



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 09:20 AM GMT

PDB ID : 3DD1
Title : Crystal structure of glycogen phosphorylase complexed with an anthranilimide based inhibitor GSK254
Authors : Nolte, R.T.
Deposited on : 2008-06-04
Resolution : 2.57 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>

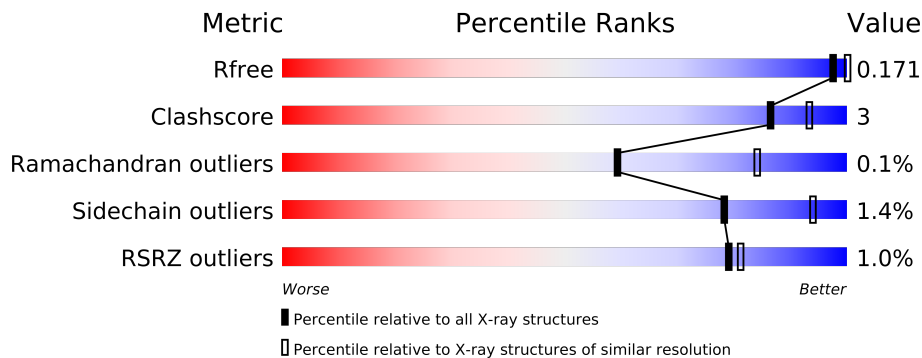
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.57 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	1891 (2.60-2.56)
Clashscore	79885	2358 (2.60-2.56)
Ramachandran outliers	78287	2316 (2.60-2.56)
Sidechain outliers	78261	2316 (2.60-2.56)
RSRZ outliers	66119	1891 (2.60-2.56)

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	A	901	-	X
2	NBG	B	901	-	X
6	MES	B	904	-	X
6	MES	B	905	-	X
7	MPD	A	908	-	X
7	MPD	B	907	-	X
7	MPD	B	908	-	X

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 13886 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.

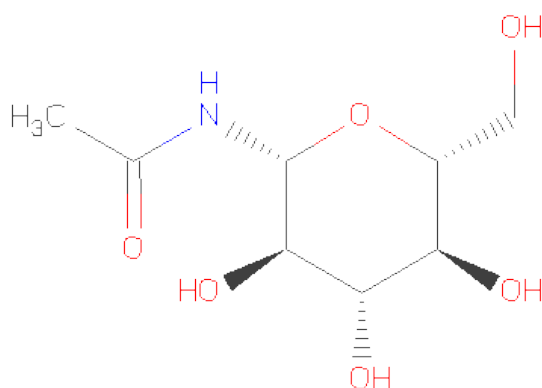
- Molecule 1 is a protein called Glycogen phosphorylase, liver form.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	811	Total	C	N	O	P	S	0	4	0
			6582	4217	1120	1214	1	30			
1	B	805	Total	C	N	O	S		0	3	0
			6538	4198	1107	1202	31				

There are 4 discrepancies between the modelled and reference sequences:

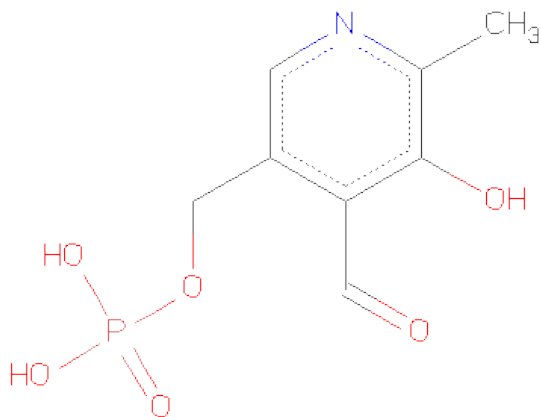
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P06737
A	0	GLY	-	EXPRESSION TAG	UNP P06737
B	-1	GLY	-	EXPRESSION TAG	UNP P06737
B	0	GLY	-	EXPRESSION TAG	UNP P06737

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



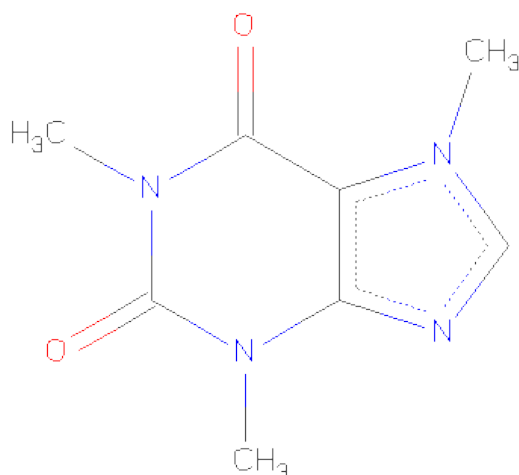
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



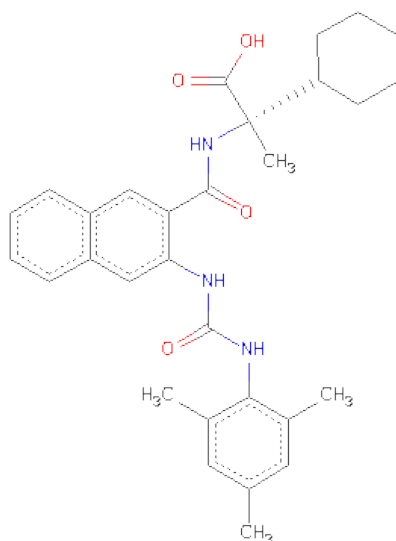
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 4 is CAFFEINE (three-letter code: CFF) (formula: C₈H₁₀N₄O₂).



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

- Molecule 5 is 2-CYCLOHEXYL-N-[(3-[(2,4,6-TRIMETHYLPHENYL)CARBAMOYL]AMINO}NAPHTHALEN-2-YL)CARBONYL]-D-ALANINE (three-letter code: 25D) (formula: $C_{30}H_{35}N_3O_4$).



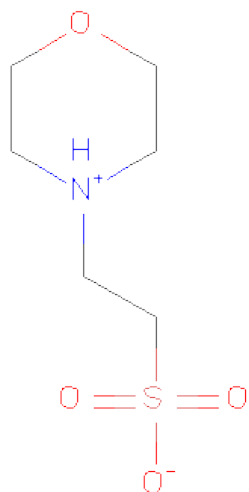
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			37	30	3	4		

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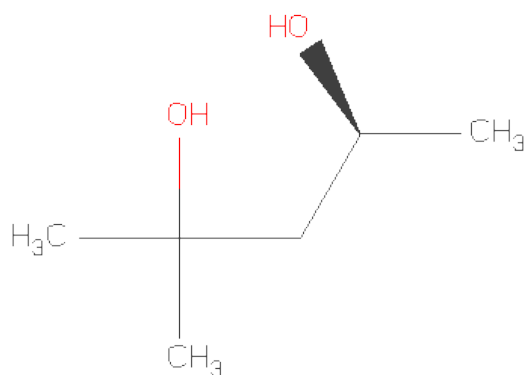
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			37	30	3	4		

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONICACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



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

- Molecule 7 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C₆H₁₄O₂).



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

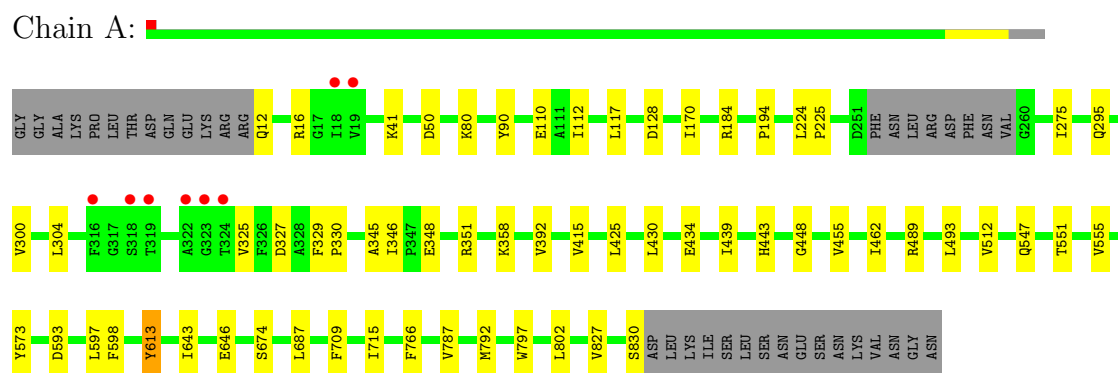
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	272	Total	O	0	0
			272	272		
8	B	268	Total	O	0	0
			268	268		

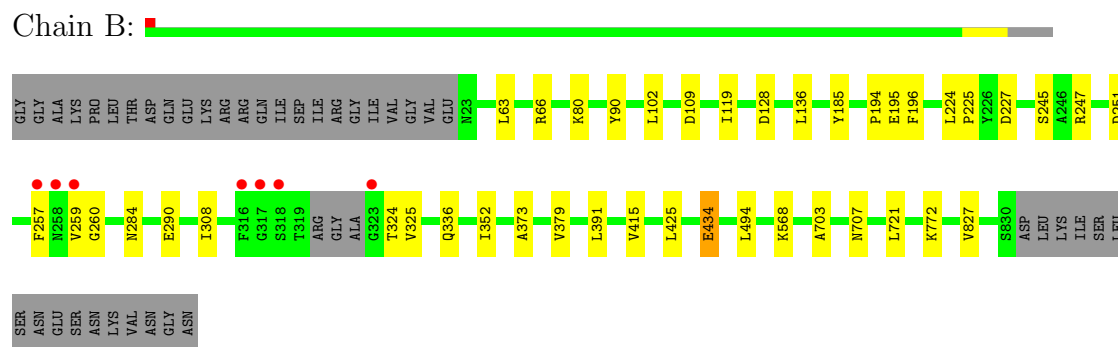
3 Residue-property plots

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



- Molecule 1: Glycogen phosphorylase, liver form



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	124.10Å 124.10Å 123.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.27 – 2.57 30.97 – 2.57	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.27-2.57) 100.0 (30.97-2.57)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.39 (at 2.57Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.167 , 0.207 0.154 , 0.171	Depositor DCC
R_{free} test set	2049 reflections (3.13%)	DCC
Wilson B-factor (Å ²)	38.4	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 17.6	EDS
Estimated twinning fraction	0.026 for -h,-k,l 0.097 for h,-h-k,-l 0.028 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 67542 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13886	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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: MPD, SEP, CFF, PLP, 25D, 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	0.36	0/6716	0.52	0/9084
1	B	0.36	0/6685	0.51	0/9044
All	All	0.36	0/13401	0.51	0/18128

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	6547	34	1
1	B	6538	0	6500	23	0
2	A	15	0	15	0	0
2	B	15	0	15	1	0
3	A	15	0	7	0	0
3	B	15	0	7	0	0
4	A	14	0	10	1	0
4	B	14	0	10	0	0
5	A	37	0	34	1	0
5	B	37	0	34	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	24	0	24	0	0
7	A	24	0	42	10	0
7	B	16	0	28	4	0
8	A	272	0	0	2	0
8	B	268	0	0	1	1
All	All	13886	0	13273	68	1

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 3.

All (68) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:A:906:MPD:HM1	7:A:906:MPD:H53	1.37	1.07
7:A:907:MPD:H11	7:A:907:MPD:H52	1.67	0.76
7:A:906:MPD:HM1	7:A:906:MPD:C5	2.16	0.73
1:B:194:PRO:HA	1:B:224:LEU:HD13	1.73	0.70
1:B:109[A]:ASP:OD1	1:B:119:ILE:HD13	1.92	0.69
1:B:308:ILE:HD13	1:B:352:ILE:HG21	1.82	0.60
1:B:415:VAL:HG22	1:B:425:LEU:HD11	1.85	0.58
5:B:906:25D:H5B	5:B:906:25D:H25B	1.86	0.56
7:B:907:MPD:H52	7:B:907:MPD:HM3	1.88	0.54
1:B:224:LEU:HD23	1:B:247:ARG:NH1	2.23	0.53
1:A:613:TYR:CE2	4:A:903:CFF:H123	2.43	0.53
1:A:351:ARG:HH12	7:A:906:MPD:HM2	1.72	0.53
1:A:766:PHE:CD1	7:A:908:MPD:H52	2.44	0.53
1:A:392:VAL:HG21	1:A:439:ILE:HD12	1.90	0.53
1:A:224:LEU:HD12	1:A:225:PRO:HD2	1.92	0.52
7:A:906:MPD:CM	8:A:1080:HOH:O	2.56	0.52
1:A:415:VAL:HG22	1:A:425:LEU:HD11	1.92	0.51
1:B:379:VAL:HG22	8:B:1083:HOH:O	2.10	0.51
1:B:336:GLN:OE1	1:B:373:ALA:HB3	2.12	0.50
1:A:346:ILE:HD13	1:A:448:GLY:HA3	1.94	0.50
1:B:284:ASN:OD1	2:B:901:NBG:H82	2.12	0.49
7:B:908:MPD:H12	7:B:908:MPD:H52	1.94	0.49
1:B:80:LYS:HB3	1:B:827:VAL:HG12	1.93	0.49
1:A:194:PRO:HB3	1:B:185:TYR:CD1	2.48	0.48
1:A:300:VAL:HG13	1:A:345:ALA:HA	1.94	0.48
1:B:109[A]:ASP:OD1	1:B:119:ILE:HG21	2.14	0.48
1:B:259:VAL:HG12	1:B:260:GLY:N	2.28	0.48
1:A:547:GLN:O	1:A:551:THR:HG23	2.13	0.47
1:A:80:LYS:HB3	1:A:827:VAL:HG12	1.95	0.47
1:A:766:PHE:CE1	7:A:908:MPD:H52	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:687:LEU:HD12	1:A:797:TRP:CH2	2.50	0.46
1:A:415:VAL:HG23	1:A:425:LEU:HD21	1.97	0.46
1:A:493:LEU:HD21	1:A:512:VAL:HG11	1.96	0.46
1:A:358:LYS:CG	7:A:907:MPD:H53	2.45	0.46
1:A:709:PHE:CD2	1:A:787:VAL:HG22	2.51	0.46
7:A:906:MPD:CM	7:A:906:MPD:H53	2.25	0.45
1:A:455:VAL:HG23	1:A:674:SER:HB2	1.99	0.45
7:B:907:MPD:H11	7:B:907:MPD:H52	1.99	0.45
1:A:170:ILE:HG12	1:A:646:GLU:HG2	1.97	0.45
1:B:66:ARG:NH2	1:B:102:LEU:HD22	2.32	0.44
1:A:304:LEU:HD12	1:A:348:GLU:CG	2.47	0.44
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.99	0.44
1:A:555:VAL:HG21	1:A:643:ILE:CD1	2.48	0.44
1:A:802:LEU:HD12	1:A:802:LEU:O	2.18	0.44
1:B:721:LEU:HD23	1:B:772:LYS:HD3	1.98	0.44
1:B:195:GLU:HG2	1:B:196:PHE:CD2	2.53	0.44
1:B:136:LEU:HD23	1:B:136:LEU:C	2.37	0.44
1:A:300:VAL:CG1	1:A:345:ALA:HA	2.48	0.44
1:B:227:ASP:OD2	5:B:906:25D:H1B	2.17	0.43
1:B:224:LEU:HD12	1:B:225:PRO:HD2	2.00	0.43
7:A:906:MPD:HM3	8:A:1080:HOH:O	2.18	0.43
1:A:275:ILE:O	1:A:295:GLN:HG2	2.18	0.43
1:B:494:LEU:C	1:B:494:LEU:HD23	2.38	0.43
1:A:434:GLU:N	1:A:434:GLU:OE1	2.52	0.43
7:B:907:MPD:H11	7:B:907:MPD:C5	2.49	0.43
5:A:905:25D:O22	5:A:905:25D:N10	2.49	0.42
1:B:703:ALA:O	1:B:707:ASN:ND2	2.46	0.42
1:B:194:PRO:CA	1:B:224:LEU:HD13	2.46	0.42
1:A:597:LEU:HD12	1:A:598:PHE:N	2.34	0.42
1:A:41:LYS:NZ	1:A:50:ASP:OD2	2.52	0.42
1:B:290:GLU:HG3	1:B:391:LEU:HD11	2.01	0.42
1:A:430:LEU:HD22	1:A:443:HIS:HB3	2.02	0.41
1:A:597:LEU:HD21	1:A:792:MET:SD	2.61	0.41
1:A:325:VAL:HG12	1:A:327:ASP:H	1.86	0.41
1:A:462:ILE:HD11	1:A:715:ILE:CD1	2.51	0.41
1:A:687:LEU:HD12	1:A:797:TRP:CZ3	2.56	0.40
1:A:112:ILE:HG23	1:A:117:LEU:HB2	2.03	0.40
1:B:63:LEU:HD12	1:B:63:LEU:C	2.42	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	Distance(Å)	Clash(Å)
1:A:110:GLU:OE1	8:B:974:HOH:O[2_535]	2.15	0.05

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	810/848 (96%)	791 (98%)	19 (2%)	0	100	100
1	B	804/848 (95%)	783 (97%)	20 (2%)	1 (0%)	59	84
All	All	1614/1696 (95%)	1574 (98%)	39 (2%)	1 (0%)	59	84

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	434	GLU

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	706/738 (96%)	696 (99%)	10 (1%)	78	94
1	B	704/738 (95%)	695 (99%)	9 (1%)	80	94
All	All	1410/1476 (96%)	1391 (99%)	19 (1%)	78	94

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	16	ARG
1	A	90	TYR
1	A	128	ASP

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Mol	Chain	Res	Type
1	A	184	ARG
1	A	489	ARG
1	A	573	TYR
1	A	593	ASP
1	A	613	TYR
1	A	830	SER
1	B	90	TYR
1	B	128	ASP
1	B	245	SER
1	B	251	ASP
1	B	257	PHE
1	B	324	THR
1	B	325	VAL
1	B	434	GLU
1	B	568	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	408	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	6.25	3 (33%)	10,12,14	0.87	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	18.06	1.23	1.11
1	A	14	SEP	P-O1P	3.22	1.62	1.51
1	A	14	SEP	CA-C	2.54	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 ⓘ

15 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	0.84	1 (6%)	21,21,21	0.73	0
3	PLP	A	902	1	14,15,16	1.06	1 (7%)	20,22,23	0.90	0
4	CFF	A	903	-	15,15,15	2.54	6 (40%)	18,23,23	3.02	5 (27%)
5	25D	A	905	-	40,40,40	0.97	0	58,58,58	1.28	7 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	MPD	A	906	-	7,7,7	0.30	0	10,10,10	0.42	0
7	MPD	A	907	-	7,7,7	0.33	0	10,10,10	0.31	0
7	MPD	A	908	-	7,7,7	0.25	0	10,10,10	0.30	0
2	NBG	B	901	-	15,15,15	0.71	1 (6%)	21,21,21	0.71	0
3	PLP	B	902	1	14,15,16	0.97	1 (7%)	20,22,23	0.90	0
4	CFF	B	903	-	15,15,15	2.61	6 (40%)	18,23,23	3.09	5 (27%)
6	MES	B	904	-	12,12,12	1.96	1 (8%)	16,16,16	2.14	5 (31%)
6	MES	B	905	-	12,12,12	2.02	1 (8%)	16,16,16	2.27	6 (37%)
5	25D	B	906	-	40,40,40	1.06	1 (2%)	58,58,58	1.01	3 (5%)
7	MPD	B	907	-	7,7,7	0.29	0	10,10,10	0.29	0
7	MPD	B	908	-	7,7,7	0.26	0	10,10,10	0.24	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NBG	A	901	-	-	0/5/26/26	0/1/1/1
3	PLP	A	902	1	-	0/6/6/8	0/1/1/1
4	CFF	A	903	-	-	0/0/0/0	0/0/2/2
5	25D	A	905	-	-	0/29/37/37	0/2/4/4
7	MPD	A	906	-	-	0/5/5/5	0/0/0/0
7	MPD	A	907	-	-	0/5/5/5	0/0/0/0
7	MPD	A	908	-	-	0/5/5/5	0/0/0/0
2	NBG	B	901	-	-	0/5/26/26	0/1/1/1
3	PLP	B	902	1	-	0/6/6/8	0/1/1/1
4	CFF	B	903	-	-	0/0/0/0	0/0/2/2
6	MES	B	904	-	-	0/6/14/14	0/1/1/1
6	MES	B	905	-	-	0/6/14/14	0/1/1/1
5	25D	B	906	-	-	0/29/37/37	0/2/4/4
7	MPD	B	907	-	-	0/5/5/5	0/0/0/0
7	MPD	B	908	-	-	0/5/5/5	0/0/0/0

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	905	MES	C8-S	-6.10	1.67	1.78
6	B	904	MES	C8-S	-5.94	1.67	1.78
4	B	903	CFF	C4-N9	5.12	1.38	1.33
4	A	903	CFF	C4-N9	5.03	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	903	CFF	C5-N7	-5.01	1.32	1.39
4	A	903	CFF	C5-N7	-4.67	1.33	1.39
4	B	903	CFF	C2-N1	3.96	1.42	1.38
4	A	903	CFF	C2-N1	3.86	1.42	1.38
4	B	903	CFF	C2-N3	-3.44	1.34	1.38
4	A	903	CFF	C2-N3	-3.31	1.34	1.38
4	A	903	CFF	C5-C4	-3.21	1.35	1.40
2	A	901	NBG	C1-N1	3.02	1.46	1.43
4	B	903	CFF	C5-C4	-3.02	1.35	1.40
3	A	902	PLP	C2-N1	2.73	1.38	1.33
5	B	906	25D	C21-N23	2.70	1.39	1.34
2	B	901	NBG	C1-N1	2.57	1.46	1.43
4	A	903	CFF	C6-N1	2.52	1.42	1.35
4	B	903	CFF	C6-N1	2.47	1.42	1.35
3	B	902	PLP	C2-N1	2.34	1.38	1.33

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	903	CFF	N9-C4-N3	-6.89	123.62	128.19
4	A	903	CFF	N9-C4-N3	-6.66	123.77	128.19
4	A	903	CFF	C6-N1-C2	-6.44	119.43	121.69
4	B	903	CFF	C6-N1-C2	-6.04	119.57	121.69
4	B	903	CFF	C14-N7-C5	-5.94	118.17	125.61
4	A	903	CFF	C14-N7-C5	-5.54	118.67	125.61
4	B	903	CFF	N3-C2-N1	5.44	120.54	115.69
6	B	904	MES	C5-N4-C3	5.37	120.41	109.75
4	A	903	CFF	N3-C2-N1	5.17	120.30	115.69
6	B	905	MES	C5-N4-C3	4.86	119.38	109.75
4	B	903	CFF	C14-N7-C8	4.03	133.99	125.33
4	A	903	CFF	C14-N7-C8	3.85	133.59	125.33
6	B	905	MES	C7-N4-C3	3.37	120.47	111.66
5	A	905	25D	C26-C24-C32	3.31	114.57	109.07
5	A	905	25D	C26-C24-N23	-3.29	101.90	107.56
6	B	905	MES	C7-N4-C5	3.25	120.15	111.66
6	B	904	MES	C7-N4-C3	3.22	120.07	111.66
5	A	905	25D	C28-C27-C26	-3.08	106.84	112.46
6	B	904	MES	C7-N4-C5	3.01	119.52	111.66
6	B	905	MES	C2-C3-N4	-2.90	106.24	109.96
6	B	905	MES	C6-C5-N4	-2.90	106.24	109.96
5	A	905	25D	C25-C24-N23	2.90	113.85	109.46
6	B	905	MES	C8-C7-N4	-2.65	107.91	112.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	905	25D	C30-C31-C26	-2.54	107.83	112.46
5	A	905	25D	C32-C24-N23	-2.52	103.98	108.64
5	B	906	25D	C26-C24-N23	2.47	111.80	107.56
5	B	906	25D	O33-C32-C24	-2.46	118.51	123.04
6	B	904	MES	C8-C7-N4	-2.32	108.47	112.44
5	A	905	25D	O33-C32-C24	-2.06	119.26	123.04
6	B	904	MES	C6-C5-N4	-2.03	107.35	109.96
5	B	906	25D	O22-C21-N23	2.01	126.13	122.35

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%)	-0.34	8 (0%) 79 81	34, 43, 62, 79	0
1	B	805/848 (94%)	-0.36	7 (0%) 81 83	34, 43, 61, 74	0
All	All	1616/1696 (95%)	-0.35	15 (0%) 79 83	34, 43, 62, 79	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	257	PHE	4.6
1	A	316	PHE	4.2
1	B	258	ASN	3.8
1	A	323	GLY	3.7
1	A	322	ALA	3.7
1	B	259	VAL	3.5
1	A	319	THR	3.4
1	A	324	THR	3.2
1	A	18	ILE	3.0
1	B	318	SER	2.7
1	B	323	GLY	2.5
1	A	19	VAL	2.3
1	A	318	SER	2.3
1	B	317	GLY	2.2
1	B	316	PHE	2.1

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(\AA^2)	Q<0.9
1	SEP	A	14	10/11	0.22	1.09	76,77,79,79	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(\AA^2)	Q<0.9
7	MPD	B	908	8/8	0.37	44.45	102,102,102,102	0
7	MPD	B	907	8/8	0.37	13.24	88,89,89,89	0
2	NBG	B	901	15/15	0.31	10.83	77,78,79,79	0
6	MES	B	905	12/12	0.23	6.92	83,83,84,84	0
2	NBG	A	901	15/15	0.20	5.33	62,64,65,65	0
7	MPD	A	908	8/8	0.28	3.04	77,77,77,77	0
6	MES	B	904	12/12	0.20	2.77	74,74,75,75	0
7	MPD	A	906	8/8	0.18	1.74	59,60,60,60	0
4	CFF	B	903	14/14	0.14	1.26	51,51,51,51	0
5	25D	B	906	37/37	0.15	0.95	37,41,48,48	0
7	MPD	A	907	8/8	0.20	0.60	67,68,68,69	0
4	CFF	A	903	14/14	0.13	0.15	49,49,50,50	0
5	25D	A	905	37/37	0.13	-0.06	37,41,47,47	0
3	PLP	B	902	15/16	0.10	-0.76	38,39,40,40	0
3	PLP	A	902	15/16	0.10	-0.78	35,35,37,37	0

6.5 Other polymers ⓘ

There are no such residues in this entry.