



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:11 PM GMT

PDB ID : 1SHN
Title : Crystal structure of shrimp alkaline phosphatase with phosphate bound
Authors : de Backer, M.M.E.; McSweeney, S.; Lindley, P.F.; Hough, E.
Deposited on : 2004-02-26
Resolution : 2.15 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

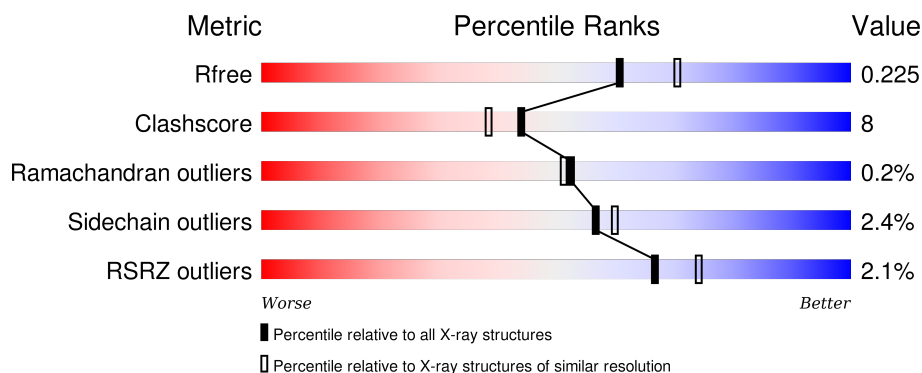
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


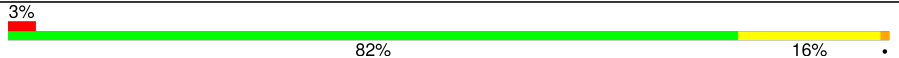
The reported resolution of this entry is 2.15 Å.

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}	91344	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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. 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	478	 2% 81% 16% 3%
1	B	478	 3% 82% 16% 1%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PO4	A	486	-	-	X	X
4	PO4	B	484	-	-	X	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7699 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.

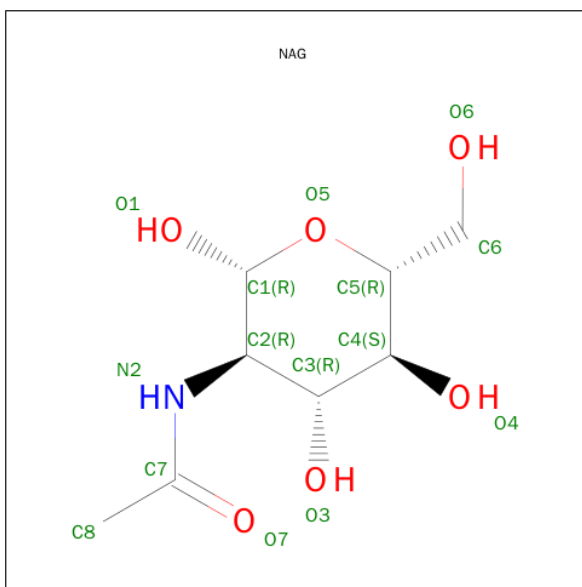
- Molecule 1 is a protein called alkaline phosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3731	2333	629	755	14			
1	B	476	Total	C	N	O	S	0	0	0
			3731	2333	629	755	14			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLU	-	CLONING ARTIFACT	UNP Q9BHT8
A	2	GLU	-	CLONING ARTIFACT	UNP Q9BHT8
A	3	ASP	-	CLONING ARTIFACT	UNP Q9BHT8
A	184	ALA	ARG	CONFLICT	UNP Q9BHT8
A	355	ALA	VAL	CONFLICT	UNP Q9BHT8
B	1	GLU	-	CLONING ARTIFACT	UNP Q9BHT8
B	2	GLU	-	CLONING ARTIFACT	UNP Q9BHT8
B	3	ASP	-	CLONING ARTIFACT	UNP Q9BHT8
B	184	ALA	ARG	CONFLICT	UNP Q9BHT8
B	355	ALA	VAL	CONFLICT	UNP Q9BHT8

- Molecule 2 is zinc (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

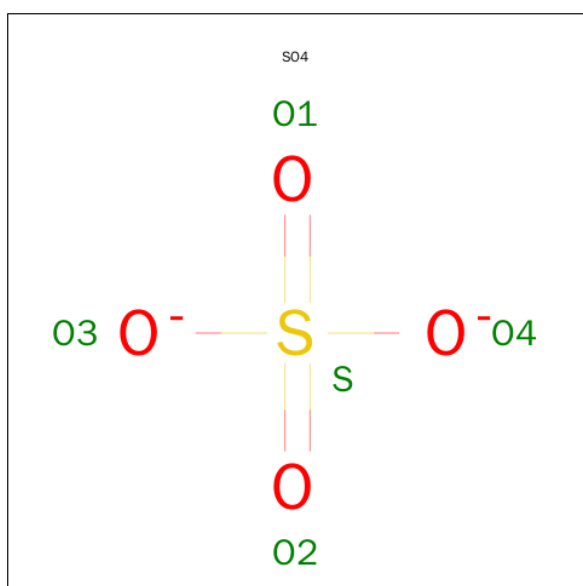
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Zn	0	0
			3	3		
3	A	3	Total	Zn	0	0
			3	3		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		

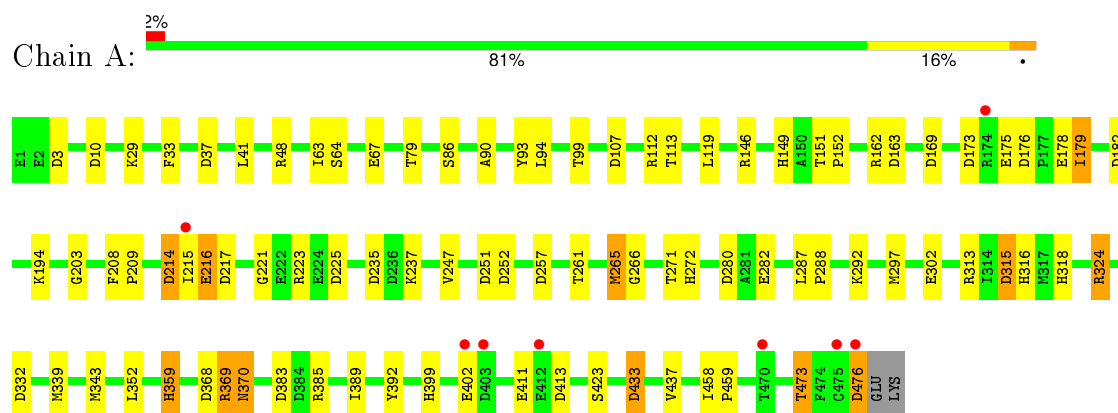
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	101	Total 101	O 101	0	0
6	B	82	Total 82	O 82	0	0

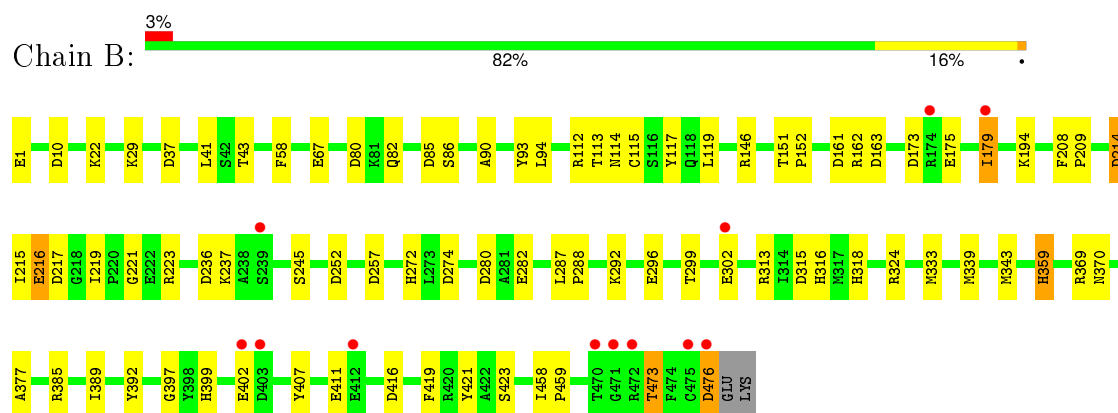
3 Residue-property plots

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: alkaline phosphatase



• Molecule 1: alkaline phosphatase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	170.68 Å 170.68 Å 83.92 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.64 – 2.15 39.64 – 2.15	Depositor EDS
% Data completeness (in resolution range)	96.3 (39.64-2.15) 96.3 (39.64-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.41 (at 2.16 Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.186 , 0.218 0.197 , 0.225	Depositor DCC
R_{free} test set	3357 reflections (5.43%)	DCC
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 37.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 66358 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7699	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.76 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.7429e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: SO4, PO4, ZN, NAG

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	1.00	4/3811 (0.1%)	1.11	29/5174 (0.6%)
1	B	1.04	8/3811 (0.2%)	1.09	19/5174 (0.4%)
All	All	1.02	12/7622 (0.2%)	1.10	48/10348 (0.5%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	117	TYR	CE1-CZ	-10.92	1.24	1.38
1	B	117	TYR	CG-CD2	-10.69	1.25	1.39
1	B	67	GLU	CD-OE2	-7.14	1.17	1.25
1	A	67	GLU	CD-OE2	-7.14	1.17	1.25
1	B	117	TYR	CE2-CZ	-6.80	1.29	1.38
1	B	67	GLU	CG-CD	-6.59	1.42	1.51
1	A	175	GLU	CD-OE2	-6.45	1.18	1.25
1	B	407	TYR	CE2-CZ	6.02	1.46	1.38
1	A	67	GLU	CG-CD	-5.96	1.43	1.51
1	B	67	GLU	CD-OE1	-5.62	1.19	1.25
1	B	1	GLU	CD-OE1	-5.53	1.19	1.25
1	A	67	GLU	CB-CG	-5.12	1.42	1.52

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	369	ARG	NE-CZ-NH2	-9.15	115.72	120.30
1	A	182	ASP	CB-CG-OD2	8.46	125.92	118.30
1	B	324	ARG	NE-CZ-NH2	-7.51	116.54	120.30
1	A	37	ASP	CB-CG-OD2	7.31	124.88	118.30
1	B	476	ASP	CB-CG-OD2	7.23	124.81	118.30
1	A	173	ASP	CB-CG-OD2	7.20	124.78	118.30
1	B	324	ARG	NE-CZ-NH1	6.96	123.78	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	274	ASP	CB-CG-OD2	6.96	124.56	118.30
1	A	324	ARG	NE-CZ-NH2	-6.76	116.92	120.30
1	A	413	ASP	CB-CG-OD2	6.67	124.30	118.30
1	B	22	LYS	CB-CG-CD	6.62	128.82	111.60
1	A	176	ASP	CB-CG-OD2	6.54	124.18	118.30
1	A	182	ASP	OD1-CG-OD2	-6.40	111.14	123.30
1	A	265	MET	CG-SD-CE	6.27	110.24	100.20
1	B	1	GLU	OE1-CD-OE2	-6.25	115.80	123.30
1	B	236	ASP	CB-CG-OD2	6.24	123.91	118.30
1	A	385	ARG	NE-CZ-NH2	-6.16	117.22	120.30
1	A	369	ARG	NE-CZ-NH1	6.13	123.37	120.30
1	A	214	ASP	CB-CG-OD2	6.10	123.79	118.30
1	A	476	ASP	CB-CA-C	-6.09	98.21	110.40
1	B	257	ASP	CB-CG-OD2	6.02	123.72	118.30
1	A	433	ASP	CB-CG-OD2	5.99	123.69	118.30
1	B	80	ASP	CB-CG-OD1	5.91	123.62	118.30
1	A	217	ASP	CB-CG-OD2	5.91	123.61	118.30
1	B	252	ASP	CB-CG-OD2	5.86	123.58	118.30
1	A	383	ASP	CB-CG-OD2	5.86	123.57	118.30
1	A	252	ASP	CB-CG-OD2	5.79	123.51	118.30
1	A	257	ASP	CB-CG-OD1	5.79	123.51	118.30
1	A	169	ASP	CB-CG-OD2	5.73	123.46	118.30
1	A	235	ASP	CB-CG-OD2	5.71	123.44	118.30
1	B	173	ASP	CB-CG-OD2	5.66	123.40	118.30
1	B	37	ASP	CB-CG-OD2	5.60	123.34	118.30
1	B	10	ASP	CB-CG-OD2	5.57	123.31	118.30
1	A	225	ASP	CB-CG-OD2	5.56	123.30	118.30
1	B	324	ARG	CG-CD-NE	-5.55	100.13	111.80
1	B	161	ASP	CB-CG-OD2	5.48	123.23	118.30
1	A	3	ASP	CB-CG-OD2	5.38	123.14	118.30
1	A	10	ASP	CB-CG-OD2	5.38	123.14	118.30
1	B	385	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	A	48	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	315	ASP	CB-CG-OD2	5.25	123.02	118.30
1	B	22	LYS	CB-CA-C	-5.19	100.02	110.40
1	B	85	ASP	CB-CG-OD1	5.13	122.91	118.30
1	A	476	ASP	CB-CG-OD2	5.04	122.84	118.30
1	B	214	ASP	CB-CG-OD2	5.04	122.84	118.30
1	A	332	ASP	CB-CG-OD2	5.03	122.83	118.30
1	A	368	ASP	CB-CG-OD1	5.01	122.81	118.30
1	A	251	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

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	3731	0	3516	58	0
1	B	3731	0	3516	57	0
2	A	14	0	13	0	0
2	B	14	0	13	4	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	5	0	0	2	0
4	B	5	0	0	3	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	A	101	0	0	3	0
6	B	82	0	0	2	0
All	All	7699	0	7058	115	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 8.

All (115) 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:B:114:ASN:HD21	2:B:483:NAG:C1	1.27	1.45
1:A:339:MET:SD	1:A:343:MET:CE	2.40	1.09
1:A:339:MET:SD	1:A:343:MET:HE3	2.00	1.01
1:B:313:ARG:HE	1:B:316:HIS:HD2	1.01	0.95
1:A:313:ARG:HE	1:A:316:HIS:HD2	1.06	0.95
1:B:114:ASN:HD21	2:B:483:NAG:C2	1.86	0.88
1:A:339:MET:CG	1:A:343:MET:CE	2.55	0.84
1:B:313:ARG:HE	1:B:316:HIS:CD2	1.93	0.83
1:A:339:MET:HG3	1:A:343:MET:CE	2.09	0.82
1:A:86:SER:OG	4:A:486:PO4:O4	1.98	0.80
1:B:86:SER:OG	4:B:484:PO4:P	2.42	0.77
1:A:339:MET:SD	1:A:343:MET:HE2	2.23	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:MET:SD	1:B:343:MET:CE	2.74	0.75
1:A:313:ARG:HE	1:A:316:HIS:CD2	1.99	0.73
1:A:339:MET:CG	1:A:343:MET:HE1	2.19	0.71
1:A:339:MET:HG3	1:A:343:MET:HE3	1.73	0.70
1:B:214:ASP:OD2	1:B:215:ILE:O	2.10	0.70
1:A:339:MET:CG	1:A:343:MET:HE3	2.17	0.69
1:A:29:LYS:HE3	1:A:302:GLU:O	1.92	0.69
1:A:339:MET:HG3	1:A:343:MET:HE1	1.72	0.69
4:B:484:PO4:O2	6:B:523:HOH:O	2.11	0.68
1:A:292:LYS:HG3	1:A:343:MET:HE2	1.77	0.66
1:A:313:ARG:NE	1:A:316:HIS:HD2	1.88	0.66
1:A:215:ILE:O	1:A:216:GLU:HB2	1.98	0.64
1:B:339:MET:SD	1:B:343:MET:HE3	2.38	0.64
1:B:146:ARG:H	1:B:272:HIS:HD2	1.46	0.64
1:B:369:ARG:O	1:B:370:ASN:HB2	1.97	0.64
1:B:359:HIS:HD2	6:B:505:HOH:O	1.83	0.61
1:A:359:HIS:HD2	6:A:488:HOH:O	1.84	0.61
1:B:58:PHE:CD2	1:B:370:ASN:OD1	2.53	0.60
1:B:58:PHE:CG	1:B:370:ASN:OD1	2.54	0.60
1:B:339:MET:HG3	1:B:343:MET:CE	2.31	0.59
1:A:292:LYS:HG3	1:A:343:MET:CE	2.33	0.59
1:B:292:LYS:HG3	1:B:343:MET:HE2	1.84	0.59
1:B:215:ILE:O	1:B:216:GLU:HB2	2.03	0.59
1:B:112:ARG:O	1:B:113:THR:HB	2.04	0.57
1:B:43:THR:OG1	1:B:318:HIS:HE1	1.87	0.57
1:B:292:LYS:HA	1:B:343:MET:HE1	1.87	0.57
1:A:203:GLY:N	1:A:271:THR:O	2.38	0.56
1:B:115:CYS:HB3	1:B:175:GLU:OE1	2.04	0.56
1:B:313:ARG:NE	1:B:316:HIS:HD2	1.87	0.56
1:A:208:PHE:CE1	1:A:221:GLY:CA	2.89	0.55
1:A:214:ASP:OD2	1:A:215:ILE:O	2.25	0.55
1:A:392:TYR:O	1:A:423:SER:HA	2.07	0.54
1:B:86:SER:OG	4:B:484:PO4:O4	2.26	0.54
1:B:29:LYS:HE3	1:B:302:GLU:O	2.06	0.54
1:A:112:ARG:O	1:A:113:THR:HB	2.08	0.54
1:A:146:ARG:H	1:A:272:HIS:HD2	1.56	0.53
1:B:146:ARG:H	1:B:272:HIS:CD2	2.27	0.53
1:A:215:ILE:HG13	6:A:511:HOH:O	2.08	0.53
1:A:119:LEU:HD11	1:A:179:ILE:HD11	1.92	0.52
1:A:473:THR:HG22	1:A:476:ASP:H	1.75	0.51
1:B:339:MET:SD	1:B:343:MET:HE2	2.49	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:MET:CG	1:B:343:MET:CE	2.88	0.51
1:B:151:THR:HB	1:B:152:PRO:CD	2.41	0.51
1:A:315:ASP:OD1	1:A:359:HIS:HE1	1.94	0.50
1:B:315:ASP:OD1	1:B:359:HIS:HE1	1.94	0.50
1:A:194:LYS:O	1:A:237:LYS:NZ	2.44	0.50
1:B:339:MET:HG3	1:B:343:MET:HE3	1.93	0.50
1:A:86:SER:OG	4:A:486:PO4:P	2.69	0.50
1:B:112:ARG:O	1:B:113:THR:CB	2.60	0.49
1:B:458:ILE:HB	1:B:459:PRO:HD3	1.95	0.49
1:B:339:MET:HG3	1:B:343:MET:HE1	1.93	0.49
1:A:280:ASP:OD1	1:A:282:GLU:HB2	2.13	0.48
1:B:392:TYR:O	1:B:423:SER:HA	2.14	0.48
1:A:370:ASN:HD22	1:A:370:ASN:N	2.12	0.48
1:A:271:THR:HG23	1:A:272:HIS:H	1.79	0.47
1:B:280:ASP:OD1	1:B:282:GLU:HB2	2.14	0.47
1:A:369:ARG:O	1:A:370:ASN:HB2	2.15	0.47
1:B:194:LYS:O	1:B:237:LYS:NZ	2.48	0.47
1:B:318:HIS:HB3	1:B:359:HIS:CD2	2.50	0.46
1:B:397:GLY:HA3	1:B:421:TYR:O	2.16	0.46
1:A:458:ILE:HB	1:A:459:PRO:HD3	1.98	0.46
1:A:247:VAL:O	1:A:266:GLY:HA2	2.16	0.45
1:B:114:ASN:CG	2:B:483:NAG:C1	2.78	0.45
1:A:162:ARG:HG3	1:A:163:ASP:N	2.31	0.45
1:A:389:ILE:HD13	1:B:82:GLN:HE22	1.81	0.44
1:B:296:GLU:O	1:B:299:THR:HG22	2.17	0.44
1:A:112:ARG:O	1:A:113:THR:CB	2.65	0.44
1:B:90:ALA:HA	1:B:93:TYR:CZ	2.53	0.44
1:A:215:ILE:O	1:A:216:GLU:CB	2.66	0.44
1:B:318:HIS:HB3	1:B:359:HIS:CG	2.53	0.44
1:A:93:TYR:CD1	1:A:94:LEU:HG	2.53	0.44
1:A:261:THR:HG22	1:A:297:MET:HE1	2.00	0.43
1:B:114:ASN:ND2	2:B:483:NAG:C2	2.65	0.43
1:B:377:ALA:HB2	1:B:389:ILE:HA	2.01	0.43
1:B:416:ASP:HB3	1:B:419:PHE:HB2	2.01	0.43
1:B:119:LEU:HD11	1:B:179:ILE:HD11	2.00	0.43
1:A:209:PRO:HA	1:A:223:ARG:HB2	2.01	0.43
1:A:287:LEU:N	1:A:288:PRO:CD	2.82	0.42
1:B:339:MET:CG	1:B:343:MET:HE3	2.49	0.42
1:A:292:LYS:CB	1:A:343:MET:HE1	2.49	0.42
1:A:359:HIS:C	1:A:433:ASP:HB2	2.40	0.42
1:B:93:TYR:CD1	1:B:94:LEU:HG	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:HIS:HB3	1:A:359:HIS:CD2	2.55	0.42
1:B:209:PRO:HA	1:B:223:ARG:HB2	2.01	0.42
1:A:271:THR:HG23	1:A:272:HIS:N	2.35	0.41
1:A:90:ALA:HA	1:A:93:TYR:CZ	2.55	0.41
1:A:149:HIS:CD2	1:A:152:PRO:HD2	2.55	0.41
1:A:437:VAL:HB	6:A:507:HOH:O	2.19	0.41
1:B:287:LEU:N	1:B:288:PRO:CD	2.83	0.41
1:A:292:LYS:HA	1:A:343:MET:HE1	2.03	0.41
1:B:292:LYS:HG3	1:B:343:MET:CE	2.48	0.41
1:A:63:ILE:O	1:A:64:SER:C	2.59	0.41
1:B:473:THR:HG22	1:B:476:ASP:H	1.86	0.41
1:A:352:LEU:C	1:A:352:LEU:HD23	2.40	0.41
1:A:79:THR:OG1	1:A:99:THR:C	2.58	0.41
1:A:151:THR:HB	1:A:152:PRO:CD	2.51	0.41
1:B:217:ASP:CB	1:B:219:ILE:HG13	2.50	0.41
1:B:208:PHE:CE2	1:B:221:GLY:CA	3.04	0.41
1:B:162:ARG:HG3	1:B:163:ASP:N	2.35	0.40
1:B:41:LEU:HA	1:B:41:LEU:HD23	1.97	0.40
1:A:292:LYS:HB2	1:A:343:MET:HE1	2.02	0.40
1:A:41:LEU:HD23	1:A:41:LEU:HA	1.98	0.40
1:B:287:LEU:HD23	1:B:333:MET:HA	2.04	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	474/478 (99%)	457 (96%)	16 (3%)	1 (0%)	52	51
1	B	474/478 (99%)	460 (97%)	13 (3%)	1 (0%)	52	51
All	All	948/956 (99%)	917 (97%)	29 (3%)	2 (0%)	52	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	GLU
1	B	216	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	394/398 (99%)	382 (97%)	12 (3%)	48	48
1	B	394/398 (99%)	387 (98%)	7 (2%)	66	71
All	All	788/796 (99%)	769 (98%)	19 (2%)	57	60

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

Mol	Chain	Res	Type
1	A	33	PHE
1	A	107	ASP
1	A	178	GLU
1	A	179	ILE
1	A	265	MET
1	A	324	ARG
1	A	359	HIS
1	A	370	ASN
1	A	399	HIS
1	A	402	GLU
1	A	411	GLU
1	A	473	THR
1	B	179	ILE
1	B	245	SER
1	B	359	HIS
1	B	399	HIS
1	B	402	GLU
1	B	411	GLU
1	B	473	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	GLN
1	A	133	GLN
1	A	158	HIS
1	A	195	ASN
1	A	272	HIS
1	A	316	HIS
1	A	322	GLN
1	A	359	HIS
1	A	370	ASN
1	A	447	HIS
1	B	82	GLN
1	B	114	ASN
1	B	133	GLN
1	B	195	ASN
1	B	272	HIS
1	B	316	HIS
1	B	318	HIS
1	B	322	GLN
1	B	359	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	$\# Z > 2$
2	NAG	A	483	1	14,14,15	1.10	1 (7%)	15,19,21	2.92	6 (40%)
4	PO4	A	486	3	4,4,4	0.95	0	6,6,6	0.49	0
5	SO4	A	487	-	4,4,4	0.43	0	6,6,6	0.51	0
2	NAG	B	483	1	14,14,15	0.90	0	15,19,21	2.48	6 (40%)
4	PO4	B	484	3	4,4,4	0.53	0	6,6,6	0.34	0
5	SO4	B	488	-	4,4,4	0.29	0	6,6,6	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	NAG	A	483	1	-	0/6/23/26	0/1/1/1
4	PO4	A	486	3	-	0/0/0/0	0/0/0/0
5	SO4	A	487	-	-	0/0/0/0	0/0/0/0
2	NAG	B	483	1	-	0/6/23/26	0/1/1/1
4	PO4	B	484	3	-	0/0/0/0	0/0/0/0
5	SO4	B	488	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	483	NAG	O5-C1	-2.30	1.39	1.43

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	483	NAG	C4-C3-C2	-2.84	106.82	111.23
2	A	483	NAG	O7-C7-C8	-2.75	117.01	122.06
2	B	483	NAG	C6-C5-C4	-2.21	107.56	113.02
2	A	483	NAG	C6-C5-C4	2.77	119.85	113.02
2	A	483	NAG	O5-C5-C6	2.89	113.60	107.35
2	B	483	NAG	C3-C4-C5	3.62	116.50	110.20
2	B	483	NAG	O5-C5-C6	3.79	115.55	107.35
2	B	483	NAG	O6-C6-C5	4.67	126.76	111.33
2	A	483	NAG	O3-C3-C4	5.05	121.70	110.34
2	B	483	NAG	C1-O5-C5	5.13	118.76	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	483	NAG	O6-C6-C5	5.71	130.21	111.33
2	A	483	NAG	C1-O5-C5	5.79	119.60	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	486	PO4	2	0
2	B	483	NAG	4	0
4	B	484	PO4	3	0

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	476/478 (99%)	-0.13	8 (1%) 73 80	19, 27, 41, 59	0
1	B	476/478 (99%)	-0.08	12 (2%) 61 69	19, 27, 41, 59	0
All	All	952/956 (99%)	-0.10	20 (2%) 67 74	19, 27, 41, 59	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	471	GLY	3.9
1	B	402	GLU	3.6
1	A	470	THR	3.6
1	B	470	THR	3.6
1	B	476	ASP	3.5
1	B	302	GLU	3.2
1	B	174	ARG	3.1
1	A	476	ASP	2.9
1	A	412	GLU	2.9
1	B	403	ASP	2.8
1	A	402	GLU	2.7
1	B	475	CYS	2.6
1	B	472	ARG	2.5
1	B	239	SER	2.4
1	A	174	ARG	2.3
1	B	412	GLU	2.3
1	A	215	ILE	2.3
1	A	475	CYS	2.2
1	B	179	ILE	2.2
1	A	403	ASP	2.1

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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	PO4	B	484	5/5	0.82	0.29	9.45	20,21,26,31	5
4	PO4	A	486	5/5	0.96	0.19	2.89	17,20,30,33	5
3	ZN	B	482	1/1	1.00	0.10	-1.61	38,38,38,38	0
3	ZN	A	484	1/1	0.98	0.07	-2.05	24,24,24,24	0
3	ZN	B	480	1/1	0.99	0.06	-2.98	23,23,23,23	0
3	ZN	B	481	1/1	0.99	0.04	-3.18	25,25,25,25	0
3	ZN	A	485	1/1	0.99	0.06	-3.58	27,27,27,27	0
3	ZN	A	479	1/1	0.84	0.08	-3.83	43,43,43,43	0
5	SO4	B	488	5/5	0.70	0.37	-	27,38,40,40	5
2	NAG	A	483	14/15	0.84	0.13	-	32,37,40,43	0
2	NAG	B	483	14/15	0.79	0.18	-	35,44,50,56	0
5	SO4	A	487	5/5	0.85	0.20	-	31,32,34,35	5

6.5 Other polymers [i](#)

There are no such residues in this entry.