



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:47 PM UTC

PDB ID : 2VX8 / pdb_00002vx8
Title : Vamp7 longin domain Hrb peptide complex
Authors : Evans, P.R.; Owen, D.J.; Luzio, J.P.
Deposited on : 2008-07-01
Resolution : 2.20 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
Xtrriage (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

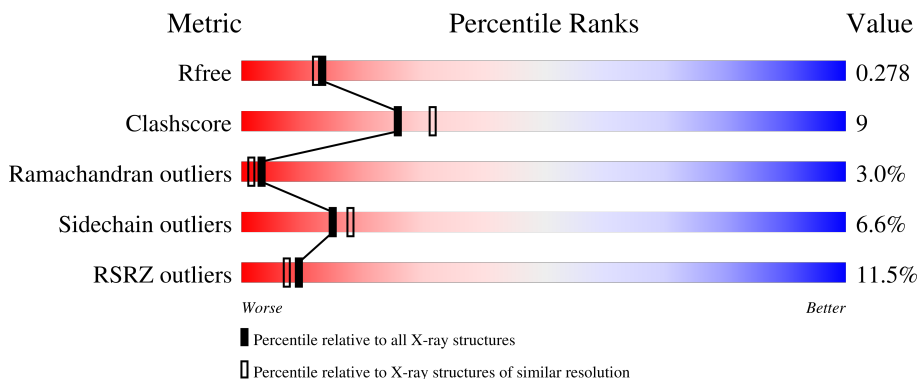
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	169	 6% 62% 14% 2% 18%
1	B	169	 2% 66% 14% 1% 18%
1	C	169	 22% 51% 21% 7% 22%
1	D	169	 6% 62% 15% 1% 21%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 4418 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 NUCLEOPORIN-LIKE PROTEIN RIP, VESICLE-ASSOCIATED MEMBRANE PROTEIN 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	136	1065	682	182	196	5	0	0	0
1	B	138	1087	696	185	201	5	0	0	0
1	C	132	1046	671	177	193	5	0	0	0
1	D	134	1047	674	176	192	5	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP P70280
A	2	SER	-	expression tag	UNP P70280
A	43	GLY	-	linker	UNP P70280
A	164	HIS	-	expression tag	UNP P70280
A	165	HIS	-	expression tag	UNP P70280
A	166	HIS	-	expression tag	UNP P70280
A	167	HIS	-	expression tag	UNP P70280
A	168	HIS	-	expression tag	UNP P70280
A	169	HIS	-	expression tag	UNP P70280
B	1	GLY	-	expression tag	UNP P70280
B	2	SER	-	expression tag	UNP P70280
B	43	GLY	-	linker	UNP P70280
B	164	HIS	-	expression tag	UNP P70280
B	165	HIS	-	expression tag	UNP P70280
B	166	HIS	-	expression tag	UNP P70280
B	167	HIS	-	expression tag	UNP P70280
B	168	HIS	-	expression tag	UNP P70280
B	169	HIS	-	expression tag	UNP P70280
C	1	GLY	-	expression tag	UNP P70280
C	2	SER	-	expression tag	UNP P70280

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Chain	Residue	Modelled	Actual	Comment	Reference
C	43	GLY	-	linker	UNP P70280
C	164	HIS	-	expression tag	UNP P70280
C	165	HIS	-	expression tag	UNP P70280
C	166	HIS	-	expression tag	UNP P70280
C	167	HIS	-	expression tag	UNP P70280
C	168	HIS	-	expression tag	UNP P70280
C	169	HIS	-	expression tag	UNP P70280
D	1	GLY	-	expression tag	UNP P70280
D	2	SER	-	expression tag	UNP P70280
D	43	GLY	-	linker	UNP P70280
D	164	HIS	-	expression tag	UNP P70280
D	165	HIS	-	expression tag	UNP P70280
D	166	HIS	-	expression tag	UNP P70280
D	167	HIS	-	expression tag	UNP P70280
D	168	HIS	-	expression tag	UNP P70280
D	169	HIS	-	expression tag	UNP P70280

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Cl 2 2	0	0
2	D	1	Total Cl 1 1	0	0

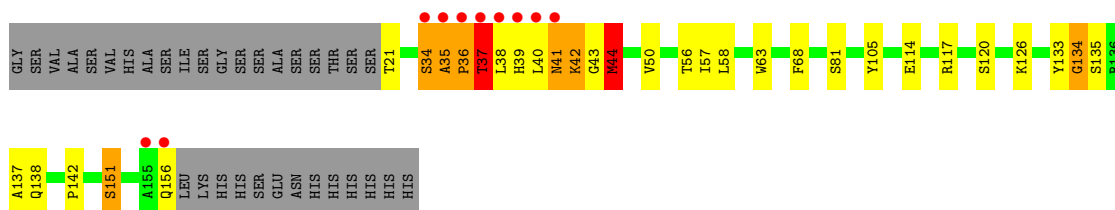
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	55	Total O 55 55	0	0
3	B	49	Total O 49 49	0	0
3	C	22	Total O 22 22	0	0
3	D	44	Total O 44 44	0	0

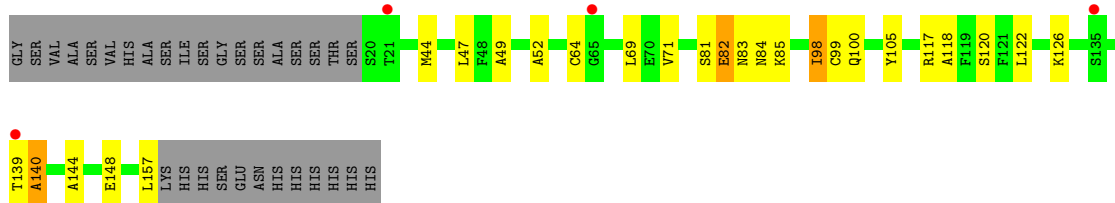
3 Residue-property plots [i](#)

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.

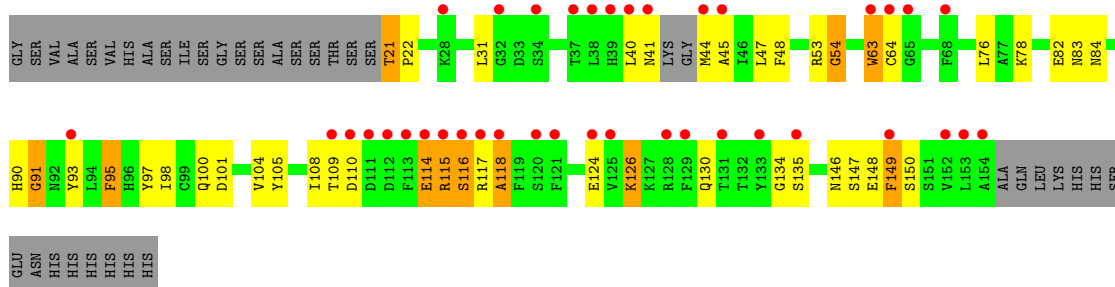
- Molecule 1: NUCLEOPORIN-LIKE PROTEIN RIP, VESICLE-ASSOCIATED MEMBRANE PROTEIN 7



- Molecule 1: NUCLEOPORIN-LIKE PROTEIN RIP, VESICLE-ASSOCIATED MEMBRANE PROTEIN 7



- Molecule 1: NUCLEOPORIN-LIKE PROTEIN RIP, VESICLE-ASSOCIATED MEMBRANE PROTEIN 7



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.51Å 115.10Å 55.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.71 – 2.20 57.71 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.0 (57.71-2.20) 99.3 (57.71-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.38 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.5.0035	Depositor
R, R_{free}	0.220 , 0.280 0.217 , 0.278	Depositor DCC
R_{free} test set	1747 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	37.4	Xtrriage
Anisotropy	0.586	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4418	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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 i

5.1 Standard geometry i

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

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	1.36	2/1089 (0.2%)	1.27	2/1477 (0.1%)
1	B	1.30	4/1111 (0.4%)	1.21	2/1505 (0.1%)
1	C	1.20	1/1069 (0.1%)	1.25	7/1448 (0.5%)
1	D	1.24	0/1069	1.33	12/1447 (0.8%)
All	All	1.27	7/4338 (0.2%)	1.27	23/5877 (0.4%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	108	ILE	CA-CB	-6.54	1.46	1.54
1	A	58	LEU	C-O	6.19	1.32	1.24
1	B	49	ALA	CA-C	5.22	1.58	1.52
1	A	138	GLN	CA-C	-5.20	1.45	1.52
1	B	98	ILE	CA-CB	-5.12	1.48	1.54
1	B	52	ALA	CA-C	5.05	1.58	1.52
1	B	71	VAL	CA-CB	5.04	1.61	1.54

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	71	VAL	CB-CA-C	-11.20	97.01	112.14
1	D	117	ARG	N-CA-C	8.31	120.26	108.54
1	D	35	ALA	CA-C-N	-7.48	112.62	120.03
1	D	35	ALA	C-N-CA	-7.48	112.62	120.03
1	C	63	TRP	N-CA-C	-6.40	103.48	113.02
1	C	104	VAL	N-CA-C	6.24	117.13	108.89
1	C	21	THR	CA-C-N	-6.04	113.73	119.89
1	C	21	THR	C-N-CA	-6.04	113.73	119.89
1	D	116	SER	CA-C-N	-5.70	115.34	123.20
1	D	116	SER	C-N-CA	-5.70	115.34	123.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	68	PHE	N-CA-C	5.67	117.46	111.28
1	C	54	GLY	N-CA-C	-5.54	101.26	111.34
1	C	97	TYR	N-CA-C	5.45	117.55	108.99
1	D	117	ARG	CA-CB-CG	-5.45	103.21	114.10
1	D	71	VAL	N-CA-CB	5.41	117.90	110.54
1	D	123	ASN	N-CA-C	5.36	116.80	111.07
1	A	37	THR	N-CA-C	5.29	122.06	110.80
1	B	69	LEU	N-CA-C	5.27	117.44	111.11
1	D	146	ASN	N-CA-C	5.27	116.83	111.14
1	D	81	SER	N-CA-C	5.21	119.50	113.20
1	C	149	PHE	N-CA-C	5.20	121.87	110.80
1	D	119	PHE	N-CA-C	5.12	117.76	111.82
1	B	140	ALA	N-CA-C	5.11	116.88	110.24

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	1065	0	1053	25	0
1	B	1087	0	1084	15	0
1	C	1046	0	1038	31	0
1	D	1047	0	1036	12	0
2	B	2	0	0	0	0
2	D	1	0	0	0	0
3	A	55	0	0	3	0
3	B	49	0	0	3	0
3	C	22	0	0	4	0
3	D	44	0	0	3	0
All	All	4418	0	4211	80	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 9.

All (80) 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:35:ALA:HB1	1:A:36:PRO:HD3	1.43	0.99
1:A:41:ASN:HA	1:A:63:TRP:CD1	1.98	0.98
1:B:44:MET:SD	1:B:157:LEU:HD21	2.06	0.96
1:A:37:THR:HG21	3:A:2006:HOH:O	1.69	0.92
1:C:44:MET:HB2	1:C:47:LEU:HD21	1.59	0.85
1:A:40:LEU:HD11	1:B:47:LEU:HD13	1.60	0.83
1:A:41:ASN:HA	1:A:63:TRP:HD1	1.41	0.82
1:D:131:THR:HG21	3:D:2036:HOH:O	1.84	0.78
1:C:93:TYR:HA	1:C:110:ASP:HA	1.67	0.75
1:A:151:SER:N	3:A:2055:HOH:O	2.20	0.74
1:A:39:HIS:C	1:A:41:ASN:H	1.94	0.74
1:A:35:ALA:CB	1:A:36:PRO:HD3	2.16	0.73
1:C:93:TYR:HB3	1:C:109:THR:O	1.91	0.71
1:C:83:ASN:OD1	1:C:100:GLN:NE2	2.25	0.70
1:C:95:PHE:CD2	1:C:95:PHE:N	2.62	0.67
1:C:147:SER:HB3	3:C:2021:HOH:O	1.95	0.67
1:D:83:ASN:OD1	3:D:2027:HOH:O	2.13	0.66
1:C:83:ASN:HD21	1:C:101:ASP:H	1.43	0.65
1:C:100:GLN:HG2	1:C:130:GLN:HE22	1.64	0.62
1:A:40:LEU:HG	1:B:64:CYS:SG	2.39	0.62
1:C:76:LEU:O	3:C:2011:HOH:O	2.16	0.61
1:A:50:VAL:HG21	1:A:57:ILE:HD12	1.84	0.59
1:B:84:ASN:HB3	3:B:2028:HOH:O	2.02	0.58
1:A:35:ALA:HB1	1:A:36:PRO:CD	2.28	0.58
1:B:140:ALA:HB1	1:B:144:ALA:HB3	1.86	0.58
1:C:114:GLU:O	1:C:116:SER:N	2.36	0.58
1:B:44:MET:HG3	1:B:157:LEU:HD11	1.87	0.56
1:C:44:MET:O	1:C:44:MET:HG3	2.07	0.55
1:A:35:ALA:CB	1:A:36:PRO:CD	2.83	0.55
1:C:53:ARG:O	1:C:54:GLY:C	2.50	0.55
1:A:37:THR:CG2	3:A:2006:HOH:O	2.39	0.55
1:D:140:ALA:HB1	1:D:144:ALA:HB3	1.89	0.55
1:A:41:ASN:HB2	1:A:44:MET:O	2.07	0.54
1:B:81:SER:O	3:B:2026:HOH:O	2.18	0.54
1:A:114:GLU:HB3	1:A:117:ARG:HD3	1.90	0.53
1:D:36:PRO:HD2	1:D:71:VAL:HG13	1.91	0.52
1:A:39:HIS:C	1:A:41:ASN:N	2.62	0.52
1:A:40:LEU:HD11	1:B:47:LEU:CD1	2.38	0.52
1:A:40:LEU:O	1:A:63:TRP:HB3	2.09	0.52
1:B:85:LYS:HG2	1:B:98:ILE:HG12	1.91	0.52
1:C:114:GLU:C	1:C:116:SER:H	2.18	0.51
1:C:83:ASN:O	1:C:84:ASN:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:GLN:HG2	1:C:130:GLN:NE2	2.26	0.51
1:A:41:ASN:O	1:A:42:LYS:C	2.55	0.51
1:A:56:THR:HG23	1:A:142:PRO:HG3	1.93	0.50
1:C:44:MET:HB2	1:C:47:LEU:CD2	2.34	0.50
1:C:82:GLU:O	3:C:2013:HOH:O	2.19	0.50
1:C:21:THR:N	1:C:22:PRO:HD2	2.26	0.49
1:D:117:ARG:HD2	1:D:120:SER:H	1.79	0.48
1:A:133:TYR:O	1:A:134:GLY:C	2.57	0.48
1:C:22:PRO:O	1:C:115:ARG:NH2	2.42	0.48
1:C:147:SER:N	3:C:2021:HOH:O	2.41	0.47
1:B:44:MET:SD	1:B:157:LEU:CD2	2.93	0.47
1:C:40:LEU:O	1:C:41:ASN:HB2	2.15	0.47
1:A:105:TYR:CE1	1:A:126:LYS:HG3	2.51	0.46
1:C:114:GLU:C	1:C:116:SER:N	2.74	0.46
1:B:83:ASN:HA	1:B:99:CYS:O	2.17	0.45
1:A:39:HIS:HB3	1:A:43:GLY:H	1.81	0.45
1:C:31:LEU:HD23	1:C:78:LYS:HD2	1.99	0.44
1:C:117:ARG:O	1:C:118:ALA:C	2.59	0.44
1:D:133:TYR:O	1:D:134:GLY:C	2.60	0.44
1:D:124:GLU:HB3	1:D:156:GLN:NE2	2.33	0.44
1:C:90:HIS:O	1:C:91:GLY:C	2.61	0.44
1:A:41:ASN:CA	1:A:63:TRP:CD1	2.88	0.43
1:D:50:VAL:HG21	1:D:57:ILE:HD12	2.01	0.42
1:C:105:TYR:CD1	1:C:105:TYR:N	2.87	0.42
1:C:63:TRP:O	1:C:64:CYS:HB3	2.18	0.42
1:D:44:MET:HE3	1:D:44:MET:HB2	1.86	0.42
1:C:21:THR:N	1:C:22:PRO:CD	2.82	0.41
1:C:95:PHE:N	1:C:95:PHE:HD2	2.17	0.41
1:B:82:GLU:H	1:B:82:GLU:HG3	1.51	0.41
1:D:58:LEU:HD23	1:D:58:LEU:HA	1.91	0.41
1:B:105:TYR:CE2	1:B:126:LYS:HA	2.55	0.41
1:C:98:ILE:HG21	1:C:126:LYS:HD3	2.01	0.41
1:D:48:PHE:O	1:D:107:CYS:HA	2.20	0.41
1:A:135:SER:C	1:A:137:ALA:N	2.79	0.41
1:C:146:ASN:O	1:C:150:SER:HB2	2.21	0.41
1:B:84:ASN:CB	3:B:2028:HOH:O	2.66	0.40
1:B:118:ALA:O	1:B:122:LEU:HG	2.21	0.40
1:D:70:GLU:HB3	3:D:2022:HOH:O	2.21	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	134/169 (79%)	119 (89%)	8 (6%)	7 (5%)	1	0
1	B	136/169 (80%)	134 (98%)	2 (2%)	0	100	100
1	C	128/169 (76%)	108 (84%)	12 (9%)	8 (6%)	1	0
1	D	128/169 (76%)	123 (96%)	4 (3%)	1 (1%)	16	16
All	All	526/676 (78%)	484 (92%)	26 (5%)	16 (3%)	3	1

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	35	ALA
1	A	42	LYS
1	A	44	MET
1	C	148	GLU
1	C	149	PHE
1	A	34	SER
1	C	115	ARG
1	D	112	ASP
1	A	36	PRO
1	A	37	THR
1	C	45	ALA
1	C	48	PHE
1	C	91	GLY
1	C	118	ALA
1	A	134	GLY
1	C	134	GLY

5.3.2 Protein sidechains [i](#)

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	114/144 (79%)	104 (91%)	10 (9%)	9	10
1	B	118/144 (82%)	112 (95%)	6 (5%)	21	27
1	C	114/144 (79%)	108 (95%)	6 (5%)	20	26
1	D	112/144 (78%)	104 (93%)	8 (7%)	13	16
All	All	458/576 (80%)	428 (93%)	30 (7%)	15	18

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR
1	A	34	SER
1	A	37	THR
1	A	38	LEU
1	A	41	ASN
1	A	44	MET
1	A	81	SER
1	A	120	SER
1	A	151	SER
1	A	156	GLN
1	B	82	GLU
1	B	100	GLN
1	B	117	ARG
1	B	120	SER
1	B	139	THR
1	B	148	GLU
1	C	95	PHE
1	C	114	GLU
1	C	116	SER
1	C	124	GLU
1	C	126	LYS
1	C	135	SER
1	D	31	LEU
1	D	44	MET
1	D	46	ILE
1	D	71	VAL
1	D	78	LYS
1	D	81	SER
1	D	117	ARG
1	D	136	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	61	HIS
1	A	74	GLN
1	A	138	GLN
1	B	39	HIS
1	B	74	GLN
1	C	123	ASN
1	C	130	GLN
1	D	61	HIS
1	D	90	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 [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	136/169 (80%)	0.29	10 (7%) 20 18	21, 34, 67, 76	0
1	B	138/169 (81%)	0.09	4 (2%) 53 50	19, 33, 56, 67	0
1	C	132/169 (78%)	1.30	38 (28%) 1 1	29, 54, 76, 80	0
1	D	134/169 (79%)	0.47	10 (7%) 20 17	27, 42, 66, 76	0
All	All	540/676 (79%)	0.53	62 (11%) 9 7	19, 40, 72, 80	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	35	ALA	5.3
1	A	36	PRO	4.8
1	A	40	LEU	4.2
1	C	154	ALA	4.1
1	A	41	ASN	4.0
1	B	135	SER	4.0
1	C	125	VAL	4.0
1	C	117	ARG	3.9
1	D	157	LEU	3.7
1	C	152	VAL	3.6
1	A	156	GLN	3.3
1	C	113	PHE	3.3
1	C	124	GLU	3.3
1	D	21	THR	3.3
1	A	34	SER	3.3
1	C	121	PHE	3.2
1	D	158	LYS	3.1
1	C	111	ASP	3.1
1	C	38	LEU	3.1
1	D	116	SER	3.1
1	C	114	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	118	ALA	3.0
1	A	37	THR	3.0
1	D	43	GLY	2.9
1	C	41	ASN	2.9
1	B	139	THR	2.8
1	C	37	THR	2.8
1	D	44	MET	2.8
1	C	32	GLY	2.8
1	C	93	TYR	2.8
1	C	63	TRP	2.7
1	C	39	HIS	2.7
1	A	38	LEU	2.7
1	B	65	GLY	2.7
1	A	39	HIS	2.6
1	C	34	SER	2.6
1	C	40	LEU	2.6
1	C	109	THR	2.6
1	D	113	PHE	2.6
1	C	45	ALA	2.5
1	C	149	PHE	2.4
1	C	65	GLY	2.4
1	C	128	ARG	2.4
1	C	131	THR	2.3
1	C	135	SER	2.3
1	C	44	MET	2.3
1	C	110	ASP	2.3
1	C	115	ARG	2.3
1	C	133	TYR	2.3
1	C	68	PHE	2.3
1	C	112	ASP	2.2
1	C	129	PHE	2.2
1	C	64	CYS	2.2
1	C	116	SER	2.2
1	A	155	ALA	2.2
1	C	120	SER	2.1
1	D	40	LEU	2.1
1	C	28	LYS	2.1
1	C	153	LEU	2.1
1	D	117	ARG	2.1
1	B	21	THR	2.0
1	D	81	SER	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(\AA^2)	Q<0.9
2	CL	D	1159	1/1	0.91	0.11	58,58,58,58	0
2	CL	B	1159	1/1	0.97	0.07	29,29,29,29	0
2	CL	B	1158	1/1	1.00	0.02	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.