



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:33 PM UTC

PDB ID : 1URB / pdb_00001urb
Title : ALKALINE PHOSPHATASE (N51MG)
Authors : Tibbitts, T.T.; Murphy, J.E.; Kantrowitz, E.R.
Deposited on : 1996-02-03
Resolution : 2.14 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

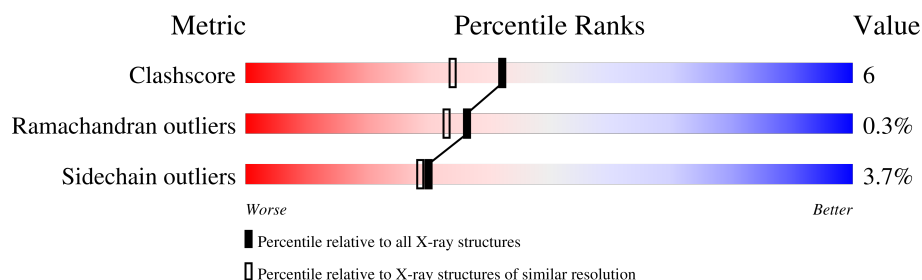
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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))
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)

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 of 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	446	
1	B	446	

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	457	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7025 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	446	Total	C	N	O	S	0	0	0
			3281	2028	579	662	12			
1	B	446	Total	C	N	O	S	0	0	0
			3281	2028	579	662	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	ASN	ASP	engineered mutation	UNP P00634
B	51	ASN	ASP	engineered mutation	UNP P00634

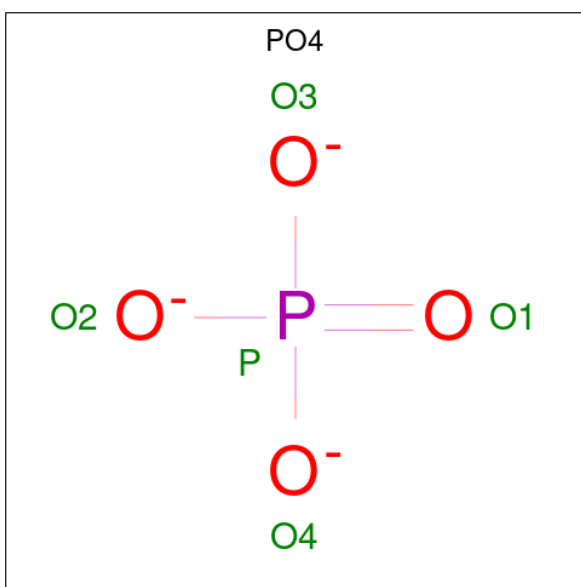
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 5 is water.

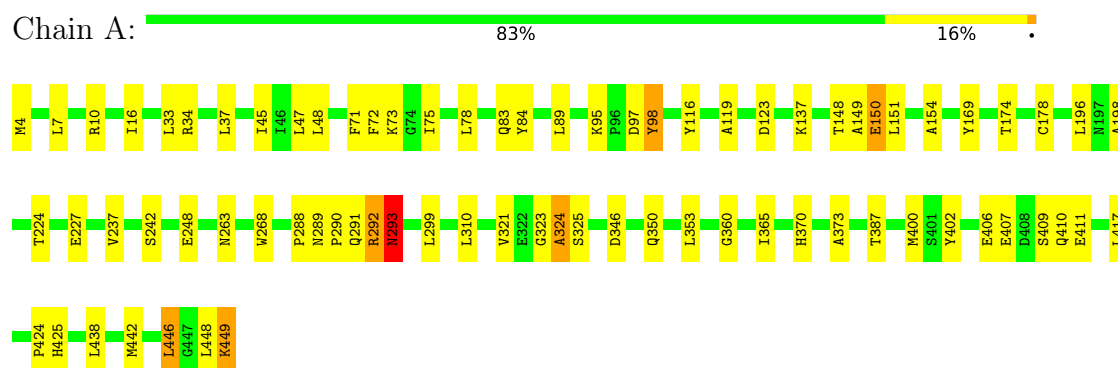
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	248	Total	O	0	0
			248	248		
5	B	191	Total	O	0	0
			191	191		

3 Residue-property plots

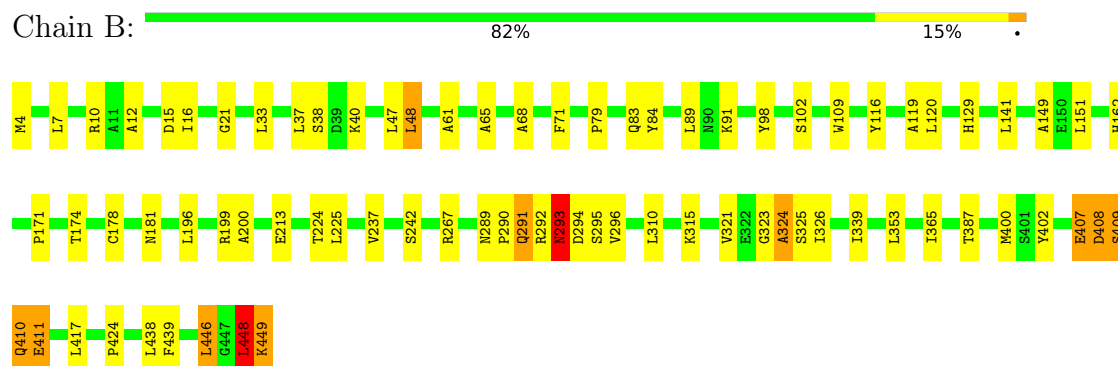
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: ALKALINE PHOSPHATASE



• Molecule 1: ALKALINE PHOSPHATASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	195.72Å 168.48Å 76.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.14	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.14)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.193 , 0.241	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7025	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.95	8/3335 (0.2%)	1.19	25/4526 (0.6%)
1	B	0.86	10/3335 (0.3%)	1.12	18/4526 (0.4%)
All	All	0.90	18/6670 (0.3%)	1.15	43/9052 (0.5%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	406	GLU	CA-C	-11.79	1.36	1.52
1	A	407	GLU	N-CA	-10.52	1.34	1.46
1	A	406	GLU	C-N	-10.37	1.16	1.33
1	A	293	ASN	C-O	10.06	1.36	1.24
1	A	407	GLU	CA-CB	-9.71	1.38	1.53
1	B	291	GLN	CG-CD	8.30	1.72	1.52
1	B	291	GLN	CB-CG	-8.06	1.28	1.52
1	B	409	SER	CA-C	7.81	1.61	1.52
1	A	292	ARG	N-CA	7.57	1.55	1.46
1	B	409	SER	C-N	7.54	1.43	1.33
1	B	410	GLN	N-CA	7.22	1.54	1.46
1	A	291	GLN	C-N	6.98	1.42	1.33
1	B	409	SER	C-O	6.87	1.32	1.24
1	A	291	GLN	C-O	6.50	1.32	1.24
1	B	448	LEU	C-O	-6.42	1.15	1.23
1	B	448	LEU	CA-C	5.98	1.61	1.53
1	B	291	GLN	N-CA	5.66	1.53	1.46
1	B	290	PRO	CA-C	5.62	1.60	1.52

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	406	GLU	CA-C-O	17.62	139.89	119.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	409	SER	CA-C-O	-11.02	108.46	120.36
1	A	406	GLU	CA-C-N	-9.64	105.37	122.15
1	A	406	GLU	C-N-CA	-9.64	105.37	122.15
1	A	293	ASN	O-C-N	9.56	135.31	122.59
1	B	98	TYR	N-CA-C	8.13	122.91	112.34
1	A	291	GLN	O-C-N	8.09	133.53	122.37
1	A	98	TYR	N-CA-C	7.96	122.09	112.38
1	B	324	ALA	N-CA-C	7.66	119.71	111.36
1	B	293	ASN	N-CA-C	7.24	126.22	110.80
1	A	293	ASN	N-CA-C	7.02	125.75	110.80
1	B	448	LEU	N-CA-CB	-6.84	100.57	110.36
1	A	291	GLN	CA-C-O	-6.43	111.49	119.28
1	A	324	ALA	N-CA-C	6.28	119.42	111.69
1	B	325	SER	N-CA-C	6.24	120.61	113.19
1	B	411	GLU	N-CA-C	6.10	119.43	110.59
1	A	154	ALA	N-CA-C	5.76	120.82	111.37
1	A	75	ILE	N-CA-C	5.74	117.16	110.62
1	A	411	GLU	N-CA-C	5.62	118.75	110.59
1	A	97	ASP	N-CA-C	-5.61	98.20	108.02
1	B	323	GLY	N-CA-C	-5.61	99.88	113.18
1	B	417	LEU	N-CA-C	5.60	117.70	109.24
1	A	373	ALA	N-CA-C	5.58	120.21	112.45
1	B	91	LYS	N-CA-C	5.58	117.81	111.11
1	B	408	ASP	N-CA-C	5.53	117.00	110.97
1	A	150	GLU	N-CA-C	-5.50	101.91	110.10
1	B	294	ASP	N-CA-C	-5.41	106.52	113.01
1	A	323	GLY	N-CA-C	-5.40	100.39	113.18
1	B	65	ALA	N-CA-C	5.34	119.52	112.89
1	A	417	LEU	N-CA-C	5.32	117.07	109.14
1	B	200	ALA	N-CA-C	-5.31	103.52	110.53
1	B	12	ALA	N-CA-C	-5.31	102.19	110.10
1	A	406	GLU	O-C-N	-5.25	115.27	122.46
1	B	326	ILE	N-CA-C	-5.18	105.66	110.53
1	B	79	PRO	N-CA-C	5.18	120.34	113.40
1	B	291	GLN	OE1-CD-NE2	-5.13	117.47	122.60
1	A	325	SER	N-CA-C	5.07	119.22	113.19
1	A	78	LEU	CA-C-N	5.03	124.33	118.85
1	A	78	LEU	C-N-CA	5.03	124.33	118.85
1	A	169	TYR	N-CA-C	5.03	116.45	110.97
1	A	360	GLY	N-CA-C	5.02	122.02	115.40
1	A	291	GLN	CA-C-N	5.01	127.76	120.79
1	A	291	GLN	C-N-CA	5.01	127.76	120.79

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	3281	0	3229	44	0
1	B	3281	0	3228	46	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	10	0	0	3	0
4	B	10	0	0	0	0
5	A	248	0	0	9	1
5	B	191	0	0	5	0
All	All	7025	0	6457	82	1

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 (82) 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:290:PRO:HB2	5:A:701:HOH:O	1.76	0.84
1:B:10:ARG:HB2	1:B:71:PHE:CE1	2.17	0.80
1:A:73:LYS:HE2	5:A:463:HOH:O	1.81	0.79
1:B:402:TYR:HB3	1:B:410:GLN:HG3	1.63	0.79
1:B:237:VAL:HG13	1:B:242:SER:HB2	1.69	0.75
1:A:402:TYR:HB3	1:A:410:GLN:HG3	1.70	0.74
1:B:408:ASP:OD1	1:B:409:SER:N	2.24	0.71
1:B:400:MET:HE3	5:B:579:HOH:O	1.89	0.70
1:A:292:ARG:O	1:A:293:ASN:HB2	1.90	0.69
1:A:288:PRO:HB3	1:A:292:ARG:CZ	2.23	0.69
1:B:48:LEU:HD13	1:B:321:VAL:HB	1.76	0.66
1:A:293:ASN:ND2	5:A:580:HOH:O	2.29	0.66
1:B:293:ASN:HB3	1:B:295:SER:H	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:VAL:HG13	1:A:242:SER:HB2	1.79	0.64
1:A:370:HIS:HB2	5:A:683:HOH:O	1.97	0.64
1:B:411:GLU:HG2	5:B:541:HOH:O	1.97	0.64
1:B:267:ARG:O	1:B:292:ARG:NH1	2.29	0.64
1:A:289:ASN:O	1:A:292:ARG:HG2	1.97	0.63
1:A:365:ILE:HD13	1:A:438:LEU:HD11	1.79	0.63
1:B:449:LYS:H	1:B:449:LYS:HD2	1.65	0.62
1:A:16:ILE:HG22	1:B:89:LEU:HD21	1.80	0.62
1:A:48:LEU:HD13	1:A:321:VAL:HB	1.82	0.61
1:A:83:GLN:HE21	1:B:83:GLN:HE21	1.50	0.60
1:A:73:LYS:HB2	1:A:350:GLN:NE2	2.17	0.59
1:B:293:ASN:HB2	1:B:296:VAL:HG23	1.83	0.59
1:B:4:MET:HE1	1:B:424:PRO:HD3	1.85	0.58
1:A:16:ILE:CG2	1:B:89:LEU:HD21	2.34	0.57
1:A:116:TYR:CZ	1:A:119:ALA:HB2	2.39	0.57
1:A:89:LEU:HD21	1:B:16:ILE:CG2	2.36	0.55
1:A:89:LEU:HD21	1:B:16:ILE:HG22	1.87	0.55
1:B:365:ILE:HD13	1:B:438:LEU:HD11	1.88	0.55
1:A:292:ARG:NH2	4:A:457:PO4:O1	2.40	0.54
1:B:149:ALA:HB2	1:B:324:ALA:CB	2.38	0.54
1:A:288:PRO:HB3	1:A:292:ARG:NH2	2.24	0.53
1:B:10:ARG:HB2	1:B:71:PHE:CD1	2.44	0.51
1:B:129:HIS:O	1:B:162:HIS:HE1	1.93	0.51
1:A:37:LEU:HD21	1:B:33:LEU:HD23	1.93	0.50
1:B:446:LEU:HB3	1:B:448:LEU:HD13	1.93	0.50
1:B:178:CYS:HB3	1:B:181:ASN:OD1	2.12	0.49
1:A:268:TRP:HD1	1:A:292:ARG:HH21	1.60	0.48
1:B:120:LEU:O	1:B:162:HIS:HA	2.13	0.48
1:B:267:ARG:HG3	5:B:493:HOH:O	2.14	0.48
1:A:73:LYS:CE	5:A:463:HOH:O	2.51	0.48
1:A:449:LYS:H	1:A:449:LYS:HD2	1.79	0.48
1:A:149:ALA:HB2	1:A:324:ALA:CB	2.44	0.48
1:A:248:GLU:HA	5:A:688:HOH:O	2.14	0.47
1:A:438:LEU:HG	1:A:442:MET:HE2	1.97	0.47
1:B:213:GLU:O	1:B:224:THR:HA	2.15	0.47
1:B:16:ILE:HG12	5:B:520:HOH:O	2.15	0.46
1:B:38:SER:OG	1:B:40:LYS:HG2	2.16	0.46
1:B:407:GLU:HB3	1:B:408:ASP:H	1.55	0.46
1:A:424:PRO:O	1:A:425:HIS:HB2	2.15	0.46
1:A:224:THR:OG1	1:A:227:GLU:HG3	2.16	0.46
1:B:199:ARG:O	1:B:199:ARG:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:ARG:O	1:B:296:VAL:HB	2.15	0.46
1:A:123:ASP:HB2	5:A:596:HOH:O	2.17	0.45
1:B:289:ASN:O	1:B:292:ARG:HD3	2.17	0.44
1:A:174:THR:HG23	1:A:178:CYS:HB2	1.99	0.44
1:A:387:THR:HA	1:A:400:MET:O	2.18	0.43
1:B:411:GLU:HA	5:B:541:HOH:O	2.18	0.43
1:A:148:THR:HG23	1:A:299:LEU:HD13	2.00	0.43
1:B:174:THR:HG23	1:B:178:CYS:HB2	2.00	0.43
1:A:45:ILE:HD12	1:A:446:LEU:HD22	2.00	0.42
1:A:292:ARG:NH1	4:A:457:PO4:O1	2.53	0.42
1:A:98:TYR:HE1	1:B:68:ALA:HB2	1.85	0.42
1:A:137:LYS:HE3	1:A:198:ALA:O	2.20	0.42
1:A:10:ARG:HB2	1:A:71:PHE:CE1	2.55	0.42
1:A:72:PHE:HB3	1:A:346:ASP:OD1	2.20	0.41
1:A:95:LYS:HB2	5:A:695:HOH:O	2.20	0.41
1:B:141:LEU:HD23	1:B:315:LYS:HB3	2.03	0.41
1:B:61:ALA:HA	1:B:339:ILE:HG23	2.03	0.41
1:B:109:TRP:O	1:B:439:PHE:HB2	2.20	0.41
1:B:33:LEU:HD12	1:B:33:LEU:HA	1.87	0.41
1:A:4:MET:HB3	5:A:534:HOH:O	2.21	0.41
1:A:150:GLU:HG3	1:A:263:ASN:OD1	2.21	0.41
1:B:15:ASP:O	1:B:21:GLY:HA3	2.21	0.41
1:B:116:TYR:CZ	1:B:119:ALA:HB2	2.55	0.41
1:B:446:LEU:HD12	1:B:446:LEU:HA	1.92	0.41
1:A:33:LEU:HD23	1:B:37:LEU:HD21	2.03	0.40
1:A:292:ARG:CZ	4:A:457:PO4:O1	2.69	0.40
1:B:171:PRO:HD3	1:B:225:LEU:HD11	2.03	0.40
1:B:387:THR:HA	1:B:400:MET:O	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:505:HOH:O	5:A:505:HOH:O[3_656]	2.13	0.07

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	444/446 (100%)	430 (97%)	13 (3%)	1 (0%)	43	42
1	B	444/446 (100%)	432 (97%)	10 (2%)	2 (0%)	24	19
All	All	888/892 (100%)	862 (97%)	23 (3%)	3 (0%)	36	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	407	GLU
1	B	293	ASN
1	A	293	ASN

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	337/337 (100%)	325 (96%)	12 (4%)	31	30
1	B	337/337 (100%)	324 (96%)	13 (4%)	28	26
All	All	674/674 (100%)	649 (96%)	25 (4%)	30	29

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

Mol	Chain	Res	Type
1	A	7	LEU
1	A	34	ARG
1	A	47	LEU

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Mol	Chain	Res	Type
1	A	84	TYR
1	A	151	LEU
1	A	196	LEU
1	A	310	LEU
1	A	353	LEU
1	A	409	SER
1	A	446	LEU
1	A	448	LEU
1	A	449	LYS
1	B	7	LEU
1	B	47	LEU
1	B	48	LEU
1	B	84	TYR
1	B	102	SER
1	B	151	LEU
1	B	196	LEU
1	B	291	GLN
1	B	310	LEU
1	B	353	LEU
1	B	446	LEU
1	B	448	LEU
1	B	449	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	235	GLN
1	A	293	ASN
1	A	388	GLN
1	A	391	ASN
1	A	410	GLN
1	B	235	GLN
1	B	276	HIS
1	B	350	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 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	$\# Z > 2$
4	PO4	A	453	2	4,4,4	1.30	0	6,6,6	1.17	0
4	PO4	A	457	-	4,4,4	1.87	2 (50%)	6,6,6	0.82	0
4	PO4	B	453	2	4,4,4	1.27	0	6,6,6	1.13	0
4	PO4	B	457	-	4,4,4	1.33	1 (25%)	6,6,6	1.11	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	457	PO4	P-O1	-2.50	1.44	1.50
4	B	457	PO4	P-O2	-2.29	1.48	1.54
4	A	457	PO4	P-O4	-2.23	1.48	1.54

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	457	PO4	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	406:GLU	C	407:GLU	N	1.16

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.