



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:08 AM GMT

PDB ID : 1ZVK
Title : Structure of Double mutant, D164N, E78H of Kumamolisin-As
Authors : Li, M.; Wlodawer, A.; Gustchina, A.; Nakayama, T.
Deposited on : 2005-06-02
Resolution : 2.04 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

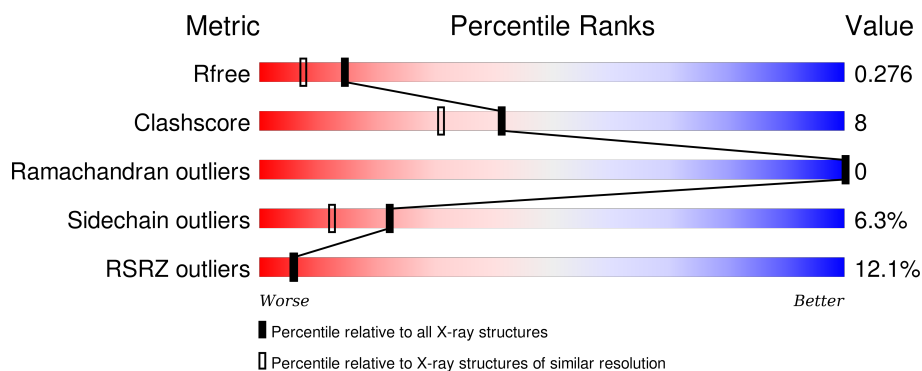
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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	358	<div> <div>13%</div> <div>77%</div> <div>21%</div> <div>..</div> </div>
1	B	358	<div> <div>11%</div> <div>80%</div> <div>17%</div> <div>..</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5502 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 kumamolisin-As.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	355	Total	C	N	O	S	0	0	1
			2528	1593	426	505	4			
1	B	355	Total	C	N	O	S	0	0	1
			2528	1593	426	505	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	78	HIS	GLU	ENGINEERED	UNP Q8GB88
A	164	ASN	ASP	ENGINEERED	UNP Q8GB88
B	78	HIS	GLU	ENGINEERED	UNP Q8GB88
B	164	ASN	ASP	ENGINEERED	UNP Q8GB88

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

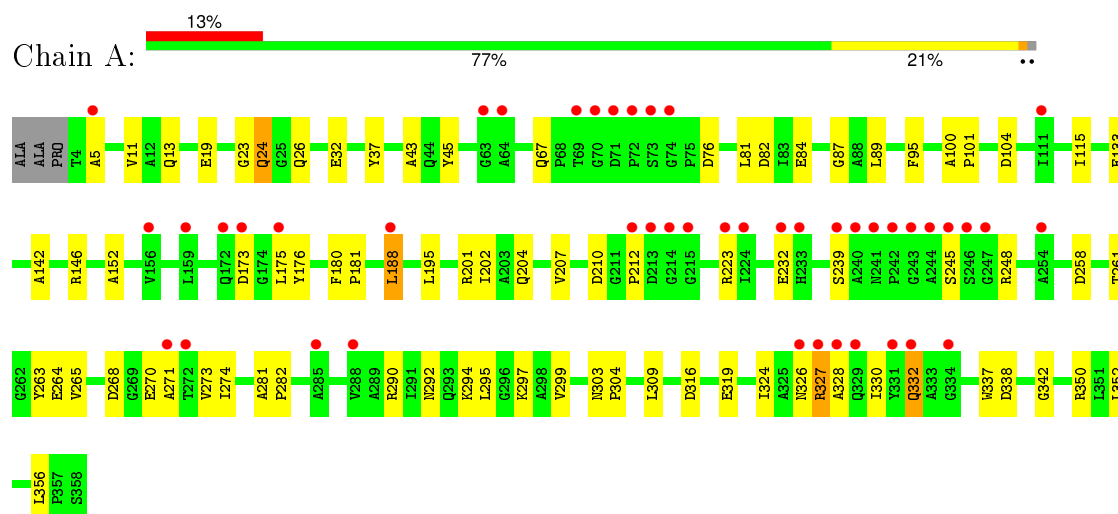
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	207	Total	O	0	0
			207	207		
3	B	237	Total	O	0	0
			237	237		

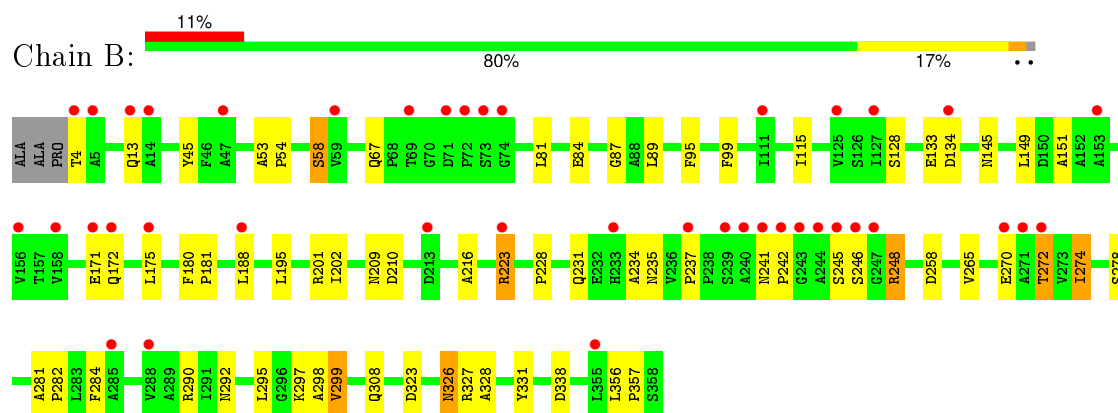
3 Residue-property plots

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: kumamolisin-As



• Molecule 1: kumamolisin-As



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.05Å 74.81Å 78.38Å 90.00° 103.08° 90.00°	Depositor
Resolution (Å)	10.00 – 2.04 36.09 – 2.04	Depositor EDS
% Data completeness (in resolution range)	93.9 (10.00-2.04) 96.8 (36.09-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 2.05Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.188 , 0.292 0.185 , 0.276	Depositor DCC
R_{free} test set	2042 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.438	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 87.4	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	1 of 41251 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5502	wwPDB-VP
Average B, all atoms (Å ²)	26.0	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 20.72 % 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 8.1833e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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:
CA

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	0.46	0/2592	1.29	14/3562 (0.4%)
1	B	0.46	0/2592	1.24	6/3562 (0.2%)
All	All	0.46	0/5184	1.27	20/7124 (0.3%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	350	ARG	NE-CZ-NH1	9.29	124.94	120.30
1	B	290	ARG	NE-CZ-NH2	-8.98	115.81	120.30
1	A	338	ASP	CB-CG-OD2	-8.92	110.27	118.30
1	B	338	ASP	CB-CG-OD2	-7.25	111.78	118.30
1	A	104	ASP	CB-CG-OD1	7.20	124.78	118.30
1	A	261	THR	C-N-CA	6.87	136.73	122.30
1	A	188	LEU	CA-CB-CG	6.48	130.21	115.30
1	B	331	TYR	CB-CG-CD1	-6.25	117.25	121.00
1	A	290	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	A	37	TYR	CB-CG-CD1	-5.81	117.52	121.00
1	A	176	TYR	CB-CG-CD1	-5.79	117.53	121.00
1	A	232	GLU	O-C-N	-5.73	113.54	122.70
1	A	173	ASP	C-N-CA	5.66	134.19	122.30
1	B	284	PHE	CG-CD1-CE1	-5.41	114.85	120.80
1	A	290	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	A	330	ILE	C-N-CA	5.23	134.79	121.70
1	B	128	SER	O-C-N	5.20	131.01	122.70
1	A	37	TYR	CB-CG-CD2	5.12	124.08	121.00
1	B	284	PHE	CZ-CE2-CD2	-5.02	114.08	120.10
1	A	316	ASP	CB-CG-OD1	5.00	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	2528	0	2418	41	0
1	B	2528	0	2418	44	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	207	0	0	8	0
3	B	237	0	0	11	0
All	All	5502	0	4836	84	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 (84) 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:295:LEU:HD12	1:B:299:VAL:HG12	1.55	0.85
1:B:326:ASN:HD22	1:B:328:ALA:H	1.22	0.85
1:B:292:ASN:OD1	1:B:299:VAL:HG13	1.82	0.79
1:B:265:VAL:HG21	1:B:274:ILE:HD13	1.67	0.77
1:B:81:LEU:HD13	1:B:274:ILE:HD11	1.70	0.74
1:B:242:PRO:HG2	3:B:1478:HOH:O	1.91	0.70
1:A:292:ASN:OD1	1:A:299:VAL:HG13	1.93	0.69
1:B:357:PRO:HD3	3:B:1166:HOH:O	1.93	0.67
1:B:228:PRO:HD2	1:B:231:GLN:HB2	1.79	0.64
1:B:145:ASN:HB2	3:B:1319:HOH:O	1.99	0.62
1:A:142:ALA:O	1:A:146:ARG:HG3	2.00	0.61
1:A:24:GLN:NE2	3:A:1362:HOH:O	2.32	0.61
1:A:152:ALA:HB1	3:A:1258:HOH:O	1.99	0.61
1:B:58:SER:HG	1:B:99:PHE:HE1	1.47	0.60
1:A:212:PRO:HG3	1:A:324:ILE:O	2.02	0.60
1:B:326:ASN:ND2	1:B:328:ALA:H	1.97	0.60
1:A:195:LEU:HD11	1:A:202:ILE:HG12	1.85	0.59
1:B:326:ASN:HD22	1:B:328:ALA:N	1.97	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:GLU:HG2	3:B:1341:HOH:O	2.04	0.57
1:B:175:LEU:HD13	1:B:223:ARG:HH21	1.69	0.57
1:B:223:ARG:HD3	3:B:2011:HOH:O	2.04	0.57
1:A:81:LEU:HD13	1:A:274:ILE:HD11	1.90	0.54
1:B:180:PHE:CG	1:B:181:PRO:HA	2.43	0.54
1:A:84:GLU:OE1	1:A:265:VAL:HB	2.08	0.54
1:A:294:LYS:HG2	1:A:352:LEU:HD21	1.90	0.54
1:A:5:ALA:HB1	1:A:264:GLU:HG3	1.90	0.53
1:B:87:GLY:HA2	1:B:95:PHE:CZ	2.44	0.52
1:A:81:LEU:HD13	1:A:274:ILE:CD1	2.40	0.52
1:A:87:GLY:HA2	1:A:95:PHE:CZ	2.44	0.52
1:B:228:PRO:HD3	1:B:248:ARG:HA	1.92	0.52
1:A:180:PHE:CG	1:A:181:PRO:HA	2.45	0.52
1:B:210:ASP:OD2	1:B:258:ASP:OD1	2.29	0.50
1:A:201:ARG:HA	3:A:1122:HOH:O	2.12	0.50
1:A:11:VAL:HG21	1:A:263:TYR:CE2	2.47	0.50
1:B:115:ILE:HD13	1:B:151:ALA:HB2	1.94	0.49
1:B:308:GLN:HB2	3:B:1294:HOH:O	2.12	0.49
1:B:270:GLU:O	1:B:272:THR:HG22	2.13	0.49
1:B:134:ASP:OD1	1:B:171:GLU:OE1	2.30	0.49
1:B:115:ILE:CD1	1:B:151:ALA:HB2	2.42	0.49
1:B:45:TYR:CE1	1:B:265:VAL:HA	2.48	0.49
1:B:81:LEU:HB2	1:B:274:ILE:HD11	1.96	0.48
1:B:81:LEU:HB2	1:B:274:ILE:CD1	2.44	0.48
1:B:195:LEU:HD11	1:B:202:ILE:HG12	1.96	0.47
1:B:298:ALA:HB3	3:B:1506:HOH:O	2.14	0.47
1:A:45:TYR:CE1	1:A:265:VAL:HA	2.50	0.47
1:A:337:TRP:HA	1:A:342:GLY:O	2.14	0.47
1:A:81:LEU:HD13	1:A:274:ILE:HG13	1.97	0.47
1:A:326:ASN:OD1	1:A:328:ALA:HB3	2.14	0.46
1:B:53:ALA:HA	1:B:54:PRO:HD3	1.86	0.46
1:B:265:VAL:CG2	1:B:274:ILE:HD13	2.44	0.46
1:A:265:VAL:HG21	1:A:274:ILE:CD1	2.46	0.46
1:A:23:GLY:O	1:A:26:GLN:HB2	2.16	0.46
1:A:45:TYR:CE2	1:A:84:GLU:HB3	2.50	0.46
1:B:13:GLN:NE2	3:B:1190:HOH:O	2.49	0.46
1:A:263:TYR:O	1:A:273:VAL:HA	2.16	0.45
1:B:223:ARG:NE	1:B:241:ASN:HD22	2.14	0.45
1:A:303:ASN:HB2	1:A:304:PRO:HD3	1.99	0.45
1:A:295:LEU:CD1	1:A:299:VAL:HG12	2.45	0.45
1:B:323:ASP:OD2	1:B:326:ASN:ND2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:ARG:HA	3:A:1017:HOH:O	2.17	0.45
1:A:13:GLN:NE2	3:A:1330:HOH:O	2.50	0.45
1:B:45:TYR:CE2	1:B:84:GLU:HB3	2.52	0.44
1:A:352:LEU:O	1:A:356:LEU:HG	2.17	0.44
1:A:43:ALA:HB2	3:A:1158:HOH:O	2.16	0.44
1:A:115:ILE:O	1:B:201:ARG:NE	2.48	0.44
1:A:100:ALA:HB1	1:A:101:PRO:HD2	1.99	0.44
1:B:54:PRO:HD2	3:B:1183:HOH:O	2.17	0.44
1:B:67:GLN:NE2	3:B:1151:HOH:O	2.50	0.43
1:B:237:PRO:HD3	3:B:1241:HOH:O	2.16	0.43
1:A:223:ARG:NE	3:A:1286:HOH:O	2.50	0.43
1:B:209:ASN:HA	1:B:216:ALA:CB	2.49	0.43
1:A:309:LEU:HA	1:A:309:LEU:HD23	1.76	0.43
1:A:32:GLU:OE2	1:A:82:ASP:OD2	2.35	0.43
1:A:281:ALA:HB3	1:A:282:PRO:HD3	2.00	0.42
1:B:281:ALA:N	1:B:282:PRO:HD2	2.34	0.42
1:A:270:GLU:HG2	1:A:271:ALA:O	2.19	0.42
1:A:332:GLN:HG2	3:A:1220:HOH:O	2.20	0.42
1:A:210:ASP:OD2	1:A:258:ASP:OD1	2.38	0.41
1:A:207:VAL:HG23	1:A:319:GLU:O	2.20	0.41
1:B:356:LEU:HA	1:B:356:LEU:HD23	1.88	0.41
1:A:81:LEU:HD13	1:A:274:ILE:CG1	2.50	0.41
1:B:234:ALA:O	1:B:235:ASN:HB3	2.20	0.41
1:A:76:ASP:OD2	1:A:268:ASP:OD2	2.39	0.41
1:B:209:ASN:HA	1:B:216:ALA:HB2	2.03	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	353/358 (99%)	341 (97%)	12 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	353/358 (99%)	345 (98%)	8 (2%)	0	100	100
All	All	706/716 (99%)	686 (97%)	20 (3%)	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	253/255 (99%)	239 (94%)	14 (6%)	27	16
1	B	253/255 (99%)	235 (93%)	18 (7%)	18	10
All	All	506/510 (99%)	474 (94%)	32 (6%)	22	12

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	A	24	GLN
1	A	67	GLN
1	A	89	LEU
1	A	133	GLU
1	A	175	LEU
1	A	188	LEU
1	A	204	GLN
1	A	239	SER
1	A	245	SER
1	A	248	ARG
1	A	297	LYS
1	A	327	ARG
1	A	332	GLN
1	B	4	THR
1	B	58	SER
1	B	89	LEU
1	B	133	GLU

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Mol	Chain	Res	Type
1	B	149	LEU
1	B	172	GLN
1	B	188	LEU
1	B	223	ARG
1	B	245	SER
1	B	246	SER
1	B	248	ARG
1	B	272	THR
1	B	274	ILE
1	B	278	SER
1	B	297	LYS
1	B	299	VAL
1	B	326	ASN
1	B	327	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	GLN
1	A	332	GLN
1	B	13	GLN
1	B	55	GLN
1	B	67	GLN
1	B	326	ASN

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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

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	355/358 (99%)	0.93	45 (12%) 5 5	12, 23, 42, 73	0
1	B	355/358 (99%)	0.83	41 (11%) 6 7	14, 22, 39, 73	0
All	All	710/716 (99%)	0.88	86 (12%) 6 6	12, 23, 41, 73	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	244	ALA	5.8
1	B	244	ALA	5.7
1	A	245	SER	5.5
1	B	245	SER	5.2
1	B	271	ALA	5.0
1	A	271	ALA	4.5
1	B	243	GLY	4.5
1	A	223	ARG	4.3
1	A	327	ARG	4.3
1	B	242	PRO	4.1
1	B	285	ALA	3.8
1	B	233	HIS	3.7
1	B	272	THR	3.7
1	A	72	PRO	3.7
1	A	328	ALA	3.6
1	B	69	THR	3.6
1	B	171	GLU	3.4
1	A	73	SER	3.4
1	A	241	ASN	3.3
1	A	242	PRO	3.3
1	B	223	ARG	3.3
1	B	240	ALA	3.2
1	A	69	THR	3.2
1	B	111	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	224	ILE	3.1
1	A	233	HIS	3.1
1	B	5	ALA	3.1
1	B	175	LEU	3.1
1	A	214	GLY	3.1
1	A	285	ALA	3.0
1	B	239	SER	3.0
1	B	156	VAL	3.0
1	B	71	ASP	2.9
1	A	172	GLN	2.9
1	A	71	ASP	2.9
1	B	72	PRO	2.9
1	B	172	GLN	2.8
1	B	14	ALA	2.8
1	B	74	GLY	2.8
1	A	239	SER	2.8
1	A	5	ALA	2.8
1	A	156	VAL	2.7
1	A	246	SER	2.7
1	B	237	PRO	2.7
1	A	334	GLY	2.6
1	A	247	GLY	2.6
1	A	74	GLY	2.6
1	B	73	SER	2.6
1	B	355	LEU	2.5
1	A	215	GLY	2.5
1	A	188	LEU	2.5
1	A	173	ASP	2.5
1	B	13	GLN	2.5
1	A	212	PRO	2.4
1	B	270	GLU	2.4
1	B	213	ASP	2.4
1	A	64	ALA	2.4
1	A	111	ILE	2.4
1	A	243	GLY	2.4
1	A	213	ASP	2.3
1	B	59	VAL	2.3
1	B	288	VAL	2.3
1	B	188	LEU	2.3
1	A	254	ALA	2.3
1	B	127	ILE	2.3
1	B	246	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	232	GLU	2.3
1	B	247	GLY	2.3
1	A	159	LEU	2.3
1	A	175	LEU	2.3
1	B	47	ALA	2.3
1	A	63	GLY	2.2
1	A	240	ALA	2.2
1	A	288	VAL	2.2
1	A	70	GLY	2.2
1	A	326	ASN	2.2
1	B	241	ASN	2.2
1	B	4	THR	2.2
1	A	272	THR	2.1
1	A	331	TYR	2.1
1	B	125	VAL	2.1
1	B	153	ALA	2.1
1	A	329	GLN	2.1
1	B	134	ASP	2.0
1	A	332	GLN	2.0
1	B	158	VAL	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. 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
2	CA	A	501	1/1	0.98	0.06	-2.25	24,24,24,24	0
2	CA	B	502	1/1	0.99	0.05	-3.07	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.