁₅NO₆).



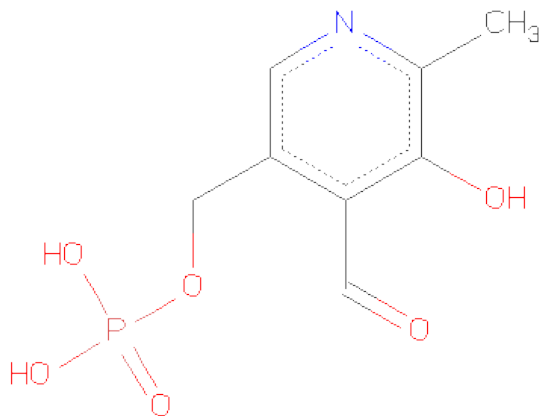
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



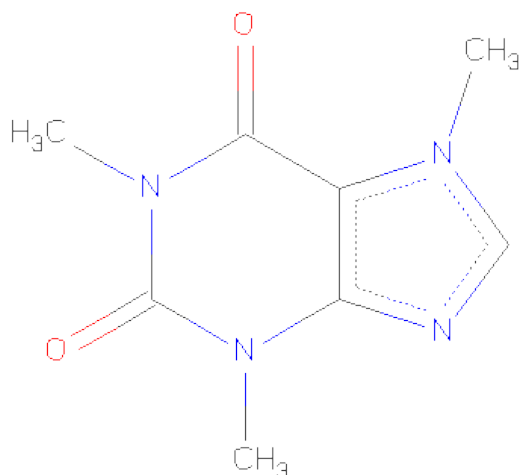
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



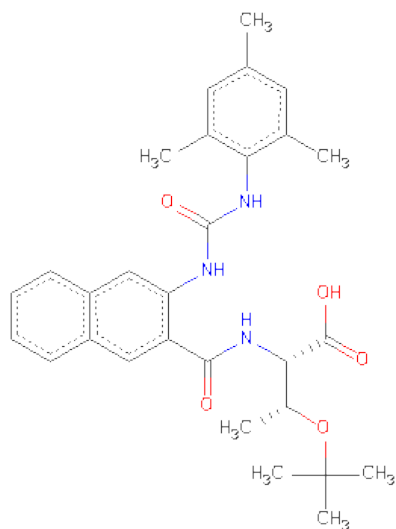
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 5 is CAFFEINE (three-letter code: CFF) (formula: $C_8H_{10}N_4O_2$).



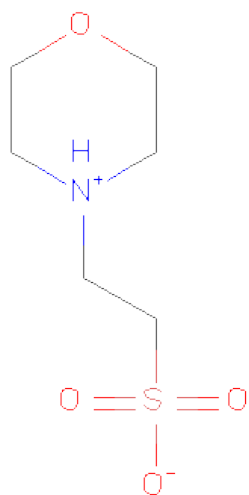
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	4	2		
5	B	1	Total	C	N	O	0	0
			14	8	4	2		

- Molecule 6 is O-TERT-BUTYL-N-[(3-{[(2,4,6-TRIMETHYLPHENYL)CARBAMOYL] AMINO}NAPHTHALEN-2-YL)CARBONYL]-L-THREONINE (three-letter code: 26B) (formula: $C_{29}H_{35}N_3O_5$).



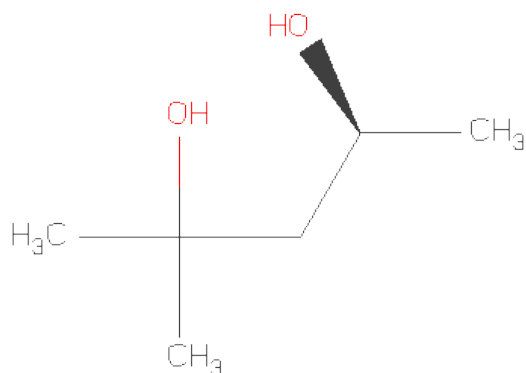
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			37	29	3	5		
6	B	1	Total	C	N	O	0	0
			37	29	3	5		
6	B	1	Total	C	N	O	0	0
			37	29	3	5		

- Molecule 7 is 2-(N-MORPHOLINO)-ETHANESULFONICACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 8 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 9 is water.

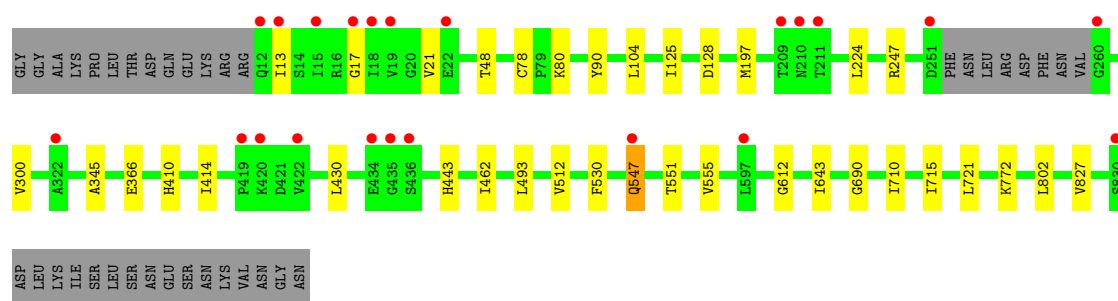
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	668	Total	O	0	0
			668	668		
9	B	685	Total	O	0	0
			685	685		

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 errors 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.

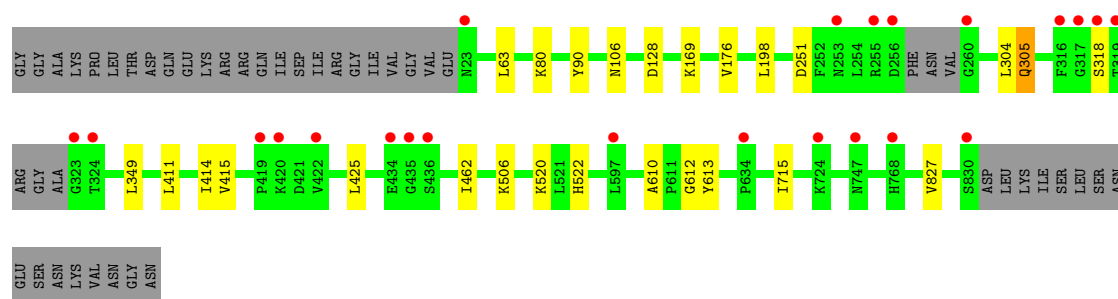
- Molecule 1: Glycogen phosphorylase, liver form

Chain A: 



- Molecule 1: Glycogen phosphorylase, liver form

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	124.40Å 124.40Å 123.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.66 – 1.80 15.49 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.9 (19.66-1.80) 96.9 (15.49-1.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.174 , 0.198 0.184 , 0.206	Depositor DCC
R_{free} test set	5803 reflections (3.12%)	DCC
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 63.0	EDS
Estimated twinning fraction	0.001 for -h,-k,l 0.016 for h,-h-k,-l 0.007 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 191942 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14698	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 26B, MPD, PLP, CFF, PO4, SEP, MES, NBG

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	0.38	0/6719	0.53	0/9094
1	B	0.38	0/6690	0.53	0/9052
All	All	0.38	0/13409	0.53	0/18146

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6582	0	6536	40	0
1	B	6539	0	6480	15	0
2	A	15	0	15	0	0
2	B	15	0	15	0	0
3	A	5	0	0	0	0
4	A	15	0	7	0	0
4	B	15	0	7	0	0
5	A	14	0	10	1	0
5	B	14	0	10	3	0
6	A	37	0	34	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	74	0	68	2	0
7	B	12	0	12	0	0
8	A	8	0	14	2	0
9	A	668	0	0	2	0
9	B	685	0	0	5	0
All	All	14698	0	13208	59	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (59) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:197[B]:MET:HE3	1:A:224[B]:LEU:HG	1.28	1.15
1:A:197[B]:MET:HE1	1:A:224[B]:LEU:CB	1.78	1.12
1:A:197[B]:MET:CE	1:A:224[B]:LEU:CB	2.29	1.10
1:A:197[B]:MET:HE1	1:A:224[B]:LEU:HB2	1.11	1.07
1:A:197[B]:MET:CE	1:A:224[B]:LEU:HB2	1.88	1.02
1:A:197[B]:MET:CE	1:A:224[B]:LEU:HG	1.96	0.96
1:A:197[B]:MET:CE	1:A:224[B]:LEU:CG	2.49	0.91
1:A:197[B]:MET:HE2	1:A:224[B]:LEU:CA	2.02	0.90
1:B:106:ASN:OD1	9:B:1591:HOH:O	1.91	0.87
1:A:197[B]:MET:HE2	1:A:224[B]:LEU:HA	1.55	0.86
1:A:547:GLN:NE2	9:A:1229:HOH:O	2.05	0.79
1:A:78[B]:CYS:SG	9:A:975:HOH:O	2.41	0.77
1:A:197[B]:MET:HE1	1:A:224[B]:LEU:CG	2.17	0.73
1:A:197[B]:MET:CE	1:A:224[B]:LEU:CA	2.64	0.70
1:A:493:LEU:HD21	1:A:512:VAL:HG22	1.75	0.68
1:A:13:ILE:HD12	1:A:104:LEU:CD2	2.26	0.66
1:A:547:GLN:O	1:A:551:THR:HG23	1.96	0.65
1:A:555[B]:VAL:HG11	1:A:643:ILE:HD11	1.78	0.65
1:B:198:LEU:HD13	1:B:305:GLN:HB3	1.82	0.61
1:A:493:LEU:HD11	1:A:512:VAL:HG11	1.85	0.58
1:B:304[A]:LEU:HD22	1:B:349:LEU:HD13	1.85	0.58
1:A:197[B]:MET:CE	1:A:224[B]:LEU:HA	2.29	0.58
1:B:522:HIS:NE2	9:B:1094:HOH:O	2.11	0.56
1:A:530:PHE:HE2	1:A:802:LEU:HD13	1.71	0.55
1:B:506:LYS:NZ	9:B:1183:HOH:O	2.40	0.55
1:A:13:ILE:HD12	1:A:104:LEU:HD23	1.91	0.52
1:B:411:LEU:HD23	1:B:414:ILE:HD12	1.91	0.52
1:A:555[A]:VAL:HG21	1:A:643:ILE:CD1	2.43	0.49
1:B:80:LYS:HB3	1:B:827:VAL:HG12	1.97	0.47
1:B:415:VAL:HG22	1:B:425:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:A:906:MPD:C1	8:A:906:MPD:O4	2.63	0.46
1:A:410:HIS:CE1	1:A:414:ILE:HD11	2.51	0.46
1:A:197[A]:MET:HE2	1:A:197[A]:MET:HB3	1.84	0.46
1:A:13:ILE:HD12	1:A:104:LEU:HD21	1.96	0.45
1:B:169:LYS:HB2	1:B:176:VAL:CG2	2.46	0.45
1:A:300:VAL:HG13	1:A:345:ALA:HA	1.98	0.45
1:B:612:GLY:C	5:B:903:CFF:H142	2.37	0.45
1:A:555[A]:VAL:HG21	1:A:643:ILE:HD11	1.97	0.45
1:B:520:LYS:NZ	9:B:1267:HOH:O	2.49	0.45
1:A:530:PHE:CE2	1:A:802:LEU:HD13	2.53	0.44
1:A:80:LYS:HB3	1:A:827:VAL:HG12	2.00	0.44
1:A:48:THR:HG22	1:A:125:ILE:HG13	1.99	0.44
6:B:906:26B:H5B	6:B:906:26B:H1	2.00	0.43
1:A:224[A]:LEU:HD22	1:A:247:ARG:HG3	2.00	0.43
1:A:300:VAL:CG1	1:A:345:ALA:HA	2.49	0.43
6:B:905:26B:H7	9:B:1585:HOH:O	2.18	0.42
1:A:493:LEU:HD11	1:A:512:VAL:CG1	2.49	0.42
1:A:430:LEU:HD22	1:A:443:HIS:HB3	2.01	0.42
1:A:612:GLY:C	5:A:904:CFF:H142	2.40	0.42
1:B:462:ILE:HD11	1:B:715:ILE:CD1	2.50	0.42
1:A:462:ILE:HD11	1:A:715:ILE:CD1	2.50	0.41
1:B:613:TYR:CE2	5:B:903:CFF:H123	2.54	0.41
1:B:63:LEU:C	1:B:63:LEU:HD12	2.41	0.41
1:B:610:ALA:CB	5:B:903:CFF:H81	2.51	0.40
1:A:17:GLY:O	1:A:21:VAL:HG23	2.21	0.40
8:A:906:MPD:H11	8:A:906:MPD:O4	2.20	0.40
1:A:721:LEU:HD23	1:A:772:LYS:HD3	2.03	0.40
1:A:690:GLY:O	1:A:710:ILE:HA	2.21	0.40
1:A:197[A]:MET:HE2	1:A:224[A]:LEU:HG	2.02	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	813/848 (96%)	794 (98%)	19 (2%)	0	100	100
1	B	805/848 (95%)	790 (98%)	15 (2%)	0	100	100
All	All	1618/1696 (95%)	1584 (98%)	34 (2%)	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	705/738 (96%)	701 (99%)	4 (1%)	92	90
1	B	703/738 (95%)	698 (99%)	5 (1%)	91	88
All	All	1408/1476 (95%)	1399 (99%)	9 (1%)	92	90

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90	TYR
1	A	128	ASP
1	A	366	GLU
1	A	547	GLN
1	B	90	TYR
1	B	128	ASP
1	B	251	ASP
1	B	305	GLN
1	B	318	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	106	ASN
1	B	539	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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	6.21	3 (33%)	10,12,14	0.94	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
1	SEP	A	14	1	-	0/6/8/10	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	14	SEP	O-C	18.01	1.23	1.11
1	A	14	SEP	P-O1P	3.06	1.61	1.51
1	A	14	SEP	CA-C	2.51	1.53	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

12 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	NBG	A	901	-	15,15,15	0.67	1 (6%)	21,21,21	0.98	1 (4%)
3	PO4	A	902	-	4,4,4	0.31	0	6,6,6	0.31	0
4	PLP	A	903	1	14,15,16	1.11	2 (14%)	20,22,23	0.87	0
5	CFF	A	904	-	15,15,15	2.45	6 (40%)	18,23,23	2.88	5 (27%)
6	26B	A	905	-	39,39,39	0.94	1 (2%)	57,57,57	1.06	3 (5%)
8	MPD	A	906	-	7,7,7	0.28	0	10,10,10	0.29	0
2	NBG	B	901	-	15,15,15	0.84	1 (6%)	21,21,21	1.11	2 (9%)
4	PLP	B	902	1	14,15,16	1.02	1 (7%)	20,22,23	0.89	0
5	CFF	B	903	-	15,15,15	2.59	7 (46%)	18,23,23	2.99	5 (27%)
7	MES	B	904	-	12,12,12	2.00	1 (8%)	16,16,16	2.14	3 (18%)
6	26B	B	905	-	39,39,39	0.93	1 (2%)	57,57,57	0.96	3 (5%)
6	26B	B	906	-	39,39,39	0.98	1 (2%)	57,57,57	1.01	2 (3%)

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	NBG	A	901	-	-	0/5/26/26	0/1/1/1
3	PO4	A	902	-	-	0/0/0/0	0/0/0/0
4	PLP	A	903	1	-	0/6/6/8	0/1/1/1
5	CFF	A	904	-	-	0/0/0/0	0/0/2/2
6	26B	A	905	-	-	0/29/29/29	0/1/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	MPD	A	906	-	-	0/5/5/5	0/0/0/0
2	NBG	B	901	-	-	0/5/26/26	0/1/1/1
4	PLP	B	902	1	-	0/6/6/8	0/1/1/1
5	CFF	B	903	-	-	0/0/0/0	0/0/2/2
7	MES	B	904	-	-	0/6/14/14	0/1/1/1
6	26B	B	905	-	-	0/29/29/29	0/1/3/3
6	26B	B	906	-	-	0/29/29/29	0/1/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	904	MES	C8-S	-6.10	1.67	1.78
5	B	903	CFF	C5-N7	-5.19	1.32	1.39
5	B	903	CFF	C4-N9	5.01	1.38	1.33
5	A	904	CFF	C4-N9	4.90	1.38	1.33
5	A	904	CFF	C5-N7	-4.82	1.33	1.39
5	B	903	CFF	C2-N1	3.61	1.42	1.38
5	B	903	CFF	C2-N3	-3.54	1.34	1.38
5	A	904	CFF	C2-N3	-3.17	1.34	1.38
5	A	904	CFF	C2-N1	3.06	1.41	1.38
2	B	901	NBG	C1-N1	3.00	1.46	1.43
5	A	904	CFF	C5-C4	-2.95	1.35	1.40
5	B	903	CFF	C5-C4	-2.76	1.36	1.40
5	A	904	CFF	C6-N1	2.53	1.42	1.35
5	B	903	CFF	C6-N1	2.50	1.42	1.35
4	A	903	PLP	C2-N1	2.47	1.38	1.33
2	A	901	NBG	C1-N1	2.32	1.46	1.43
6	B	906	26B	C8-N	2.19	1.39	1.34
4	B	902	PLP	C2-N1	2.15	1.37	1.33
6	B	905	26B	C8-N	2.14	1.38	1.34
5	B	903	CFF	C8-N9	2.10	1.38	1.34
6	A	905	26B	C8-N	2.08	1.38	1.34
4	A	903	PLP	C6-N1	2.05	1.39	1.34

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	903	CFF	N9-C4-N3	-7.42	123.27	128.19
5	A	904	CFF	N9-C4-N3	-7.18	123.43	128.19
7	B	904	MES	C5-N4-C3	6.76	123.15	109.75
5	B	903	CFF	C6-N1-C2	-5.44	119.78	121.69
5	B	903	CFF	C14-N7-C5	-5.36	118.89	125.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	904	CFF	C14-N7-C5	-5.15	119.15	125.61
5	A	904	CFF	C6-N1-C2	-5.10	119.90	121.69
5	B	903	CFF	N3-C2-N1	4.95	120.10	115.69
5	A	904	CFF	N3-C2-N1	4.92	120.07	115.69
5	B	903	CFF	C14-N7-C8	3.74	133.35	125.33
5	A	904	CFF	C14-N7-C8	3.60	133.06	125.33
6	B	906	26B	C4-O3-C2	-3.22	114.16	119.04
6	A	905	26B	C4-O3-C2	-3.18	114.23	119.04
7	B	904	MES	C7-N4-C5	2.85	119.12	111.66
6	B	906	26B	C1-C2-CA	-2.73	107.63	113.17
2	B	901	NBG	C3-C2-C1	2.54	113.70	109.91
6	A	905	26B	O3-C2-CA	2.50	110.63	106.45
6	B	905	26B	O3-C2-CA	2.40	110.46	106.45
6	B	905	26B	C4-O3-C2	-2.38	115.44	119.04
2	B	901	NBG	C1-N1-C7	2.36	125.02	122.44
7	B	904	MES	C7-N4-C3	2.32	117.72	111.66
2	A	901	NBG	O5-C1-C2	2.26	111.72	109.70
6	B	905	26B	C1-C2-CA	-2.20	108.70	113.17
6	A	905	26B	C1-C2-CA	-2.15	108.80	113.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	811/848 (95%)	-0.17	22 (2%)	52 44	22, 30, 46, 62	0
1	B	802/848 (94%)	-0.23	23 (2%)	49 41	21, 29, 46, 60	0
All	All	1613/1696 (95%)	-0.20	45 (2%)	50 43	21, 29, 46, 62	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	319	THR	7.9
1	B	318	SER	7.5
1	A	18	ILE	7.2
1	B	323	GLY	6.5
1	A	435	GLY	5.1
1	B	420	LYS	4.8
1	A	260	GLY	4.7
1	A	19	VAL	4.6
1	A	436	SER	4.6
1	B	256	ASP	4.4
1	A	322	ALA	4.3
1	A	434	GLU	4.3
1	B	435	GLY	4.3
1	A	420	LYS	4.2
1	B	434	GLU	4.1
1	A	830	SER	3.9
1	A	597	LEU	3.6
1	A	209	THR	3.6
1	B	324	THR	3.5
1	A	17	GLY	3.3
1	A	251	ASP	3.2
1	B	436	SER	3.2
1	A	12	GLN	3.2
1	B	260	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	597	LEU	3.1
1	B	255	ARG	3.0
1	A	210	ASN	3.0
1	B	768	HIS	3.0
1	B	422	VAL	2.9
1	A	13	ILE	2.9
1	B	316	PHE	2.9
1	A	15	ILE	2.9
1	B	634	PRO	2.9
1	B	317	GLY	2.7
1	A	422	VAL	2.4
1	B	830	SER	2.3
1	B	23	ASN	2.3
1	A	547	GLN	2.3
1	A	22	GLU	2.3
1	B	253	ASN	2.2
1	B	419	PRO	2.2
1	A	419	PRO	2.1
1	B	724	LYS	2.1
1	B	747	ASN	2.1
1	A	211	THR	2.0

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

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	SEP	A	14	10/11	0.27	0.72	58,59,60,60	0

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	26B	B	906	37/37	0.20	3.50	35,37,47,48	0
2	NBG	B	901	15/15	0.11	3.13	28,30,33,33	0
5	CFF	B	903	14/14	0.12	2.75	33,34,35,35	0
7	MES	B	904	12/12	0.20	2.46	44,47,49,49	0
5	CFF	A	904	14/14	0.10	2.27	32,33,34,34	0
8	MPD	A	906	8/8	0.17	2.23	40,42,43,43	0
4	PLP	A	903	15/16	0.08	1.02	23,24,29,31	0
4	PLP	B	902	15/16	0.07	0.43	23,25,29,31	0
6	26B	B	905	37/37	0.09	0.19	24,27,32,33	0
3	PO4	A	902	5/5	0.23	0.12	77,78,78,78	0
6	26B	A	905	37/37	0.08	0.02	23,26,30,31	0
2	NBG	A	901	15/15	0.06	-0.41	26,29,31,31	0

6.5 Other polymers ⓘ

There are no such residues in this entry.