



Full wwPDB X-ray Structure Validation Report i

Feb 28, 2014 – 03:20 AM GMT

PDB ID : 4B5G
Title : Substrate bound Neisseria AP endonuclease in absence of metal ions (crystal form 2)
Authors : Lu, D.; Silhan, J.; Macdonald, J.T.; Carpenter, E.P.; Jensen, K.; Tang, C.M.; Baldwin, G.S.; Freemont, P.S.
Deposited on : 2012-08-03
Resolution : 2.75 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>

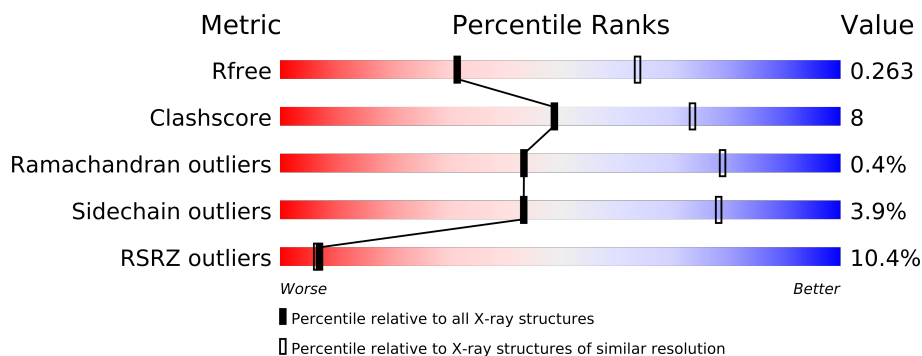
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.75 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	2406 (2.80-2.72)
Clashscore	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)
RSRZ outliers	66119	2409 (2.80-2.72)

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	259	
1	B	259	
1	C	259	
2	U	11	
2	W	11	
2	Y	11	
3	V	11	
3	X	11	
3	Z	11	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7584 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 EXODEOXYRIBONUCLEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	0	0
			2090	1331	365	382	12			
1	B	259	Total	C	N	O	S	0	0	0
			2090	1331	365	382	12			
1	C	259	Total	C	N	O	S	0	0	0
			2090	1331	365	382	12			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	101	GLY	ASP	CONFLICT	UNP C9X331
B	101	GLY	ASP	CONFLICT	UNP C9X331
C	101	GLY	ASP	CONFLICT	UNP C9X331

- Molecule 2 is a DNA chain called 5'-D(*GP*CP*TP*AP*CP*(3DR)P*CP*AP*TP*CP*GP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	U	11	Total	C	N	O	P	0	0	0
			210	101	36	63	10			
2	W	11	Total	C	N	O	P	0	0	0
			210	101	36	63	10			
2	Y	11	Total	C	N	O	P	0	0	0
			210	101	36	63	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	V	11	Total	C	N	O	P	0	0	0
			227	108	45	64	10			
3	X	11	Total	C	N	O	P	0	0	0
			227	108	45	64	10			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	Z	11	Total 227	C 108	N 45	O 64	P 10	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	O 1	0	0
4	B	1	Total 1	O 1	0	0
4	C	1	Total 1	O 1	0	0

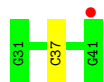
- Molecule 2: 5'-D(*GP*CP*TP*AP*CP*(3DR)P*CP*AP*TP*CP*GP)-3'

Chain U: 

There are no outlier residues recorded for this chain.

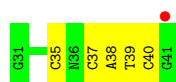
- Molecule 2: 5'-D(*GP*CP*TP*AP*CP*(3DR)P*CP*AP*TP*CP*GP)-3'

Chain W: 



- Molecule 2: 5'-D(*GP*CP*TP*AP*CP*(3DR)P*CP*AP*TP*CP*GP)-3'

Chain Y: 



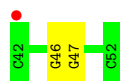
- Molecule 3: 5'-D(*CP*GP*AP*TP*GP*GP*GP*TP*AP*GP*CP)-3'

Chain V: 



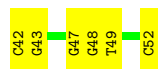
- Molecule 3: 5'-D(*CP*GP*AP*TP*GP*GP*GP*TP*AP*GP*CP)-3'

Chain X: 



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

Chain Z: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	75.24Å 75.24Å 380.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.08 – 2.75 44.08 – 2.75	Depositor EDS
% Data completeness (in resolution range)	92.5 (44.08-2.75) 93.1 (44.08-2.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.77Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: DEV_1084)	Depositor
R, R_{free}	0.232 , 0.259 0.235 , 0.263	Depositor DCC
R_{free} test set	1402 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	73.1	Xtriage
Anisotropy	0.635	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 67.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	4 of 27701 reflections (0.014%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7584	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.98% 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: 3DR

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	0.23	0/2147	0.45	1/2902 (0.0%)
1	B	0.25	0/2147	0.43	0/2902
1	C	0.26	0/2147	0.48	0/2902
2	U	0.43	0/221	1.01	0/336
2	W	0.46	0/221	1.01	0/336
2	Y	0.45	0/221	1.15	0/336
3	V	0.43	0/255	0.96	0/393
3	X	0.44	0/255	1.02	0/393
3	Z	0.43	0/255	0.94	0/393
All	All	0.29	0/7869	0.61	1/10893 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	75	ARG	NE-CZ-NH1	-5.46	117.57	120.30

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	2090	0	2013	39	0
1	B	2090	0	2013	29	0
1	C	2090	0	2013	37	0
2	U	210	0	122	0	0
2	W	210	0	122	1	0
2	Y	210	0	122	5	0
3	V	227	0	125	4	0
3	X	227	0	125	2	0
3	Z	227	0	125	5	0
4	A	1	0	0	1	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
All	All	7584	0	6780	111	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 8.

All (111) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:182:VAL:HA	1:C:186:LEU:HD23	1.64	0.77
1:B:79:ASN:HB3	1:B:99:ASP:HB2	1.67	0.76
1:A:190:ASP:OD2	1:A:219:ARG:NH2	2.20	0.71
1:C:67:SER:OG	1:C:68:GLY:N	2.25	0.70
1:A:14:SER:OG	1:A:18:LYS:NZ	2.24	0.69
1:C:131:TYR:CE1	1:C:186:LEU:HD21	2.28	0.69
1:C:190:ASP:OD2	1:C:219:ARG:NH2	2.22	0.68
1:A:9:VAL:O	4:A:2001:HOH:O	2.12	0.68
1:A:75:ARG:HH12	1:A:258:ALA:CB	2.06	0.67
1:B:67:SER:OG	1:B:68:GLY:N	2.24	0.65
1:C:131:TYR:HE1	1:C:186:LEU:HD21	1.61	0.65
1:C:64:ARG:HB2	3:Z:52:DC:H5"	1.78	0.65
1:A:104:SER:HB3	1:A:144:ILE:HG12	1.80	0.63
1:B:190:ASP:OD2	1:B:219:ARG:NH2	2.31	0.63
1:C:104:SER:HB3	1:C:144:ILE:HG12	1.81	0.63
1:C:86:ILE:HD11	1:C:89:PHE:CD2	2.33	0.62
1:A:6:SER:HB2	1:A:147:CYS:HB3	1.82	0.62
1:A:67:SER:OG	1:A:68:GLY:N	2.27	0.62
1:C:86:ILE:HD11	1:C:89:PHE:HD2	1.65	0.62
1:A:143:ASP:HB3	1:A:229:LEU:HD22	1.82	0.62
2:W:37:DC:N3	3:X:46:DG:N2	2.48	0.61
1:C:6:SER:HB2	1:C:147:CYS:HB3	1.85	0.58
1:A:69:VAL:HG23	1:A:96:VAL:HG23	1.86	0.58
1:C:193:ARG:HD3	1:C:197:PRO:HA	1.87	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:106:ILE:HD12	1:A:137:MET:HE1	1.88	0.55
1:B:158:ASP:OD1	1:B:219:ARG:NH1	2.40	0.55
1:B:243:LYS:NZ	1:B:245:SER:O	2.38	0.55
1:B:104:SER:HB3	1:B:144:ILE:HG12	1.89	0.54
1:A:13:ARG:NH1	1:A:43:ASP:HB3	2.22	0.54
1:B:79:ASN:OD1	1:B:80:VAL:N	2.41	0.54
1:B:69:VAL:HG23	1:B:96:VAL:HG23	1.89	0.54
1:C:88:GLU:HA	1:C:91:ARG:NH1	2.22	0.53
3:V:47:DG:H2"	3:V:48:DG:C8	2.43	0.53
1:C:69:VAL:HG23	1:C:96:VAL:HG23	1.90	0.52
1:C:133:MET:O	1:C:137:MET:HG3	2.09	0.52
1:B:13:ARG:NH1	1:B:43:ASP:HB3	2.25	0.52
1:A:234:VAL:HG22	1:A:253:GLU:HB3	1.92	0.52
1:A:207:ASN:OD1	3:V:47:DG:N2	2.36	0.52
1:B:35:GLN:HA	1:B:69:VAL:HG12	1.92	0.52
1:C:35:GLN:HA	1:C:69:VAL:HG12	1.91	0.51
1:B:181:LYS:HG2	1:B:185:LYS:HD2	1.91	0.51
1:A:75:ARG:HH12	1:A:258:ALA:HB2	1.75	0.51
1:C:165:ASN:O	1:C:171:PHE:HB3	2.11	0.51
1:C:38:LYS:O	1:C:65:GLY:HA2	2.11	0.50
1:A:193:ARG:HD3	1:A:197:PRO:HA	1.94	0.50
3:Z:47:DG:H2"	3:Z:48:DG:C8	2.48	0.49
1:A:104:SER:HB2	1:A:142:ARG:HH21	1.77	0.49
1:B:179:ILE:HD12	1:B:222:TYR:HE2	1.78	0.49
1:B:152:ILE:O	1:B:222:TYR:OH	2.19	0.49
1:C:117:GLU:OE2	1:C:121:GLN:NE2	2.46	0.48
1:C:57:HIS:CE1	1:C:80:VAL:HG21	2.48	0.48
1:C:13:ARG:NH1	1:C:43:ASP:HB3	2.28	0.48
1:A:159:LEU:HD11	1:A:162:TRP:HA	1.95	0.48
1:A:59:HIS:CE1	1:A:93:GLY:HA2	2.48	0.47
1:C:13:ARG:O	1:C:17:LYS:HG3	2.15	0.47
1:C:117:GLU:O	1:C:121:GLN:HG2	2.14	0.47
1:A:35:GLN:HA	1:A:69:VAL:HG12	1.95	0.47
1:A:137:MET:HE2	1:A:144:ILE:HG21	1.96	0.47
1:A:243:LYS:NZ	1:A:245:SER:O	2.44	0.47
1:C:40:GLN:NE2	1:C:62:GLU:O	2.48	0.47
1:C:245:SER:OG	1:C:246:ASP:N	2.47	0.47
1:A:245:SER:OG	1:A:246:ASP:N	2.48	0.46
1:A:8:ASN:HB3	1:A:247:HIS:CG	2.50	0.46
1:A:87:GLU:OE2	1:C:243:LYS:NZ	2.48	0.46
1:C:8:ASN:HB3	1:C:247:HIS:CG	2.50	0.46
1:B:59:HIS:CE1	1:B:93:GLY:HA2	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:41:GLU:OE1	1:A:58:TRP:NE1	2.33	0.46
1:A:210:GLN:HB2	1:A:214:LYS:HE2	1.98	0.46
1:B:40:GLN:NE2	1:B:62:GLU:O	2.49	0.46
1:C:173:PRO:O	1:C:177:GLU:HG2	2.16	0.46
1:C:104:SER:HB2	1:C:142:ARG:HH21	1.80	0.45
1:A:13:ARG:O	1:A:17:LYS:HG2	2.17	0.45
1:A:1:MET:N	1:A:256:TYR:O	2.42	0.45
1:A:200:PRO:O	1:A:219:ARG:HD3	2.16	0.45
3:Z:48:DG:H2''	3:Z:49:DT:H5'	1.98	0.45
1:B:119:ARG:NH1	1:B:122:VAL:HG21	2.32	0.45
1:C:79:ASN:HB3	1:C:99:ASP:HB2	1.99	0.44
1:C:181:LYS:HE3	1:C:181:LYS:HB2	1.62	0.44
1:A:165:ASN:O	1:A:171:PHE:HB3	2.18	0.44
1:B:63:LYS:HG2	1:B:64:ARG:N	2.32	0.44
1:A:18:LYS:NZ	3:V:50:DA:OP1	2.47	0.44
1:A:133:MET:O	1:A:137:MET:HG3	2.18	0.44
1:B:133:MET:O	1:B:137:MET:HG3	2.18	0.43
1:B:50:ASN:OD1	1:B:56:GLY:N	2.51	0.43
1:B:8:ASN:HB3	1:B:247:HIS:CG	2.54	0.43
1:B:245:SER:OG	1:B:246:ASP:N	2.51	0.42
1:A:82:ILE:HD12	1:A:82:ILE:HA	1.71	0.42
1:C:208:ARG:NH1	2:Y:37:DC:O4'	2.53	0.42
1:C:211:ALA:HB2	2:Y:38:DA:H4'	2.01	0.42
1:C:59:HIS:CE1	1:C:93:GLY:HA2	2.55	0.42
1:A:81:GLN:HB3	1:A:97:ARG:HB3	2.01	0.42
1:A:13:ARG:HH21	3:V:51:DG:H3'	1.85	0.42
1:C:119:ARG:NH2	2:Y:35:DC:OP1	2.53	0.42
3:Z:42:DC:H2'	3:Z:43:DG:C8	2.53	0.42
1:A:14:SER:HG	1:A:18:LYS:NZ	2.17	0.42
1:B:6:SER:HB2	1:B:147:CYS:HB3	2.02	0.42
1:B:136:ALA:O	1:B:140:GLU:HG3	2.20	0.41
1:B:177:GLU:O	1:B:181:LYS:HG3	2.20	0.41
1:C:38:LYS:HE2	1:C:38:LYS:HB3	1.86	0.41
2:Y:39:DT:H2''	2:Y:40:DC:C6	2.54	0.41
1:B:122:VAL:HG12	1:B:125:ARG:NH2	2.36	0.41
1:A:150:TRP:CD1	1:A:222:TYR:HB2	2.55	0.41
1:B:11:GLY:HA2	1:B:38:LYS:HB2	2.01	0.41
1:A:154:HIS:CE1	1:A:183:ILE:HD12	2.56	0.41
1:C:193:ARG:NH1	1:C:196:TYR:O	2.54	0.41
1:B:207:ASN:OD1	3:X:47:DG:N2	2.53	0.41
3:Z:47:DG:H2''	3:Z:48:DG:N7	2.35	0.41
1:B:110:LEU:HA	1:B:111:PRO:HD3	1.89	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:137:MET:CE	1:A:144:ILE:HG21	2.51	0.40
1:C:204:TRP:HH2	2:Y:37:DC:H5'	1.86	0.40
1:B:57:HIS:CE1	1:B:80:VAL:HG21	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	257/259 (99%)	244 (95%)	12 (5%)	1 (0%)	43	79
1	B	257/259 (99%)	245 (95%)	11 (4%)	1 (0%)	43	79
1	C	257/259 (99%)	245 (95%)	11 (4%)	1 (0%)	43	79
All	All	771/777 (99%)	734 (95%)	34 (4%)	3 (0%)	43	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	93	GLY
1	A	93	GLY
1	B	93	GLY

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	215/215 (100%)	207 (96%)	8 (4%)	45	80
1	B	215/215 (100%)	208 (97%)	7 (3%)	50	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	215/215 (100%)	205 (95%)	10 (5%)	36	71
All	All	645/645 (100%)	620 (96%)	25 (4%)	43	78

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	GLU
1	A	82	ILE
1	A	84	MET
1	A	108	LEU
1	A	138	LYS
1	A	159	LEU
1	A	177	GLU
1	A	253	GLU
1	B	1	MET
1	B	75	ARG
1	B	84	MET
1	B	88	GLU
1	B	108	LEU
1	B	133	MET
1	B	159	LEU
1	C	1	MET
1	C	108	LEU
1	C	118	GLU
1	C	122	VAL
1	C	131	TYR
1	C	159	LEU
1	C	172	LEU
1	C	222	TYR
1	C	237	HIS
1	C	253	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	154	HIS
1	A	161	ASN
1	B	161	ASN
1	B	247	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

3 non-standard protein/DNA/RNA residues 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	3DR	U	36	2	9,11,12	0.62	0	11,14,17	0.75	0
2	3DR	W	36	2	9,11,12	0.63	0	11,14,17	0.72	0
2	3DR	Y	36	2	9,11,12	0.63	0	11,14,17	0.73	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	3DR	U	36	2	-	0/4/15/16	0/1/1/1
2	3DR	W	36	2	-	0/4/15/16	0/1/1/1
2	3DR	Y	36	2	-	0/4/15/16	0/1/1/1

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.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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	259/259 (100%)	0.79	23 (8%) 10 9	74, 93, 117, 162	0
1	B	259/259 (100%)	0.90	39 (15%) 3 3	77, 96, 128, 161	0
1	C	259/259 (100%)	0.78	23 (8%) 10 9	76, 96, 126, 150	0
2	U	11/11 (100%)	0.61	0 100 100	95, 103, 119, 120	0
2	W	11/11 (100%)	0.64	1 (9%) 9 9	101, 110, 122, 124	0
2	Y	11/11 (100%)	0.81	1 (9%) 9 9	98, 103, 119, 122	0
3	V	11/11 (100%)	0.63	0 100 100	91, 103, 124, 135	0
3	X	11/11 (100%)	0.78	1 (9%) 9 9	94, 111, 132, 136	0
3	Z	11/11 (100%)	0.81	0 100 100	91, 111, 123, 135	0
All	All	843/843 (100%)	0.81	88 (10%) 7 6	74, 96, 124, 162	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	115	SER	8.4
1	B	259	GLU	6.5
1	B	258	ALA	5.7
1	A	115	SER	5.6
1	C	114	SER	5.4
1	B	66	TYR	5.2
1	A	258	ALA	5.2
1	A	153	ALA	5.1
1	B	115	SER	4.7
1	B	174	GLU	4.6
1	C	65	GLY	4.3
1	A	257	ALA	4.2
1	C	120	GLN	4.2
1	A	185	LYS	3.9
1	C	137	MET	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	253	GLU	3.7
1	B	170	GLY	3.6
1	B	114	SER	3.5
1	C	198	ASP	3.5
1	B	87	GLU	3.5
1	B	185	LYS	3.5
1	C	170	GLY	3.4
1	B	138	LYS	3.3
1	B	208	ARG	3.2
1	B	117	GLU	3.2
1	C	44	LEU	3.2
1	A	210	GLN	3.0
1	B	188	TRP	2.9
1	B	131	TYR	2.9
1	C	116	ALA	2.8
1	C	257	ALA	2.8
1	B	65	GLY	2.8
1	B	91	ARG	2.7
1	A	242	GLU	2.7
1	C	161	ASN	2.7
2	W	41	DG	2.6
1	B	144	ILE	2.6
1	A	124	TYR	2.6
1	B	254	TYR	2.6
1	A	161	ASN	2.6
1	A	253	GLU	2.6
1	B	153	ALA	2.6
1	B	198	ASP	2.5
1	B	44	LEU	2.5
1	B	216	VAL	2.5
1	A	114	SER	2.5
1	B	145	VAL	2.5
1	B	63	LYS	2.5
1	C	112	SER	2.5
1	A	171	PHE	2.5
1	C	138	LYS	2.5
1	A	102	ARG	2.5
1	A	101	GLY	2.4
1	A	218	TRP	2.4
1	A	120	GLN	2.4
1	C	113	GLY	2.4
1	A	259	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	147	CYS	2.4
1	C	185	LYS	2.4
1	A	89	PHE	2.4
1	C	172	LEU	2.3
1	A	254	TYR	2.3
1	B	2	LEU	2.3
1	A	188	TRP	2.3
1	C	218	TRP	2.3
1	C	66	TYR	2.3
1	B	161	ASN	2.2
1	C	188	TRP	2.2
1	B	112	SER	2.2
1	B	127	LEU	2.2
3	X	42	DC	2.2
1	B	139	ASN	2.2
1	A	131	TYR	2.1
1	C	157	ILE	2.1
2	Y	41	DG	2.1
1	B	178	TRP	2.1
1	B	110	LEU	2.1
1	C	124	TYR	2.1
1	C	174	GLU	2.1
1	B	89	PHE	2.1
1	A	207	ASN	2.1
1	B	171	PHE	2.1
1	B	42	ALA	2.1
1	A	170	GLY	2.1
1	B	218	TRP	2.1
1	B	257	ALA	2.1
1	C	9	VAL	2.1
1	B	4	ILE	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(\AA^2)	Q<0.9
2	3DR	Y	36	11/12	0.24	-0.48	92,100,111,117	0
2	3DR	U	36	11/12	0.20	-0.93	89,92,99,104	0
2	3DR	W	36	11/12	0.15	-1.84	92,100,109,109	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.