



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:33 AM UTC

PDB ID : 1KH5 / pdb_00001kh5
Title : E. COLI ALKALINE PHOSPHATASE MUTANT (D330N) MIMIC OF THE
TRANSITION STATES WITH ALUMINIUM FLUORIDE
Authors : Le Du, M.H.; Lamoure, C.; Muller, B.H.; Bulgakov, O.V.; Lajeunesse, E.
Deposited on : 2001-11-29
Resolution : 2.00 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

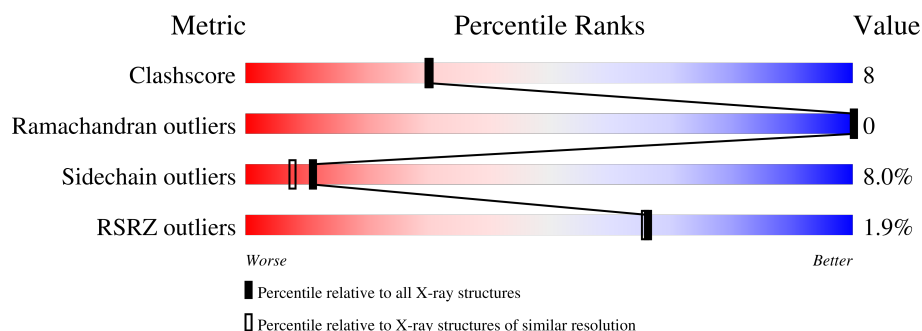
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	449	2% 76% 20% ..
1	B	449	2% 76% 19% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6879 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	444	Total	C	N	O	S	0	0	0
			3260	2014	578	657	11			
1	B	444	Total	C	N	O	S	0	0	0
			3260	2014	578	657	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ASN	ASP	conflict	UNP P00634
A	35	ASN	ASP	conflict	UNP P00634
A	176	GLN	GLU	conflict	UNP P00634
A	228	GLU	GLN	conflict	UNP P00634
A	230	GLU	GLN	conflict	UNP P00634
A	330	ASN	ASP	engineered mutation	UNP P00634
B	515	ASN	ASP	conflict	UNP P00634
B	535	ASN	ASP	conflict	UNP P00634
B	676	GLN	GLU	conflict	UNP P00634
B	728	GLU	GLN	conflict	UNP P00634
B	730	GLU	GLN	conflict	UNP P00634
B	830	ASN	ASP	engineered mutation	UNP P00634

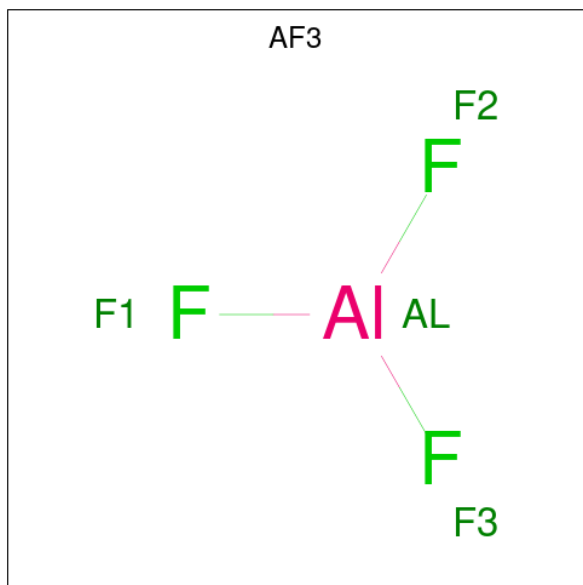
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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

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

- Molecule 4 is ALUMINUM FLUORIDE (CCD ID: AF3) (formula: AlF_3).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Al F 4 1 3	0	0
4	B	1	Total Al F 4 1 3	0	0

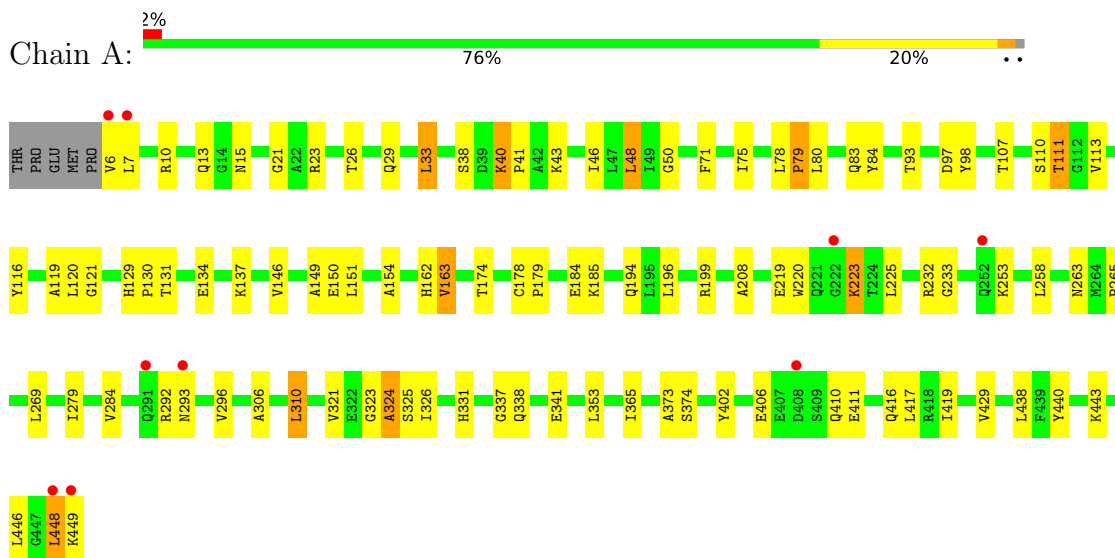
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	174	Total O 174 174	0	0
5	B	171	Total O 171 171	0	0

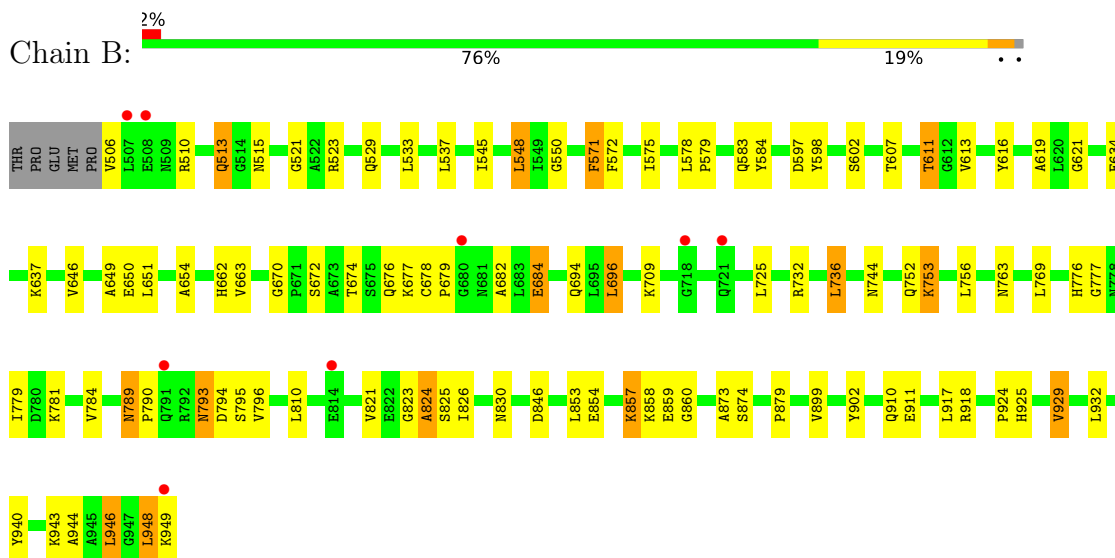
3 Residue-property plots

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 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 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	163.62Å 163.62Å 138.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.00 10.00 – 2.01	Depositor EDS
% Data completeness (in resolution range)	94.0 (10.00-2.00) 94.3 (10.00-2.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.01Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.194 , 0.228 0.210 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	26.7	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6879	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: AF3, ZN, MG

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	0.59	0/3313	1.08	18/4496 (0.4%)
1	B	0.58	0/3313	1.08	26/4496 (0.6%)
All	All	0.59	0/6626	1.08	44/8992 (0.5%)

There are no bond length outliers.

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	154	ALA	N-CA-C	9.24	122.20	111.11
1	A	324	ALA	N-CA-C	8.98	121.15	111.36
1	B	654	ALA	N-CA-C	8.54	121.36	111.11
1	B	824	ALA	N-CA-C	8.50	120.62	111.36
1	B	911	GLU	N-CA-C	7.59	122.19	110.42
1	A	98	TYR	N-CA-C	7.49	120.32	111.71
1	A	325	SER	N-CA-C	7.29	122.02	113.20
1	A	326	ILE	N-CA-C	-7.17	103.48	110.72
1	B	598	TYR	N-CA-C	7.11	119.88	111.71
1	B	826	ILE	N-CA-C	-6.83	103.86	110.42
1	A	373	ALA	N-CA-C	6.75	119.63	111.40
1	A	411	GLU	N-CA-C	6.59	120.64	110.42
1	B	873	ALA	N-CA-C	6.51	119.70	111.69
1	B	789	ASN	CA-C-N	6.41	126.33	119.28
1	B	789	ASN	C-N-CA	6.41	126.33	119.28
1	B	575	ILE	N-CA-C	6.32	117.83	110.62
1	B	825	SER	N-CA-C	6.16	120.66	113.20
1	A	323	GLY	N-CA-C	-6.11	98.69	113.18
1	B	672	SER	N-CA-C	6.08	117.58	111.07
1	A	79	PRO	N-CA-C	6.05	121.50	113.57
1	B	918	ARG	N-CA-C	6.02	118.96	110.23
1	B	823	GLY	N-CA-C	-5.71	99.64	113.18

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	50	GLY	N-CA-C	-5.63	99.84	113.18
1	A	374	SER	N-CA-C	5.62	118.50	110.24
1	B	579	PRO	N-CA-C	5.54	121.23	113.53
1	B	874	SER	N-CA-C	5.49	118.31	110.24
1	A	97	ASP	N-CA-C	-5.48	98.42	108.02
1	A	43	LYS	N-CA-C	-5.48	104.84	112.45
1	B	929	VAL	N-CA-CB	-5.47	106.19	112.21
1	B	550	GLY	N-CA-C	-5.45	100.26	113.18
1	B	513	GLN	N-CA-C	5.43	118.12	111.82
1	A	75	ILE	N-CA-C	5.35	116.72	110.62
1	B	537	LEU	N-CA-C	5.31	117.33	107.99
1	B	597	ASP	N-CA-C	-5.30	98.61	107.99
1	B	860	GLY	N-CA-C	5.26	122.35	115.40
1	B	830	ASN	N-CA-C	-5.13	105.60	111.14
1	B	670	GLY	CA-C-N	5.11	124.56	119.24
1	B	670	GLY	C-N-CA	5.11	124.56	119.24
1	A	78	LEU	CA-C-N	5.09	124.59	119.19
1	A	78	LEU	C-N-CA	5.09	124.59	119.19
1	A	416	GLN	N-CA-C	-5.09	103.76	110.43
1	B	578	LEU	CA-C-N	5.08	124.69	119.05
1	B	578	LEU	C-N-CA	5.08	124.69	119.05
1	A	93	THR	N-CA-C	5.05	118.60	112.23

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	3260	0	3202	56	0
1	B	3260	0	3202	57	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	4	0	0	0	0
5	A	174	0	0	1	0
5	B	171	0	0	4	0
All	All	6879	0	6404	109	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 (109) 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:111:THR:CG2	1:A:113:VAL:HG12	2.03	0.87
1:B:943:LYS:HE2	1:B:949:LYS:HA	1.66	0.78
1:A:7:LEU:HB2	1:A:10:ARG:HE	1.50	0.76
1:B:944:ALA:HA	1:B:949:LYS:HE3	1.67	0.75
1:B:510:ARG:HH22	1:B:529:GLN:NE2	1.87	0.72
1:A:111:THR:HG22	1:A:113:VAL:HG12	1.71	0.72
1:B:611:THR:CG2	1:B:613:VAL:HG12	2.20	0.72
1:A:111:THR:HG21	1:A:113:VAL:HG12	1.73	0.68
1:A:134:GLU:OE2	1:A:162:HIS:HE1	1.76	0.68
1:B:548:LEU:HD13	1:B:821:VAL:HB	1.75	0.67
1:A:443:LYS:HE2	1:A:449:LYS:HA	1.77	0.66
1:B:634:GLU:OE2	1:B:662:HIS:HE1	1.77	0.66
1:A:10:ARG:HH22	1:A:29:GLN:NE2	1.94	0.66
1:B:506:VAL:N	1:B:529:GLN:HE21	1.93	0.66
1:B:513:GLN:HG2	1:B:523:ARG:O	1.97	0.65
1:A:48:LEU:HD13	1:A:321:VAL:HB	1.79	0.64
1:B:611:THR:HG22	1:B:613:VAL:HG12	1.78	0.64
1:B:753:LYS:HA	1:B:753:LYS:HE2	1.81	0.63
1:A:107:THR:O	1:A:111:THR:HB	2.00	0.61
1:A:443:LYS:HE2	1:A:449:LYS:HD3	1.82	0.60
1:A:23:ARG:HD2	1:B:940:TYR:CE2	2.37	0.59
1:B:607:THR:O	1:B:611:THR:HB	2.03	0.59
1:B:515:ASN:O	1:B:521:GLY:HA3	2.03	0.59
1:B:902:TYR:HB3	1:B:910:GLN:HG3	1.86	0.58
1:B:676:GLN:HG3	1:B:677:LYS:HG3	1.85	0.57
1:B:946:LEU:HB3	1:B:948:LEU:HD13	1.86	0.57
1:B:793:ASN:HD22	1:B:795:SER:H	1.52	0.57
1:B:736:LEU:HD11	1:B:756:LEU:HD23	1.86	0.57
1:B:510:ARG:HH22	1:B:529:GLN:HE22	1.53	0.56
1:A:220:TRP:HD1	1:A:223:LYS:HZ1	1.54	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:611:THR:HG21	1:B:613:VAL:HG12	1.86	0.56
1:B:857:LYS:NZ	1:B:857:LYS:HB2	2.19	0.55
1:A:419:ILE:HG23	1:A:429:VAL:HG13	1.88	0.55
1:B:611:THR:HG21	5:B:1311:HOH:O	2.05	0.55
1:A:38:SER:OG	1:A:40:LYS:HG3	2.08	0.53
1:B:777:GLY:HA2	1:B:781:LYS:HD3	1.91	0.53
1:B:781:LYS:N	1:B:781:LYS:HD2	2.23	0.53
1:A:130:PRO:HD2	5:A:1072:HOH:O	2.08	0.52
1:B:650:GLU:H	1:B:763:ASN:ND2	2.07	0.52
1:B:682:ALA:HB1	1:B:684:GLU:OE1	2.09	0.52
1:A:13:GLN:OE1	1:A:26:THR:HG22	2.09	0.52
1:A:179:PRO:O	1:A:185:LYS:HD2	2.11	0.51
1:B:621:GLY:O	1:B:662:HIS:HD2	1.93	0.51
1:A:10:ARG:HD2	1:B:932:LEU:O	2.11	0.50
1:A:40:LYS:HD3	1:A:41:PRO:O	2.12	0.50
1:A:337:GLY:O	1:A:341:GLU:HG2	2.12	0.49
1:A:149:ALA:HA	1:A:263:ASN:HD22	1.77	0.49
1:A:150:GLU:H	1:A:263:ASN:ND2	2.10	0.49
1:A:162:HIS:H	1:A:194:GLN:NE2	2.11	0.49
1:A:137:LYS:HE3	1:A:199:ARG:O	2.13	0.48
1:A:15:ASN:O	1:A:21:GLY:HA3	2.12	0.48
1:A:402:TYR:HB3	1:A:410:GLN:HG3	1.96	0.47
1:B:649:ALA:HA	1:B:763:ASN:HD22	1.78	0.47
1:B:879:PRO:HA	1:B:899:VAL:HG21	1.96	0.47
1:B:650:GLU:HG3	1:B:763:ASN:ND2	2.30	0.47
1:B:879:PRO:HA	1:B:899:VAL:CG2	2.45	0.47
1:A:116:TYR:CZ	1:A:119:ALA:HB2	2.50	0.47
1:B:650:GLU:H	1:B:763:ASN:HD22	1.64	0.46
1:A:365:ILE:HD13	1:A:438:LEU:HD11	1.98	0.46
1:B:924:PRO:O	1:B:925:HIS:HB2	2.14	0.46
1:A:13:GLN:HG2	1:A:23:ARG:O	2.15	0.46
1:B:858:LYS:HD3	1:B:859:GLU:N	2.31	0.46
1:B:949:LYS:NZ	1:B:949:LYS:HB2	2.31	0.46
1:B:572:PHE:HB3	1:B:846:ASP:OD1	2.16	0.45
1:A:110:SER:O	1:A:131:THR:HA	2.17	0.45
1:B:854:GLU:HA	1:B:857:LYS:HE3	1.98	0.45
1:B:744:ASN:HB2	5:B:1352:HOH:O	2.17	0.45
1:A:6:VAL:N	1:A:29:GLN:HE21	2.14	0.45
1:B:678:CYS:N	1:B:679:PRO:HD3	2.33	0.44
1:A:120:LEU:HB2	1:A:163:VAL:HG12	2.00	0.44
1:B:637:LYS:HG2	5:B:1081:HOH:O	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:GLY:O	1:A:162:HIS:HD2	2.00	0.44
1:B:649:ALA:HB2	1:B:824:ALA:CB	2.48	0.44
1:A:406:GLU:OE1	1:B:776:HIS:HE1	2.01	0.44
1:B:789:ASN:HA	1:B:790:PRO:HD3	1.77	0.43
1:A:33:LEU:HD22	1:A:33:LEU:HA	1.85	0.43
1:B:744:ASN:HA	5:B:1351:HOH:O	2.18	0.43
1:A:440:TYR:CE2	1:B:523:ARG:HD2	2.54	0.43
1:A:220:TRP:CD1	1:A:223:LYS:HZ1	2.35	0.43
1:A:331:HIS:ND1	1:A:410:GLN:O	2.52	0.43
1:B:616:TYR:CZ	1:B:619:ALA:HB2	2.54	0.42
1:B:793:ASN:HB3	1:B:796:VAL:HG23	2.02	0.42
1:B:674:THR:HG23	1:B:678:CYS:HB2	2.02	0.42
1:A:162:HIS:H	1:A:194:GLN:HE22	1.68	0.42
1:B:510:ARG:NH2	1:B:529:GLN:NE2	2.60	0.42
1:A:265:PRO:HB2	1:A:292:ARG:HG3	2.01	0.41
1:B:793:ASN:HD22	1:B:794:ASP:N	2.19	0.41
1:A:149:ALA:HB2	1:A:324:ALA:CB	2.50	0.41
1:A:338:GLN:NE2	1:A:402:TYR:OH	2.53	0.41
1:B:637:LYS:HE2	1:B:637:LYS:HB3	1.92	0.41
1:B:650:GLU:N	1:B:763:ASN:HD22	2.19	0.41
1:A:448:LEU:HA	1:A:448:LEU:HD12	1.80	0.41
1:B:545:ILE:HD12	1:B:946:LEU:HD22	2.03	0.41
1:A:306:ALA:O	1:A:310:LEU:HB2	2.21	0.41
1:A:448:LEU:O	1:A:449:LYS:C	2.63	0.41
1:A:10:ARG:HH22	1:A:29:GLN:CD	2.28	0.41
1:A:111:THR:HG22	1:A:113:VAL:H	1.85	0.41
1:B:662:HIS:H	1:B:694:GLN:HE22	1.69	0.41
1:A:233:GLY:O	1:A:253:LYS:HD3	2.20	0.41
1:A:46:ILE:HG22	1:A:48:LEU:HD22	2.02	0.40
1:A:129:HIS:HA	1:A:130:PRO:HD3	1.91	0.40
1:A:79:PRO:HG2	1:A:80:LEU:HD22	2.02	0.40
1:A:208:ALA:HB2	1:A:258:LEU:HB3	2.03	0.40
1:A:293:ASN:HB2	1:A:296:VAL:HG23	2.03	0.40
1:B:510:ARG:HB2	1:B:571:PHE:CD1	2.57	0.40
1:B:696:LEU:HD12	1:B:696:LEU:HA	1.90	0.40
1:A:7:LEU:HD13	1:A:7:LEU:HA	1.83	0.40
1:A:150:GLU:H	1:A:263:ASN:HD22	1.69	0.40
1:A:174:THR:HG23	1:A:178:CYS:HB2	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	442/449 (98%)	434 (98%)	8 (2%)	0	100	100
1	B	442/449 (98%)	435 (98%)	7 (2%)	0	100	100
All	All	884/898 (98%)	869 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	333/340 (98%)	309 (93%)	24 (7%)	13	10
1	B	333/340 (98%)	304 (91%)	29 (9%)	9	6
All	All	666/680 (98%)	613 (92%)	53 (8%)	11	8

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LEU
1	A	40	LYS
1	A	48	LEU
1	A	71	PHE
1	A	83	GLN
1	A	84	TYR
1	A	111	THR
1	A	146	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	151	LEU
1	A	163	VAL
1	A	184	GLU
1	A	196	LEU
1	A	219	GLU
1	A	223	LYS
1	A	225	LEU
1	A	232	ARG
1	A	269	LEU
1	A	279	ILE
1	A	284	VAL
1	A	310	LEU
1	A	353	LEU
1	A	417	LEU
1	A	446	LEU
1	A	448	LEU
1	B	533	LEU
1	B	548	LEU
1	B	571	PHE
1	B	583	GLN
1	B	584	TYR
1	B	602	SER
1	B	611	THR
1	B	646	VAL
1	B	651	LEU
1	B	663	VAL
1	B	684	GLU
1	B	696	LEU
1	B	709	LYS
1	B	725	LEU
1	B	732	ARG
1	B	736	LEU
1	B	752	GLN
1	B	753	LYS
1	B	769	LEU
1	B	779	ILE
1	B	784	VAL
1	B	793	ASN
1	B	810	LEU
1	B	853	LEU
1	B	857	LYS
1	B	917	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	929	VAL
1	B	946	LEU
1	B	948	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	29	GLN
1	A	35	ASN
1	A	83	GLN
1	A	145	ASN
1	A	162	HIS
1	A	194	GLN
1	A	263	ASN
1	A	276	HIS
1	A	293	ASN
1	A	338	GLN
1	B	513	GLN
1	B	515	ASN
1	B	529	GLN
1	B	583	GLN
1	B	625	HIS
1	B	645	ASN
1	B	662	HIS
1	B	694	GLN
1	B	763	ASN
1	B	776	HIS
1	B	793	ASN
1	B	829	GLN
1	B	935	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	AF3	A	453	5,2,1	0,3,3	-	-	-		
4	AF3	B	953	5,2,1	0,3,3	-	-	-		

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	444/449 (98%)	0.22	9 (2%) 65 64	13, 23, 50, 73	0
1	B	444/449 (98%)	0.03	8 (1%) 67 67	14, 23, 51, 79	0
All	All	888/898 (98%)	0.12	17 (1%) 66 66	13, 23, 51, 79	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	408	ASP	3.8
1	A	6	VAL	3.7
1	A	7	LEU	3.3
1	A	293	ASN	2.8
1	B	718	GLY	2.7
1	A	252	GLN	2.5
1	A	222	GLY	2.5
1	B	507	LEU	2.5
1	B	949	LYS	2.5
1	B	508	GLU	2.4
1	B	721	GLN	2.3
1	A	448	LEU	2.2
1	B	680	GLY	2.2
1	A	291	GLN	2.1
1	A	449	LYS	2.1
1	B	791	GLN	2.1
1	B	814	GLU	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	ZN	B	950	1/1	0.80	0.07	16,16,16,16	0
4	AF3	B	953	4/4	0.80	0.24	26,31,33,34	0
4	AF3	A	453	4/4	0.86	0.20	33,37,38,41	0
3	MG	B	952	1/1	0.92	0.14	6,6,6,6	0
2	ZN	B	951	1/1	0.93	0.12	25,25,25,25	0
2	ZN	A	451	1/1	0.93	0.10	25,25,25,25	0
3	MG	A	452	1/1	0.94	0.04	12,12,12,12	0
2	ZN	A	450	1/1	0.98	0.05	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.