



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 07:56 AM GMT

PDB ID : 4A09
Title : STRUCTURE OF HSDDDB1-DRDDB2 BOUND TO A 15 BP CPD-DUPLEX
(PURINE AT D-1 POSITION) AT 3.1 Å RESOLUTION (CPD 2)
Authors : Scrima, A.; Fischer, E.S.; Iwai, S.; Gut, H.; Thoma, N.H.
Deposited on : 2011-09-08
Resolution : 3.10 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>

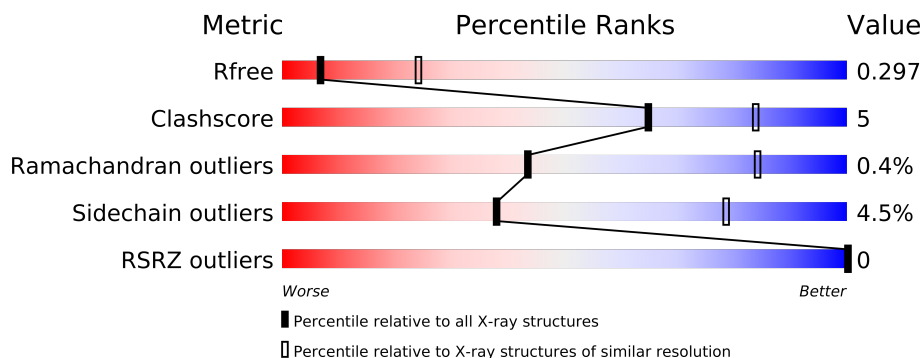
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.10 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	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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	1159	
2	B	382	
3	G	14	
4	H	16	

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

Mol	Type	Chain	Res	Geometry	Electron density
5	CA	B	1456	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12113 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 DNA DAMAGE-BINDING PROTEIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1105	Total	C	N	O	S	0	0	0
			8646	5484	1453	1662	47			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	EXPRESSION TAG	UNP Q16531
A	-17	HIS	-	EXPRESSION TAG	UNP Q16531
A	-16	HIS	-	EXPRESSION TAG	UNP Q16531
A	-15	HIS	-	EXPRESSION TAG	UNP Q16531
A	-14	HIS	-	EXPRESSION TAG	UNP Q16531
A	-13	HIS	-	EXPRESSION TAG	UNP Q16531
A	-12	HIS	-	EXPRESSION TAG	UNP Q16531
A	-11	VAL	-	EXPRESSION TAG	UNP Q16531
A	-10	ASP	-	EXPRESSION TAG	UNP Q16531
A	-9	GLU	-	EXPRESSION TAG	UNP Q16531
A	-8	ASN	-	EXPRESSION TAG	UNP Q16531
A	-7	LEU	-	EXPRESSION TAG	UNP Q16531
A	-6	TYR	-	EXPRESSION TAG	UNP Q16531
A	-5	PHE	-	EXPRESSION TAG	UNP Q16531
A	-4	GLN	-	EXPRESSION TAG	UNP Q16531
A	-3	GLY	-	EXPRESSION TAG	UNP Q16531
A	-2	GLY	-	EXPRESSION TAG	UNP Q16531
A	-1	GLY	-	EXPRESSION TAG	UNP Q16531
A	0	ARG	-	EXPRESSION TAG	UNP Q16531
A	194	ALA	GLU	ENGINEERED MUTATION	UNP Q16531

- Molecule 2 is a protein called DNA DAMAGE-BINDING PROTEIN 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	354	Total	C	N	O	S	0	0	0
			2839	1804	498	526	11			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	76	MET	-	EXPRESSION TAG	UNP Q2YDS1
B	77	HIS	-	EXPRESSION TAG	UNP Q2YDS1
B	78	HIS	-	EXPRESSION TAG	UNP Q2YDS1
B	79	HIS	-	EXPRESSION TAG	UNP Q2YDS1
B	80	HIS	-	EXPRESSION TAG	UNP Q2YDS1
B	81	HIS	-	EXPRESSION TAG	UNP Q2YDS1
B	82	HIS	-	EXPRESSION TAG	UNP Q2YDS1
B	83	ARG	-	EXPRESSION TAG	UNP Q2YDS1
B	84	ARG	-	EXPRESSION TAG	UNP Q2YDS1
B	85	LEU	-	EXPRESSION TAG	UNP Q2YDS1
B	86	VAL	-	EXPRESSION TAG	UNP Q2YDS1
B	87	PRO	-	EXPRESSION TAG	UNP Q2YDS1
B	88	ARG	-	EXPRESSION TAG	UNP Q2YDS1
B	89	GLY	-	EXPRESSION TAG	UNP Q2YDS1
B	90	SER	-	EXPRESSION TAG	UNP Q2YDS1
B	91	GLY	-	EXPRESSION TAG	UNP Q2YDS1
B	92	GLY	-	EXPRESSION TAG	UNP Q2YDS1
B	93	ARG	-	EXPRESSION TAG	UNP Q2YDS1
B	180	GLN	LEU	VARIANT	UNP Q2YDS1
B	214	ARG	TRP	VARIANT	UNP Q2YDS1

- Molecule 3 is a DNA chain called 5'-D(*GP*GP*TP*GP*AP*AP*AP*(TTD)P*AP*GP*C P*AP*GP*GP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	14	Total	C	N	O	P	0	0	0
			313	149	64	86	14			

- Molecule 4 is a DNA chain called 5'-D(*CP*CP*TP*GP*CP*TP*CP*CP*TP*TP*TP*CP *AP*CP*CP*C)-3'.

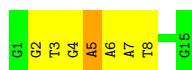
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	15	Total	C	N	O	P	0	0	0
			292	142	44	92	14			

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		

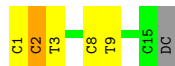
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	16	Total 16	O 16	0	0
6	B	4	Total 4	O 4	0	0
6	G	2	Total 2	O 2	0	0



- Molecule 4: 5'-D(*CP*CP*TP*GP*CP*TP*CP*CP*TP*TP*TP*CP*AP*CP*CP*C)-3'

Chain H:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	111.65Å 122.94Å 154.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.27 – 3.10 48.27 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.27-3.10) 99.8 (48.27-3.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.55 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.245 , 0.308 0.239 , 0.297	Depositor DCC
R_{free} test set	1955 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 9.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 39092 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	12113	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% 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: CA, TTD

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	0.32	0/8803	0.51	0/11924
2	B	0.32	0/2913	0.52	0/3957
3	G	0.61	0/308	1.03	1/473 (0.2%)
4	H	0.77	0/323	1.24	1/494 (0.2%)
All	All	0.35	0/12347	0.56	2/16848 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	5	DA	P-O3'-C3'	5.15	125.88	119.70
4	H	2	DC	P-O3'-C3'	5.01	125.71	119.70

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	8646	0	8626	80	0
2	B	2839	0	2785	38	0
3	G	313	0	170	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	292	0	172	4	0
5	B	1	0	0	0	0
6	A	16	0	0	0	0
6	B	4	0	0	0	0
6	G	2	0	0	0	0
All	All	12113	0	11753	126	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 5.

All (126) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:81:THR:HG22	1:A:83:LYS:H	1.41	0.86
1:A:167:VAL:HG12	1:A:180:PHE:HB3	1.65	0.78
1:A:482:GLU:HB3	1:A:483:PRO:HD3	1.67	0.75
1:A:184:ASP:HB2	1:A:185:PRO:HD2	1.70	0.71
1:A:329:GLY:HA3	1:A:384:GLU:HG2	1.73	0.70
2:B:141:ARG:HG2	2:B:141:ARG:HH11	1.55	0.70
2:B:249:ARG:HE	2:B:291:ASP:HB3	1.58	0.68
4:H:1:DC:H2"	4:H:2:DC:C5	2.29	0.67
2:B:323:HIS:NE2	2:B:342:THR:HG21	2.10	0.66
2:B:350:ARG:HG2	2:B:363:ILE:HG12	1.77	0.65
4:H:1:DC:H2"	4:H:2:DC:H5	1.62	0.65
1:A:654:ASP:HA	1:A:675:GLU:HG3	1.78	0.64
1:A:18:CYS:HB2	1:A:313:CYS:SG	2.37	0.64
1:A:1051:LEU:HB2	1:A:1089:ILE:HD13	1.80	0.64
1:A:507:GLN:NE2	1:A:553:SER:H	1.93	0.64
1:A:197:LEU:H	1:A:197:LEU:HD23	1.63	0.62
1:A:413:LEU:HB3	1:A:424:THR:HB	1.82	0.62
1:A:656:PRO:HB2	1:A:671:VAL:HB	1.82	0.61
2:B:211:SER:HB3	2:B:243:VAL:HG13	1.82	0.60
1:A:839:GLU:H	2:B:103:THR:HG21	1.66	0.60
2:B:193:ASP:HB2	2:B:214:ARG:HD3	1.84	0.59
1:A:402:ILE:HG22	1:A:404:LEU:HD13	1.83	0.59
2:B:443:SER:HB2	2:B:450:LEU:HB2	1.84	0.58
2:B:263:LEU:HB2	2:B:272:PHE:HB3	1.84	0.57
1:A:953:TRP:HB2	1:A:970:ASN:HB2	1.85	0.57
1:A:16:ASN:HD22	1:A:36:ASN:H	1.53	0.56
2:B:307:ASP:OD1	2:B:309:ARG:HG2	2.05	0.55
1:A:476:VAL:HG13	1:A:490:TRP:HB3	1.88	0.55
2:B:305:LEU:HD12	2:B:319:ALA:HB3	1.89	0.54
1:A:273:LEU:HB2	1:A:281:PHE:HB2	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:969:GLU:HG2	1:A:970:ASN:N	2.22	0.53
2:B:369:ARG:HH21	2:B:395:ASP:HA	1.73	0.53
2:B:140:HIS:HB2	2:B:453:ASN:HB2	1.91	0.53
2:B:134:LEU:HA	2:B:137:TYR:CD1	2.45	0.52
1:A:1089:ILE:HG21	1:A:1094:ILE:HD11	1.91	0.51
2:B:279:ALA:HB1	2:B:299:VAL:HG23	1.90	0.51
2:B:388:ILE:O	2:B:408:ILE:HA	2.10	0.51
2:B:367:PRO:HG2	2:B:392:ARG:HG3	1.92	0.51
1:A:567:ARG:HH11	1:A:576:LEU:HD21	1.76	0.51
1:A:1102:ARG:N	1:A:1103:PRO:HD2	2.26	0.51
1:A:504:ASN:HD22	1:A:506:SER:H	1.59	0.50
1:A:905:HIS:CD2	1:A:933:LEU:HD21	2.47	0.50
1:A:870:VAL:HA	1:A:883:SER:O	2.12	0.49
1:A:81:THR:HB	1:A:85:ASN:HB2	1.93	0.49
1:A:507:GLN:HE22	1:A:553:SER:H	1.58	0.49
2:B:102:GLN:O	2:B:103:THR:HG22	2.13	0.49
2:B:141:ARG:CG	2:B:141:ARG:HH11	2.21	0.49
2:B:260:ARG:HA	2:B:275:LYS:HA	1.95	0.49
2:B:289:ARG:HD2	2:B:337:SER:HB2	1.95	0.49
1:A:684:SER:HB3	1:A:687:TYR:HB2	1.95	0.48
1:A:184:ASP:HB2	1:A:185:PRO:CD	2.40	0.48
1:A:504:ASN:ND2	1:A:506:SER:H	2.10	0.48
1:A:452:VAL:HB	1:A:470:GLN:HE22	1.78	0.48
1:A:851:PHE:HB3	1:A:858:LEU:HD22	1.96	0.48
1:A:813:ALA:HA	1:A:833:THR:HG22	1.96	0.47
1:A:285:LEU:HB3	1:A:297:LEU:HD11	1.96	0.47
2:B:307:ASP:HB2	2:B:318:ILE:HD11	1.97	0.47
1:A:929:SER:HB2	1:A:950:ASN:O	2.14	0.47
2:B:441:LEU:HB3	2:B:452:TRP:HB2	1.97	0.47
1:A:329:GLY:HA3	1:A:384:GLU:CG	2.41	0.46
2:B:242:CYS:O	2:B:254:THR:HG23	2.14	0.46
1:A:124:ILE:HG12	1:A:131:ILE:HG12	1.98	0.46
1:A:1030:PHE:CZ	1:A:1038:GLY:HA3	2.51	0.46
3:G:4:DG:H2''	3:G:5:DA:C8	2.51	0.46
4:H:2:DC:C2'	4:H:3:DT:H71	2.46	0.46
1:A:459:PHE:HB3	1:A:471:ILE:HD12	1.98	0.46
2:B:279:ALA:CB	2:B:299:VAL:HG23	2.46	0.45
2:B:382:HIS:CG	2:B:383:PRO:HD2	2.51	0.45
1:A:1089:ILE:CG2	1:A:1094:ILE:HD11	2.46	0.45
1:A:731:GLN:HA	1:A:796:GLN:NE2	2.32	0.45
1:A:1100:ILE:HD12	1:A:1104:LYS:HB3	1.99	0.45
1:A:507:GLN:HE22	1:A:553:SER:N	2.15	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:891:TYR:HB3	1:A:899:LEU:HG	1.98	0.45
1:A:731:GLN:HA	1:A:796:GLN:HE21	1.81	0.44
1:A:928:ARG:HG2	1:A:947:ARG:HH12	1.82	0.44
1:A:374:GLN:HE21	1:A:391:ARG:HB2	1.82	0.44
3:G:8:TTD:O4'	3:G:8:TTD:O2	2.36	0.44
1:A:282:MET:HB2	1:A:305:LEU:HD11	1.99	0.44
2:B:333:ASN:HB3	2:B:381:TRP:CE2	2.52	0.44
1:A:181:VAL:HA	1:A:189:HIS:O	2.18	0.44
2:B:148:ARG:HA	2:B:447:PHE:CE2	2.52	0.44
1:A:436:LEU:HA	1:A:445:GLU:HA	2.00	0.44
1:A:649:VAL:HG22	1:A:659:ILE:HB	2.00	0.44
1:A:463:VAL:HB	1:A:521:ILE:HG21	2.00	0.43
2:B:334:PRO:HG2	2:B:383:PRO:HA	1.99	0.43
2:B:405:THR:HG22	2:B:421:ARG:HB2	1.99	0.43
2:B:141:ARG:NH1	2:B:141:ARG:CG	2.80	0.43
1:A:1000:LEU:HD11	1:A:1030:PHE:CE1	2.53	0.43
1:A:10:GLN:HB3	1:A:1037:ILE:HB	2.01	0.43
1:A:564:ILE:HG23	1:A:588:PRO:HD3	2.00	0.43
1:A:258:ILE:HD13	1:A:273:LEU:HD13	2.01	0.43
2:B:394:PRO:HB3	2:B:402:ASP:HB3	2.00	0.43
1:A:472:THR:HG23	1:A:475:SER:H	1.84	0.43
1:A:372:GLN:HA	1:A:1014:MET:HG2	2.00	0.43
3:G:2:DG:H2''	3:G:3:DT:OP2	2.18	0.43
1:A:889:ARG:HD2	1:A:891:TYR:CZ	2.54	0.43
1:A:600:HIS:CD2	1:A:618:ILE:HG12	2.54	0.43
1:A:22:HIS:HA	1:A:30:ASN:HD22	1.84	0.43
1:A:504:ASN:HD21	1:A:507:GLN:HG2	1.83	0.43
2:B:272:PHE:CZ	2:B:274:GLU:HB2	2.54	0.42
2:B:217:THR:OG1	2:B:254:THR:HG21	2.19	0.42
1:A:33:ILE:HD12	1:A:42:TYR:HE2	1.83	0.42
4:H:8:DC:H1'	4:H:9:DT:H71	2.02	0.42
1:A:265:ASP:OD2	1:A:269:SER:HB2	2.19	0.42
2:B:367:PRO:HB2	2:B:393:TYR:O	2.20	0.42
2:B:325:LYS:HB3	2:B:326:PRO:HD2	2.00	0.42
1:A:396:ILE:HG12	1:A:673:LEU:HD11	2.01	0.42
1:A:921:ILE:HB	1:A:933:LEU:HB2	2.02	0.42
1:A:928:ARG:HG2	1:A:947:ARG:NH1	2.35	0.42
1:A:455:GLN:HB3	1:A:472:THR:OG1	2.19	0.41
2:B:128:GLU:N	2:B:129:PRO:HD2	2.35	0.41
3:G:6:DA:H2''	3:G:7:DA:OP2	2.20	0.41
3:G:8:TTD:H6	3:G:8:TTD:H2''	1.68	0.41
1:A:1074:ARG:O	1:A:1085:ALA:HB2	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:743:GLN:HA	1:A:749:THR:HG22	2.02	0.41
1:A:108:VAL:HG11	1:A:143:ILE:HD11	2.02	0.41
1:A:765:VAL:HG12	1:A:806:GLN:HB3	2.03	0.41
1:A:81:THR:CG2	1:A:82:ALA:N	2.83	0.41
1:A:644:LEU:HG	1:A:645:SER:H	1.86	0.41
1:A:571:LEU:HD23	1:A:571:LEU:HA	1.90	0.41
1:A:6:VAL:HG22	1:A:1040:VAL:HG22	2.02	0.41
1:A:81:THR:HG22	1:A:82:ALA:N	2.35	0.40
2:B:382:HIS:CD2	2:B:383:PRO:HD2	2.56	0.40
1:A:408:LYS:HA	1:A:678:TYR:CE2	2.55	0.40
1:A:311:ALA:HB2	1:A:324:VAL:HG13	2.02	0.40
1:A:465:HIS:CD2	1:A:523:PRO:HD3	2.57	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	1095/1159 (94%)	1011 (92%)	80 (7%)	4 (0%)	43	84
2	B	352/382 (92%)	327 (93%)	23 (6%)	2 (1%)	33	78
All	All	1447/1541 (94%)	1338 (92%)	103 (7%)	6 (0%)	43	84

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	407	ILE
1	A	417	PRO
1	A	688	PRO
2	B	193	ASP
2	B	118	ILE
1	A	564	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	967/1014 (95%)	923 (95%)	44 (5%)	37	78
2	B	313/335 (93%)	300 (96%)	13 (4%)	40	81
All	All	1280/1349 (95%)	1223 (96%)	57 (4%)	38	78

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	18	CYS
1	A	54	GLU
1	A	207	TRP
1	A	235	GLU
1	A	241	ASN
1	A	304	LEU
1	A	312	GLU
1	A	314	LEU
1	A	318	ASP
1	A	319	ASN
1	A	334	VAL
1	A	343	GLN
1	A	392	ASN
1	A	449	MET
1	A	476	VAL
1	A	478	LEU
1	A	563	ASP
1	A	576	LEU
1	A	587	ILE
1	A	594	THR
1	A	618	ILE
1	A	626	ARG
1	A	636	THR
1	A	639	ARG
1	A	644	LEU
1	A	695	ASN
1	A	708	GLN
1	A	728	GLU

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Mol	Chain	Res	Type
1	A	867	LYS
1	A	881	LEU
1	A	887	THR
1	A	898	GLU
1	A	901	THR
1	A	914	LEU
1	A	969	GLU
1	A	970	ASN
1	A	993	GLN
1	A	1000	LEU
1	A	1050	LEU
1	A	1052	LEU
1	A	1086	THR
1	A	1093	LEU
1	A	1106	GLN
2	B	103	THR
2	B	116	GLN
2	B	148	ARG
2	B	202	GLN
2	B	262	LEU
2	B	274	GLU
2	B	293	LEU
2	B	308	LEU
2	B	312	LYS
2	B	374	LEU
2	B	389	VAL
2	B	393	TYR
2	B	453	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	30	ASN
1	A	85	ASN
1	A	156	ASN
1	A	234	GLN
1	A	240	HIS
1	A	241	ASN
1	A	267	ASN
1	A	374	GLN
1	A	392	ASN

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Mol	Chain	Res	Type
1	A	456	GLN
1	A	481	GLN
1	A	504	ASN
1	A	522	HIS
1	A	683	ASN
1	A	727	GLN
1	A	796	GLN
1	A	806	GLN
1	A	809	GLN
1	A	885	ASN
1	A	950	ASN
1	A	970	ASN
1	A	990	GLN
1	A	1034	ASN
1	A	1049	ASN
1	A	1055	GLN
1	A	1106	GLN
2	B	102	GLN
2	B	107	HIS
2	B	119	HIS
2	B	159	HIS
2	B	181	ASN
2	B	269	HIS
2	B	370	GLN
2	B	424	ASN
2	B	453	ASN

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
3	TTD	G	8	3	43,45,46	2.32	7 (16%)	71,74,77	2.43	15 (21%)

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	TTD	G	8	3	-	0/23/109/110	0/0/6/6

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	8	TTD	P-OP1	12.12	1.60	1.46
3	G	8	TTD	C1R-N1T	3.97	1.51	1.45
3	G	8	TTD	C1'-N1	3.32	1.50	1.45
3	G	8	TTD	C2-N1	3.23	1.43	1.36
3	G	8	TTD	PB-O5P	3.13	1.63	1.51
3	G	8	TTD	C2T-N1T	2.37	1.41	1.36
3	G	8	TTD	C6-N1	2.23	1.51	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	8	TTD	O4R-C1R-N1T	11.56	123.18	108.76
3	G	8	TTD	C5-C4-N3	6.52	121.91	116.07
3	G	8	TTD	C5T-C4T-N3T	6.51	121.90	116.07
3	G	8	TTD	N3-C2-N1	5.51	122.62	116.74
3	G	8	TTD	N3T-C2T-N1T	4.90	121.97	116.74
3	G	8	TTD	O4-C4-C5	-4.55	119.28	122.92
3	G	8	TTD	O4T-C4T-C5T	-3.49	120.13	122.92
3	G	8	TTD	C4'-O4R-C1R	-3.34	100.96	109.44
3	G	8	TTD	C4-N3-C2	-3.19	121.21	126.84
3	G	8	TTD	C4T-N3T-C2T	-3.01	121.52	126.84
3	G	8	TTD	C2R-C1R-N1T	-2.79	111.66	115.68
3	G	8	TTD	O2-C2-N3	-2.78	115.85	121.42
3	G	8	TTD	C2'-C1'-N1	-2.53	112.03	115.68
3	G	8	TTD	C5-C5T-C6T	2.32	91.31	88.37
3	G	8	TTD	O4R-C1R-C2R	-2.25	101.82	106.25

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 ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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	1105/1159 (95%)	-0.05	0 100 100	39, 56, 80, 96	0
2	B	354/382 (92%)	-0.13	0 100 100	33, 49, 66, 75	0
3	G	14/14 (100%)	0.33	0 100 100	56, 73, 100, 102	0
4	H	15/16 (93%)	0.29	0 100 100	47, 74, 107, 108	0
All	All	1488/1571 (94%)	-0.06	0 100 100	33, 54, 79, 108	0

There are no RSRZ outliers to report.

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
3	TTD	G	8	40/41	0.23	-0.19	63,66,66,66	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
5	CA	B	1456	1/1	0.30	12.14	31,31,31,31	0

6.5 Other polymers ⓘ

There are no such residues in this entry.