



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 12:20 pm BST

PDB ID : 5IZO
Title : Bacillus NanoRNase A (H103A) + 2 divalent cations + PO4 at the active site
Authors : Schmier, B.J.; Malhotra, A.; Nellersa, C.M.
Deposited on : 2016-03-25
Resolution : 1.95 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

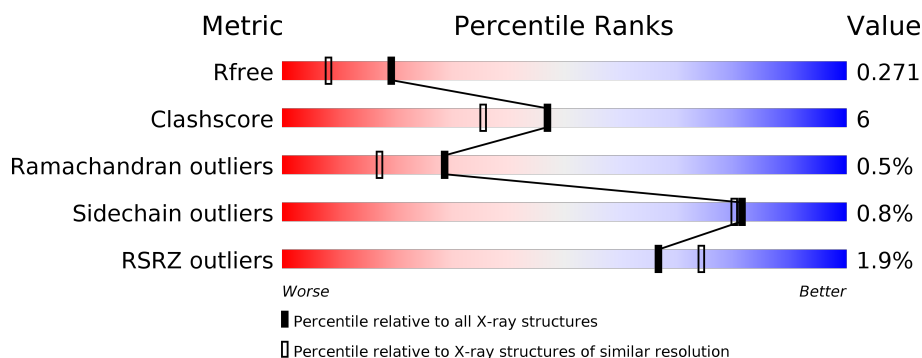
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	333	<div> <div>5%</div> <div> <div></div> <div>72%</div> <div>15%</div> <div>12%</div> </div> </div>
1	B	333	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>• •</div> </div> </div>
1	C	333	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>17%</div> <div>• 5%</div> </div> </div>
1	D	333	<div> <div>%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>5%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10085 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Bifunctional oligoribonuclease and PAP phosphatase NrnA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	293	Total	C	N	O	S	11	0	0
			2193	1401	358	428	6			
1	B	320	Total	C	N	O	S	15	0	0
			2462	1569	400	486	7			
1	C	315	Total	C	N	O	S	6	0	0
			2446	1557	403	480	6			
1	D	315	Total	C	N	O	S	13	0	0
			2433	1551	405	472	5			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP O34600
A	-19	GLY	-	expression tag	UNP O34600
A	-18	SER	-	expression tag	UNP O34600
A	-17	SER	-	expression tag	UNP O34600
A	-16	HIS	-	expression tag	UNP O34600
A	-15	HIS	-	expression tag	UNP O34600
A	-14	HIS	-	expression tag	UNP O34600
A	-13	HIS	-	expression tag	UNP O34600
A	-12	HIS	-	expression tag	UNP O34600
A	-11	HIS	-	expression tag	UNP O34600
A	-10	GLU	-	expression tag	UNP O34600
A	-9	ASN	-	expression tag	UNP O34600
A	-8	LEU	-	expression tag	UNP O34600
A	-7	TYR	-	expression tag	UNP O34600
A	-6	PHE	-	expression tag	UNP O34600
A	-5	GLN	-	expression tag	UNP O34600
A	-4	SER	-	expression tag	UNP O34600
A	-3	MET	-	expression tag	UNP O34600
A	-2	ALA	-	expression tag	UNP O34600
A	-1	SER	-	expression tag	UNP O34600
A	103	ALA	HIS	engineered mutation	UNP O34600

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	MET	-	initiating methionine	UNP O34600
B	-19	GLY	-	expression tag	UNP O34600
B	-18	SER	-	expression tag	UNP O34600
B	-17	SER	-	expression tag	UNP O34600
B	-16	HIS	-	expression tag	UNP O34600
B	-15	HIS	-	expression tag	UNP O34600
B	-14	HIS	-	expression tag	UNP O34600
B	-13	HIS	-	expression tag	UNP O34600
B	-12	HIS	-	expression tag	UNP O34600
B	-11	HIS	-	expression tag	UNP O34600
B	-10	GLU	-	expression tag	UNP O34600
B	-9	ASN	-	expression tag	UNP O34600
B	-8	LEU	-	expression tag	UNP O34600
B	-7	TYR	-	expression tag	UNP O34600
B	-6	PHE	-	expression tag	UNP O34600
B	-5	GLN	-	expression tag	UNP O34600
B	-4	SER	-	expression tag	UNP O34600
B	-3	MET	-	expression tag	UNP O34600
B	-2	ALA	-	expression tag	UNP O34600
B	-1	SER	-	expression tag	UNP O34600
B	103	ALA	HIS	engineered mutation	UNP O34600
C	-20	MET	-	initiating methionine	UNP O34600
C	-19	GLY	-	expression tag	UNP O34600
C	-18	SER	-	expression tag	UNP O34600
C	-17	SER	-	expression tag	UNP O34600
C	-16	HIS	-	expression tag	UNP O34600
C	-15	HIS	-	expression tag	UNP O34600
C	-14	HIS	-	expression tag	UNP O34600
C	-13	HIS	-	expression tag	UNP O34600
C	-12	HIS	-	expression tag	UNP O34600
C	-11	HIS	-	expression tag	UNP O34600
C	-10	GLU	-	expression tag	UNP O34600
C	-9	ASN	-	expression tag	UNP O34600
C	-8	LEU	-	expression tag	UNP O34600
C	-7	TYR	-	expression tag	UNP O34600
C	-6	PHE	-	expression tag	UNP O34600
C	-5	GLN	-	expression tag	UNP O34600
C	-4	SER	-	expression tag	UNP O34600
C	-3	MET	-	expression tag	UNP O34600
C	-2	ALA	-	expression tag	UNP O34600
C	-1	SER	-	expression tag	UNP O34600
C	103	ALA	HIS	engineered mutation	UNP O34600

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-20	MET	-	initiating methionine	UNP O34600
D	-19	GLY	-	expression tag	UNP O34600
D	-18	SER	-	expression tag	UNP O34600
D	-17	SER	-	expression tag	UNP O34600
D	-16	HIS	-	expression tag	UNP O34600
D	-15	HIS	-	expression tag	UNP O34600
D	-14	HIS	-	expression tag	UNP O34600
D	-13	HIS	-	expression tag	UNP O34600
D	-12	HIS	-	expression tag	UNP O34600
D	-11	HIS	-	expression tag	UNP O34600
D	-10	GLU	-	expression tag	UNP O34600
D	-9	ASN	-	expression tag	UNP O34600
D	-8	LEU	-	expression tag	UNP O34600
D	-7	TYR	-	expression tag	UNP O34600
D	-6	PHE	-	expression tag	UNP O34600
D	-5	GLN	-	expression tag	UNP O34600
D	-4	SER	-	expression tag	UNP O34600
D	-3	MET	-	expression tag	UNP O34600
D	-2	ALA	-	expression tag	UNP O34600
D	-1	SER	-	expression tag	UNP O34600
D	103	ALA	HIS	engineered mutation	UNP O34600

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mn 2 2	0	0
2	A	2	Total Mn 2 2	0	0
2	D	2	Total Mn 2 2	0	0
2	C	2	Total Mn 2 2	0	0

- 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		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		

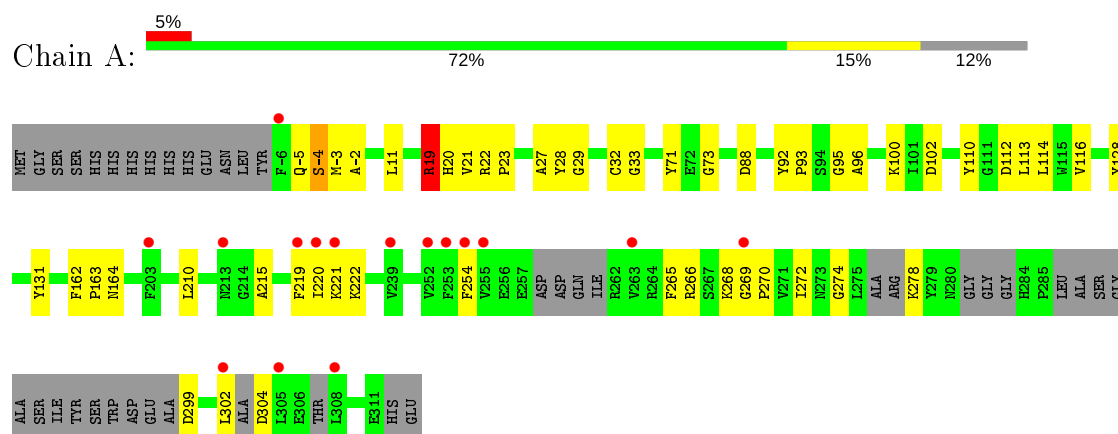
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	119	Total	O	0	0
			119	119		
4	B	148	Total	O	0	0
			148	148		
4	C	143	Total	O	0	0
			143	143		
4	D	113	Total	O	0	0
			113	113		

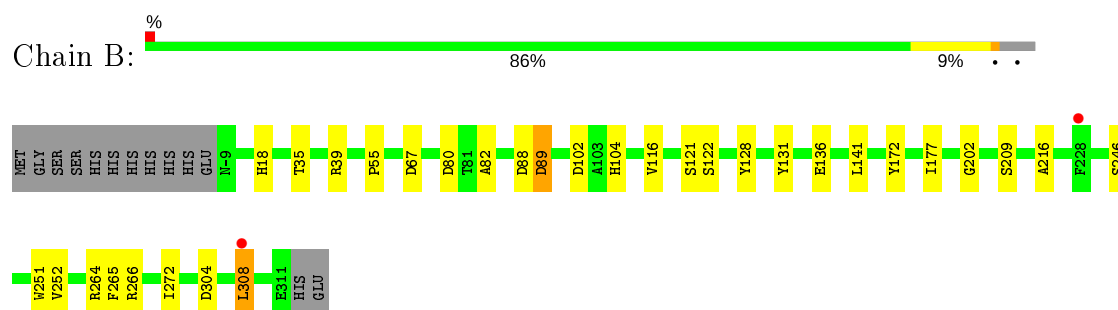
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

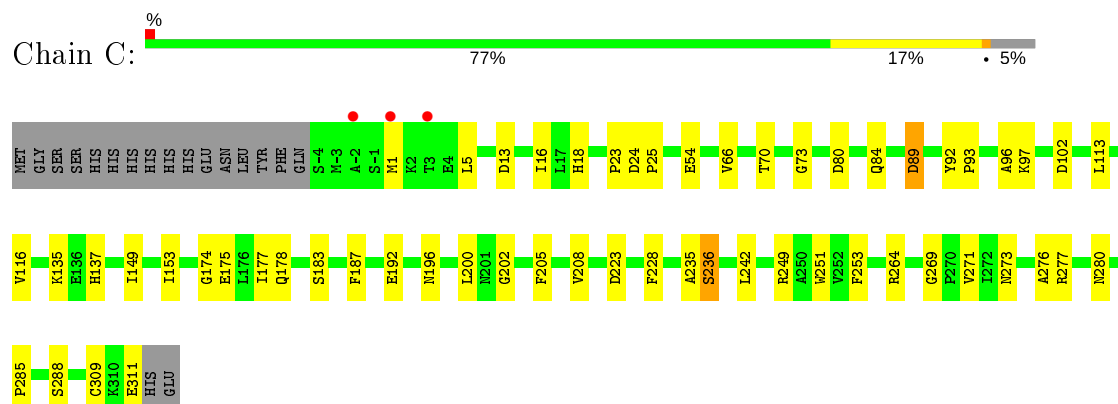
- Molecule 1: Bifunctional oligoribonuclease and PAP phosphatase NrnA



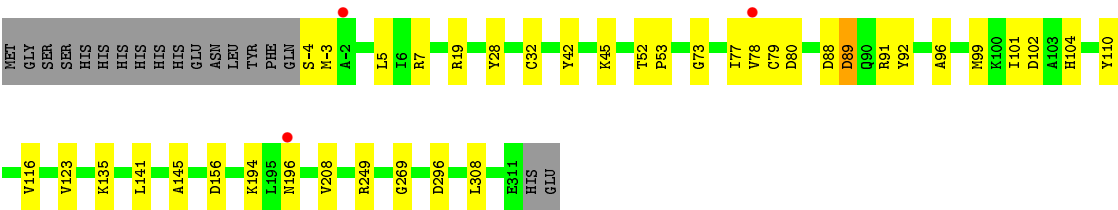
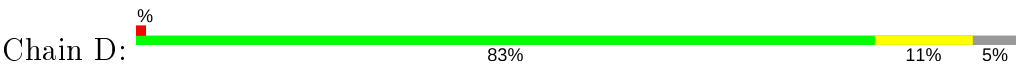
- Molecule 1: Bifunctional oligoribonuclease and PAP phosphatase NrnA



- Molecule 1: Bifunctional oligoribonuclease and PAP phosphatase NrnA



● Molecule 1: Bifunctional oligoribonuclease and PAP phosphatase NrnA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.65Å 119.64Å 124.14Å 90.00° 91.59° 90.00°	Depositor
Resolution (Å)	47.34 – 1.95 47.34 – 1.95	Depositor EDS
% Data completeness (in resolution range)	93.3 (47.34-1.95) 93.3 (47.34-1.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.212 , 0.267 0.225 , 0.271	Depositor DCC
R_{free} test set	5032 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	37.8	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.013 for -h,-l,-k 0.037 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10085	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, MN

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	0.93	1/2232 (0.0%)	0.88	3/3025 (0.1%)
1	B	1.03	0/2514	0.86	1/3418 (0.0%)
1	C	1.05	0/2498	0.93	2/3392 (0.1%)
1	D	0.98	0/2485	0.92	1/3376 (0.0%)
All	All	1.00	1/9729 (0.0%)	0.90	7/13211 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	-4	SER	CA-CB	5.13	1.60	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	19	ARG	NE-CZ-NH2	-6.93	116.83	120.30
1	B	67	ASP	CB-CA-C	-6.59	97.22	110.40
1	A	114	LEU	CA-CB-CG	6.01	129.12	115.30
1	C	97	LYS	CD-CE-NZ	5.70	124.80	111.70
1	C	16	ILE	CG1-CB-CG2	-5.47	99.36	111.40
1	D	7	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	A	222	LYS	N-CA-C	5.05	124.63	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	19	ARG	Sidechain
1	D	249	ARG	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2193	0	2046	39	0
1	B	2462	0	2370	21	0
1	C	2446	0	2374	33	0
1	D	2433	0	2364	26	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	119	0	0	2	0
4	B	148	0	0	0	0
4	C	143	0	0	2	0
4	D	113	0	0	1	0
All	All	10085	0	9154	116	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (116) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:ARG:HG3	1:A:27:ALA:HB1	1.59	0.83
1:A:19:ARG:NH2	1:A:88:ASP:OD2	2.24	0.70
1:A:-5:GLN:O	1:A:-4:SER:C	2.35	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:92:TYR:CD1	1:C:93:PRO:HD3	2.34	0.62
1:A:-5:GLN:O	1:A:-3:MET:N	2.33	0.62
1:A:220:ILE:HG22	1:A:220:ILE:O	1.99	0.61
1:A:21:VAL:O	1:A:22:ARG:HB2	2.01	0.61
1:A:92:TYR:CG	1:A:93:PRO:HD3	2.36	0.61
1:C:249:ARG:NH1	1:C:309:CYS:O	2.35	0.60
1:D:80:ASP:HA	1:D:102:ASP:OD1	2.01	0.60
1:A:272:ILE:C	1:A:274:GLY:H	2.05	0.60
1:C:149:ILE:O	1:C:153:ILE:HG13	2.02	0.59
1:D:5:LEU:HD22	1:D:99:MET:SD	2.42	0.59
1:B:88:ASP:O	1:B:89:ASP:CB	2.50	0.59
1:B:304:ASP:O	1:B:308:LEU:HB2	2.03	0.58
1:C:92:TYR:CG	1:C:93:PRO:HD3	2.38	0.58
1:A:73:GLY:HA2	1:A:96:ALA:HB2	1.86	0.58
1:D:208:VAL:HG13	1:D:208:VAL:O	2.04	0.57
1:C:280:ASN:HB3	4:C:574:HOH:O	2.04	0.57
1:C:223:ASP:N	1:C:223:ASP:OD1	2.38	0.56
1:A:-5:GLN:C	1:A:-3:MET:N	2.58	0.56
1:C:84:GLN:HB3	1:C:92:TYR:OH	2.06	0.55
1:A:-5:GLN:O	1:A:-2:ALA:N	2.39	0.55
1:D:88:ASP:O	1:D:89:ASP:HB3	2.07	0.55
1:B:209:SER:O	1:B:216:ALA:HA	2.06	0.55
1:B:265:PHE:HB2	1:B:272:ILE:HD13	1.88	0.54
1:A:22:ARG:N	1:A:23:PRO:CD	2.70	0.54
1:B:131:TYR:CE1	1:B:141:LEU:HB2	2.44	0.53
1:D:80:ASP:CA	1:D:123:VAL:HG21	2.39	0.52
1:A:128:TYR:O	1:A:131:TYR:HB3	2.10	0.52
1:D:102:ASP:OD2	1:D:104:HIS:HB2	2.09	0.52
1:D:102:ASP:O	1:D:116:VAL:HA	2.09	0.52
1:A:-5:GLN:HG3	1:A:-3:MET:H	1.75	0.52
1:B:128:TYR:O	1:B:131:TYR:HB3	2.10	0.52
1:D:194:LYS:HB3	1:D:196:ASN:OD1	2.09	0.52
1:B:102:ASP:O	1:B:116:VAL:HA	2.10	0.51
1:D:88:ASP:O	1:D:89:ASP:CB	2.59	0.50
1:C:13:ASP:OD2	1:D:296:ASP:HB2	2.11	0.50
1:A:92:TYR:N	1:A:93:PRO:CD	2.75	0.49
1:D:102:ASP:HB2	4:D:555:HOH:O	2.11	0.49
1:C:236:SER:OG	1:C:264:ARG:NH2	2.40	0.49
1:D:42:TYR:CB	1:D:45:LYS:HD2	2.43	0.48
1:D:308:LEU:HD12	1:D:308:LEU:O	2.13	0.48
1:C:80:ASP:HA	1:C:102:ASP:OD1	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:77:ILE:HG12	1:D:99:MET:HE3	1.96	0.48
1:C:205:PHE:O	1:C:208:VAL:HG12	2.14	0.48
1:B:252:VAL:HA	1:B:264:ARG:O	2.14	0.47
1:A:162:PHE:HB3	1:A:163:PRO:HD2	1.95	0.47
1:B:136:GLU:CD	1:B:136:GLU:H	2.17	0.47
1:D:73:GLY:HA2	1:D:96:ALA:HB2	1.97	0.47
1:A:274:GLY:O	1:A:278:LYS:HB2	2.15	0.47
1:C:135:LYS:C	1:C:137:HIS:H	2.17	0.47
1:C:73:GLY:HA2	1:C:96:ALA:HB2	1.97	0.46
1:B:80:ASP:HA	1:B:102:ASP:OD1	2.15	0.46
1:C:174:GLY:O	1:C:177:ILE:HG22	2.16	0.46
1:A:219:PHE:HA	1:A:254:PHE:HB2	1.97	0.45
1:C:1:MET:CE	1:C:113:LEU:HD23	2.46	0.45
1:B:88:ASP:O	1:B:89:ASP:HB3	2.16	0.45
1:A:272:ILE:HD12	1:A:272:ILE:HA	1.80	0.45
1:D:52:THR:HA	1:D:53:PRO:HD3	1.83	0.45
1:C:242:LEU:HD22	1:C:251:TRP:CD1	2.51	0.45
1:A:28:TYR:O	1:A:32:CYS:HB2	2.17	0.45
1:A:11:LEU:HA	1:A:11:LEU:HD23	1.87	0.44
1:C:102:ASP:O	1:C:116:VAL:HA	2.17	0.44
1:A:102:ASP:O	1:A:116:VAL:HA	2.17	0.44
1:A:274:GLY:HA3	4:A:606:HOH:O	2.16	0.44
1:B:131:TYR:CZ	1:B:141:LEU:HB2	2.52	0.44
1:B:121:SER:O	1:B:122:SER:HB3	2.17	0.44
1:C:276:ALA:HB2	1:C:288:SER:HB3	2.00	0.44
1:D:141:LEU:HD12	1:D:145:ALA:HB3	1.99	0.44
1:B:246:SER:HB2	1:C:192:GLU:HG2	1.99	0.44
1:A:71:TYR:O	1:A:95:GLY:HA2	2.17	0.44
1:C:18:HIS:CE1	1:C:89:ASP:HB3	2.53	0.44
1:D:194:LYS:HB3	1:D:194:LYS:HE2	1.93	0.43
1:B:202:GLY:HA2	1:C:202:GLY:HA2	2.00	0.43
1:A:29:GLY:O	1:A:33:GLY:HA3	2.19	0.43
1:C:200:LEU:HD21	1:C:235:ALA:HB2	1.99	0.43
1:D:42:TYR:HB3	1:D:45:LYS:HD2	2.00	0.43
1:C:24:ASP:HB2	1:C:25:PRO:CD	2.48	0.43
1:C:273:ASN:O	1:C:277:ARG:HG3	2.19	0.43
1:D:-4:SER:OG	1:D:-3:MET:N	2.51	0.43
1:A:265:PHE:C	1:A:266:ARG:HG2	2.38	0.43
1:A:268:LYS:HA	1:A:268:LYS:HD2	1.85	0.43
1:A:272:ILE:C	1:A:274:GLY:N	2.72	0.43
1:D:91:ARG:O	1:D:92:TYR:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:196:ASN:HB2	1:C:228:PHE:O	2.19	0.43
1:B:18:HIS:CE1	1:B:89:ASP:HB3	2.54	0.43
1:C:175:GLU:O	1:C:178:GLN:HG2	2.19	0.42
1:D:28:TYR:O	1:D:32:CYS:HB2	2.18	0.42
1:A:210:LEU:HA	1:A:215:ALA:O	2.19	0.42
1:A:92:TYR:CD2	1:A:93:PRO:HD3	2.55	0.42
1:C:183:SER:O	1:C:187:PHE:CD2	2.72	0.42
1:C:280:ASN:CB	4:C:574:HOH:O	2.66	0.42
1:A:112:ASP:C	1:A:113:LEU:HD12	2.39	0.42
1:A:302:LEU:O	1:A:304:ASP:N	2.52	0.42
1:C:66:VAL:HG13	1:C:70:THR:HB	2.02	0.42
1:A:162:PHE:HB3	1:A:163:PRO:CD	2.49	0.42
1:A:302:LEU:HB3	4:A:602:HOH:O	2.20	0.42
1:A:19:ARG:HG2	1:A:20:HIS:N	2.35	0.42
1:C:23:PRO:HG2	1:C:54:GLU:HB2	2.00	0.42
1:B:177:ILE:HA	1:B:177:ILE:HD12	1.83	0.41
1:B:35:THR:O	1:B:39:ARG:HG3	2.20	0.41
1:D:194:LYS:HE2	1:D:196:ASN:OD1	2.20	0.41
1:D:78:VAL:HG11	1:D:110:TYR:OH	2.21	0.41
1:B:251:TRP:CE2	1:B:266:ARG:HB2	2.55	0.41
1:C:271:VAL:HG22	1:C:285:PRO:HB3	2.03	0.41
1:C:1:MET:O	1:C:5:LEU:HG	2.20	0.41
1:C:242:LEU:HD12	1:C:242:LEU:N	2.36	0.41
1:A:164:ASN:N	1:A:164:ASN:OD1	2.53	0.41
1:D:79:CYS:HA	1:D:101:ILE:O	2.21	0.41
1:A:269:GLY:O	1:A:270:PRO:C	2.59	0.40
1:B:128:TYR:HD2	1:B:172:TYR:CD2	2.39	0.40
1:D:80:ASP:N	1:D:123:VAL:HG21	2.36	0.40
1:A:299:ASP:O	1:A:302:LEU:HB2	2.21	0.40
1:A:100:LYS:HG3	1:A:110:TYR:CZ	2.56	0.40
1:B:82:ALA:HB2	1:B:104:HIS:CB	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	276/333 (83%)	255 (92%)	20 (7%)	1 (0%)	34	22
1	B	318/333 (96%)	305 (96%)	12 (4%)	1 (0%)	41	30
1	C	313/333 (94%)	303 (97%)	8 (3%)	2 (1%)	25	14
1	D	313/333 (94%)	299 (96%)	12 (4%)	2 (1%)	25	14
All	All	1220/1332 (92%)	1162 (95%)	52 (4%)	6 (0%)	29	17

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	221	LYS
1	B	89	ASP
1	D	269	GLY
1	C	89	ASP
1	C	269	GLY
1	D	89	ASP

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	220/286 (77%)	219 (100%)	1 (0%)	88	88
1	B	261/286 (91%)	259 (99%)	2 (1%)	81	80
1	C	261/286 (91%)	258 (99%)	3 (1%)	73	71
1	D	257/286 (90%)	255 (99%)	2 (1%)	81	80
All	All	999/1144 (87%)	991 (99%)	8 (1%)	81	80

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ARG
1	B	55	PRO

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Mol	Chain	Res	Type
1	B	308	LEU
1	C	236	SER
1	C	253	PHE
1	C	311	GLU
1	D	135	LYS
1	D	156	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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	PO4	D	403	2	4,4,4	0.92	0	6,6,6	0.42	0
3	PO4	C	403	2	4,4,4	0.92	0	6,6,6	0.43	0
3	PO4	B	403	2	4,4,4	0.92	0	6,6,6	0.43	0
3	PO4	A	403	2	4,4,4	0.92	0	6,6,6	0.43	0

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	293/333 (87%)	0.65	16 (5%)	25 34	27, 44, 73, 89	10 (3%)
1	B	320/333 (96%)	0.32	2 (0%)	89 93	28, 39, 52, 79	6 (1%)
1	C	315/333 (94%)	0.25	3 (0%)	82 87	28, 37, 48, 72	4 (1%)
1	D	315/333 (94%)	0.34	3 (0%)	82 87	32, 42, 56, 76	6 (1%)
All	All	1243/1332 (93%)	0.39	24 (1%)	66 74	27, 40, 62, 89	26 (2%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	253	PHE	6.9
1	A	252	VAL	6.3
1	A	219	PHE	6.1
1	A	255	VAL	6.1
1	A	308	LEU	4.7
1	A	203	PHE	3.6
1	A	239	VAL	3.4
1	A	254	PHE	2.9
1	A	220	ILE	2.9
1	A	302	LEU	2.6
1	C	-2	ALA	2.6
1	A	221	LYS	2.5
1	A	305	LEU	2.5
1	A	269	GLY	2.1
1	A	263	VAL	2.1
1	C	3	THR	2.1
1	B	308	LEU	2.1
1	A	213	ASN	2.1
1	A	-6	PHE	2.1
1	C	1	MET	2.0
1	B	228	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	78	VAL	2.0
1	D	-2	ALA	2.0
1	D	196	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PO4	C	403	5/5	0.85	0.21	53,57,58,61	0
3	PO4	B	403	5/5	0.90	0.15	40,54,58,58	0
3	PO4	A	403	5/5	0.91	0.14	48,54,58,59	0
3	PO4	D	403	5/5	0.91	0.11	53,54,58,60	0
2	MN	D	401	1/1	0.95	0.16	42,42,42,42	0
2	MN	D	402	1/1	0.96	0.12	44,44,44,44	0
2	MN	C	402	1/1	0.98	0.18	35,35,35,35	0
2	MN	B	402	1/1	0.99	0.17	37,37,37,37	0
2	MN	A	401	1/1	0.99	0.11	41,41,41,41	0
2	MN	B	401	1/1	0.99	0.14	38,38,38,38	0
2	MN	C	401	1/1	0.99	0.12	39,39,39,39	0
2	MN	A	402	1/1	1.00	0.08	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.