



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:05 AM UTC

PDB ID : 5F17 / pdb_00005f17
Title : Structure of EAV NSP11 K170A mutant at 3.19Å
Authors : Zhang, M.F.; Chen, Z.Z.
Deposited on : 2015-11-30
Resolution : 3.20 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
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

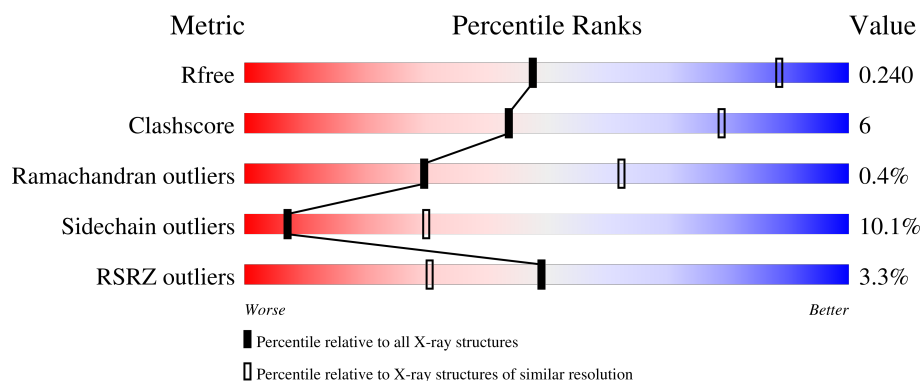
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	219	0% 83% 15% .
1	B	219	3% 80% 19% .
1	C	219	83% 15% .
1	D	219	6% 73% 17% 5% 5%
1	E	219	4% 70% 26% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	219	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: a small red segment at the beginning labeled '5%', a large green segment labeled '72%', a yellow segment labeled '21%', and a small grey segment at the end labeled '5%'.

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9879 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 Non-structural protein 11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1690	1088	280	311	11			
1	B	219	Total	C	N	O	S	0	0	0
			1667	1073	277	307	10			
1	C	219	Total	C	N	O	S	0	0	0
			1674	1076	278	309	11			
1	D	209	Total	C	N	O	S	0	0	0
			1609	1040	265	293	11			
1	E	211	Total	C	N	O	S	0	0	0
			1628	1049	270	298	11			
1	F	209	Total	C	N	O	S	0	0	0
			1611	1041	264	296	10			

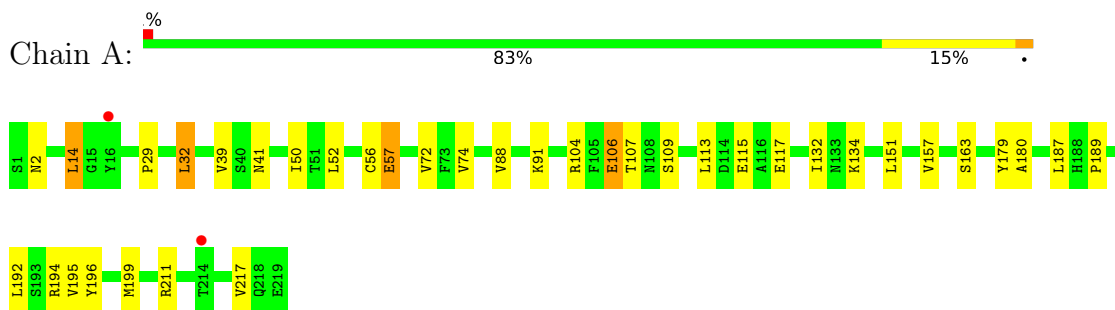
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	170	ALA	LYS	engineered mutation	UNP P19811
B	170	ALA	LYS	engineered mutation	UNP P19811
C	170	ALA	LYS	engineered mutation	UNP P19811
D	170	ALA	LYS	engineered mutation	UNP P19811
E	170	ALA	LYS	engineered mutation	UNP P19811
F	170	ALA	LYS	engineered mutation	UNP P19811

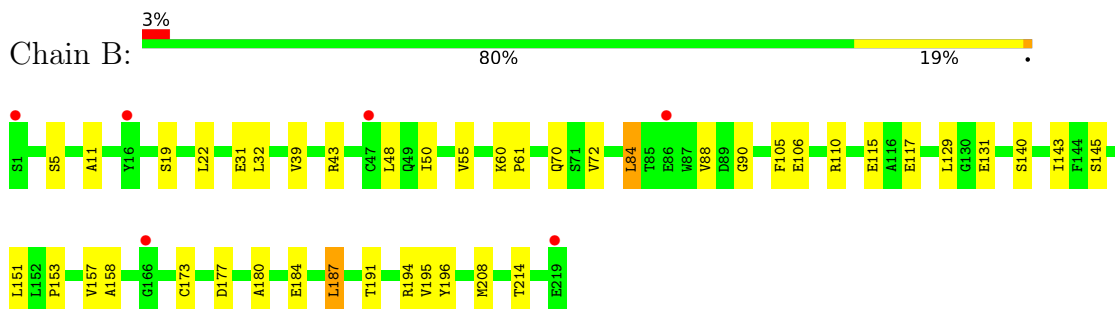
3 Residue-property plots

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.

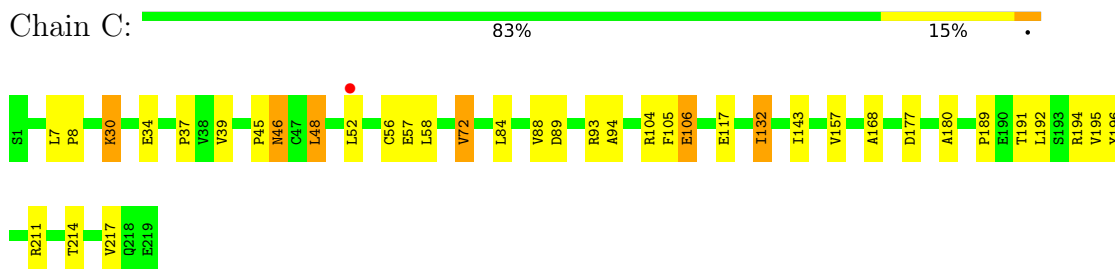
- Molecule 1: Non-structural protein 11



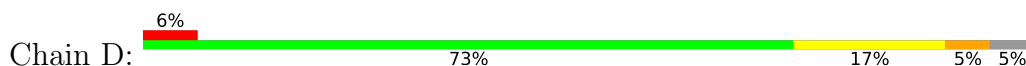
- Molecule 1: Non-structural protein 11

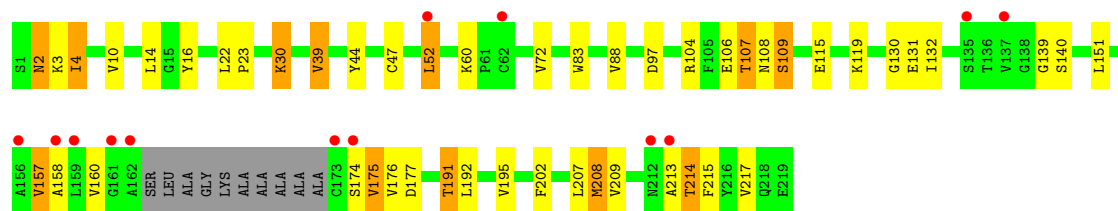


- Molecule 1: Non-structural protein 11

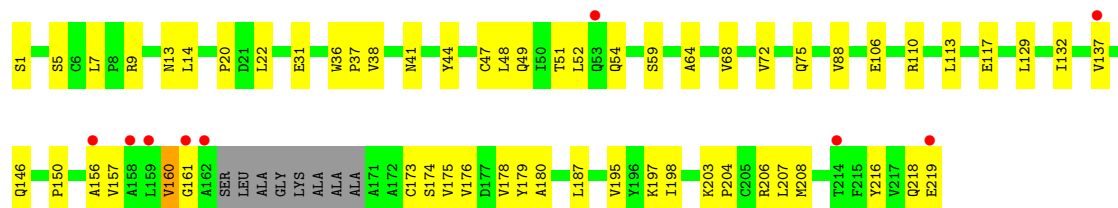


- Molecule 1: Non-structural protein 11

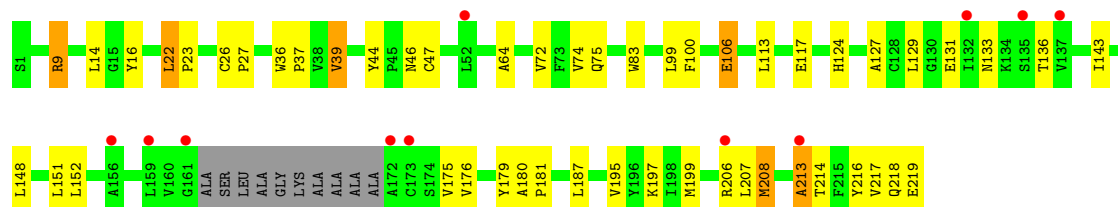
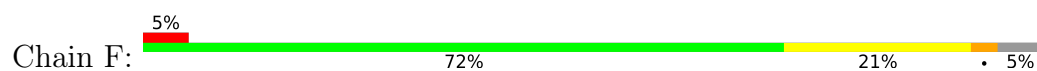




• Molecule 1: Non-structural protein 11



• Molecule 1: Non-structural protein 11



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	249.18Å 249.18Å 226.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.20 50.00 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-3.20) 99.7 (50.00-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.215 , 0.243 0.216 , 0.240	Depositor DCC
R_{free} test set	2102 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	95.5	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 81.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9879	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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](#)

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	0.31	0/1742	0.75	0/2380
1	B	0.32	0/1718	0.79	0/2352
1	C	0.31	0/1726	0.81	0/2362
1	D	0.34	0/1660	0.82	1/2269 (0.0%)
1	E	0.35	0/1678	0.83	1/2291 (0.0%)
1	F	0.37	0/1662	0.81	3/2271 (0.1%)
All	All	0.33	0/10186	0.80	5/13925 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	22	LEU	CA-C-N	6.08	125.48	118.85
1	F	22	LEU	C-N-CA	6.08	125.48	118.85
1	E	156	ALA	N-CA-C	-5.87	100.48	109.41
1	F	213	ALA	N-CA-C	5.87	117.46	108.30
1	D	139	GLY	N-CA-C	5.01	117.22	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1690	0	1634	14	0
1	B	1667	0	1588	14	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1674	0	1597	19	0
1	D	1609	0	1522	20	0
1	E	1628	0	1564	28	0
1	F	1611	0	1527	24	0
All	All	9879	0	9432	117	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 6.

All (117) 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:D:2:ASN:O	1:D:4:ILE:N	2.22	0.73
1:E:9:ARG:HD3	1:E:160:VAL:HG11	1.70	0.72
1:C:56:CYS:SG	1:C:57:GLU:N	2.66	0.67
1:E:208:MET:HB2	1:E:216:TYR:HB2	1.85	0.59
1:F:9:ARG:NH2	1:F:106:GLU:OE2	2.37	0.57
1:B:11:ALA:HB1	1:B:39:VAL:HG11	1.87	0.57
1:E:13:ASN:HD21	1:E:160:VAL:HG22	1.70	0.57
1:C:189:PRO:HD2	1:C:211:ARG:HG3	1.86	0.57
1:A:117:GLU:HG3	1:A:180:ALA:HB3	1.87	0.56
1:C:132:ILE:HD11	1:C:168:ALA:HB3	1.86	0.56
1:C:88:VAL:HG11	1:C:93:ARG:HH12	1.70	0.56
1:C:117:GLU:HG3	1:C:180:ALA:HB3	1.88	0.56
1:A:72:VAL:HG21	1:A:106:GLU:HG3	1.89	0.55
1:A:163:SER:HB2	1:E:68:VAL:HG21	1.90	0.54
1:E:146:GLN:H	1:E:146:GLN:CD	2.16	0.54
1:A:194:ARG:HG2	1:A:196:TYR:CZ	2.43	0.54
1:F:16:TYR:HB3	1:F:39:VAL:HG22	1.91	0.53
1:F:206:ARG:HB2	1:F:218:GLN:HB3	1.90	0.53
1:F:117:GLU:HG3	1:F:181:PRO:HD3	1.89	0.53
1:E:218:GLN:HG3	1:E:219:GLU:HG3	1.90	0.53
1:D:191:THR:OG1	1:D:192:LEU:N	2.41	0.52
1:F:133:ASN:H	1:F:136:THR:HG22	1.76	0.51
1:C:52:LEU:H	1:C:52:LEU:HD12	1.74	0.51
1:D:131:GLU:H	1:D:140:SER:HB3	1.75	0.51
1:A:104:ARG:HA	1:A:107:THR:HG22	1.92	0.51
1:B:48:LEU:HD11	1:B:84:LEU:HG	1.92	0.51
1:F:131:GLU:HA	1:F:217:VAL:H	1.76	0.50
1:F:99:LEU:N	1:F:199:MET:O	2.34	0.50
1:C:72:VAL:HG21	1:C:106:GLU:HG3	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:30:LYS:H	1:D:30:LYS:CD	2.24	0.50
1:F:218:GLN:HG3	1:F:219:GLU:HG3	1.94	0.49
1:E:31:GLU:OE2	1:E:31:GLU:N	2.38	0.49
1:E:5:SER:HB2	1:E:22:LEU:HD13	1.95	0.49
1:D:30:LYS:H	1:D:30:LYS:HD3	1.78	0.49
1:E:20:PRO:HD3	1:E:38:VAL:HG21	1.94	0.49
1:D:107:THR:HG22	1:D:109:SER:HB3	1.94	0.48
1:B:19:SER:HB2	1:B:39:VAL:HG23	1.95	0.48
1:A:56:CYS:SG	1:A:57:GLU:N	2.86	0.48
1:F:127:ALA:HA	1:F:214:THR:HG22	1.95	0.48
1:C:194:ARG:HG2	1:C:196:TYR:CZ	2.49	0.48
1:D:16:TYR:HB3	1:D:39:VAL:HG22	1.96	0.48
1:D:2:ASN:HD22	1:D:52:LEU:HD13	1.79	0.48
1:B:110:ARG:HD3	1:B:143:ILE:HG12	1.96	0.47
1:E:117:GLU:HG3	1:E:180:ALA:HB3	1.96	0.47
1:F:44:TYR:HB2	1:F:47:CYS:HB3	1.94	0.47
1:F:148:LEU:HD13	1:F:152:LEU:HD21	1.96	0.47
1:F:213:ALA:HB1	1:F:214:THR:HG23	1.97	0.47
1:B:5:SER:HB2	1:B:22:LEU:HD22	1.96	0.47
1:E:54:GLN:HG3	1:E:59:SER:HB2	1.96	0.47
1:D:60:LYS:HE3	1:D:97:ASP:HA	1.97	0.47
1:D:22:LEU:HA	1:D:23:PRO:HD3	1.78	0.46
1:F:113:LEU:HD12	1:F:179:TYR:HD1	1.80	0.46
1:F:64:ALA:HB2	1:F:100:PHE:HB3	1.98	0.46
1:F:36:TRP:CG	1:F:37:PRO:HD2	2.51	0.46
1:A:107:THR:HG23	1:A:109:SER:H	1.80	0.46
1:A:29:PRO:HG2	1:A:32:LEU:HB2	1.98	0.45
1:D:10:VAL:HG13	1:D:202:PHE:HD1	1.81	0.45
1:C:104:ARG:HB3	1:C:143:ILE:HD13	1.99	0.45
1:D:104:ARG:HB2	1:D:177:ASP:OD1	2.15	0.45
1:D:157:VAL:HG23	1:D:174:SER:HA	1.98	0.45
1:C:46:ASN:ND2	1:C:89:ASP:OD1	2.50	0.45
1:D:115:GLU:HG2	1:D:119:LYS:HD3	1.99	0.45
1:B:105:PHE:CE1	1:B:177:ASP:HB2	2.52	0.44
1:E:20:PRO:HD3	1:E:38:VAL:CG2	2.46	0.44
1:C:58:LEU:HD22	1:C:94:ALA:HB2	1.98	0.44
1:F:26:CYS:HA	1:F:27:PRO:HD3	1.87	0.44
1:E:113:LEU:HD12	1:E:179:TYR:CD1	2.52	0.44
1:E:173:CYS:SG	1:E:174:SER:N	2.90	0.44
1:C:88:VAL:HG11	1:C:93:ARG:NH1	2.32	0.44
1:E:206:ARG:HB2	1:E:218:GLN:HB3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:VAL:HG22	1:A:107:THR:HG21	1.99	0.44
1:A:91:LYS:HE2	1:A:91:LYS:HB3	1.70	0.44
1:A:41:ASN:ND2	1:A:50:ILE:O	2.44	0.43
1:C:34:GLU:O	1:C:45:PRO:HG2	2.18	0.43
1:F:117:GLU:HG3	1:F:180:ALA:HB3	2.01	0.43
1:D:209:VAL:HG12	1:D:215:PHE:HB3	1.99	0.43
1:F:36:TRP:CD2	1:F:37:PRO:HD2	2.54	0.43
1:E:176:VAL:HG12	1:E:178:VAL:H	1.84	0.42
1:C:105:PHE:CE1	1:C:177:ASP:HB2	2.54	0.42
1:B:60:LYS:HA	1:B:61:PRO:HD3	1.89	0.42
1:D:107:THR:O	1:D:108:ASN:HB2	2.19	0.42
1:B:140:SER:HA	1:B:145:SER:HB3	2.02	0.42
1:D:44:TYR:HB2	1:D:47:CYS:HB3	2.00	0.42
1:E:198:ILE:HD13	1:E:207:LEU:HD22	2.02	0.42
1:F:113:LEU:HD12	1:F:179:TYR:CD1	2.55	0.42
1:B:184:GLU:CD	1:B:187:LEU:HD11	2.44	0.42
1:E:203:LYS:HA	1:E:204:PRO:HD3	1.91	0.42
1:B:208:MET:HE1	1:F:216:TYR:CD1	2.55	0.42
1:B:43:ARG:NH2	1:B:90:GLY:O	2.52	0.41
1:E:22:LEU:HD21	1:E:41:ASN:OD1	2.19	0.41
1:D:214:THR:OG1	1:D:215:PHE:N	2.53	0.41
1:B:117:GLU:HG3	1:B:180:ALA:HB3	2.02	0.41
1:C:30:LYS:HE2	1:C:30:LYS:H	1.85	0.41
1:F:208:MET:H	1:F:208:MET:HG2	1.47	0.41
1:A:113:LEU:HD12	1:A:179:TYR:CD1	2.56	0.41
1:A:189:PRO:HD2	1:A:211:ARG:HG3	2.01	0.41
1:B:194:ARG:HG2	1:B:196:TYR:CZ	2.56	0.41
1:C:7:LEU:HA	1:C:8:PRO:HD3	1.91	0.41
1:E:208:MET:H	1:E:208:MET:HG2	1.63	0.41
1:A:14:LEU:HD12	1:A:14:LEU:HA	1.80	0.41
1:F:37:PRO:HA	1:F:46:ASN:O	2.20	0.41
1:E:44:TYR:HB2	1:E:47:CYS:HB3	2.03	0.41
1:E:113:LEU:HD12	1:E:179:TYR:HD1	1.86	0.41
1:F:22:LEU:HA	1:F:23:PRO:HD3	1.72	0.41
1:B:153:PRO:HG2	1:B:158:ALA:HB1	2.03	0.41
1:C:48:LEU:HD11	1:C:84:LEU:HD22	2.02	0.41
1:D:208:MET:HB3	1:D:208:MET:HE3	1.87	0.41
1:E:197:LYS:HE2	1:E:197:LYS:HB2	1.95	0.41
1:C:105:PHE:CD2	1:C:143:ILE:HD12	2.56	0.41
1:E:64:ALA:C	1:E:75:GLN:HB2	2.46	0.41
1:C:37:PRO:HA	1:C:46:ASN:O	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:158:ALA:HA	1:D:175:VAL:O	2.21	0.40
1:E:36:TRP:CG	1:E:37:PRO:HD2	2.56	0.40
1:F:64:ALA:C	1:F:75:GLN:HB2	2.47	0.40
1:E:110:ARG:NH1	1:E:150:PRO:O	2.55	0.40
1:E:49:GLN:HG2	1:E:51:THR:HG23	2.04	0.40
1:E:161:GLY:N	1:E:203:LYS:HD2	2.37	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	217/219 (99%)	206 (95%)	10 (5%)	1 (0%)	24	59
1	B	217/219 (99%)	205 (94%)	12 (6%)	0	100	100
1	C	217/219 (99%)	205 (94%)	12 (6%)	0	100	100
1	D	205/219 (94%)	190 (93%)	11 (5%)	4 (2%)	6	31
1	E	207/219 (94%)	191 (92%)	16 (8%)	0	100	100
1	F	205/219 (94%)	191 (93%)	14 (7%)	0	100	100
All	All	1268/1314 (96%)	1188 (94%)	75 (6%)	5 (0%)	30	62

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	3	LYS
1	A	134	LYS
1	D	213	ALA
1	D	2	ASN
1	D	130	GLY

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	181/184 (98%)	164 (91%)	17 (9%)	8	33
1	B	175/184 (95%)	156 (89%)	19 (11%)	6	26
1	C	177/184 (96%)	164 (93%)	13 (7%)	13	43
1	D	170/184 (92%)	147 (86%)	23 (14%)	4	19
1	E	175/184 (95%)	159 (91%)	16 (9%)	9	34
1	F	170/184 (92%)	152 (89%)	18 (11%)	6	27
All	All	1048/1104 (95%)	942 (90%)	106 (10%)	7	30

All (106) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	14	LEU
1	A	32	LEU
1	A	39	VAL
1	A	52	LEU
1	A	57	GLU
1	A	88	VAL
1	A	106	GLU
1	A	115	GLU
1	A	132	ILE
1	A	151	LEU
1	A	157	VAL
1	A	187	LEU
1	A	192	LEU
1	A	195	VAL
1	A	199	MET
1	A	217	VAL
1	B	31	GLU
1	B	32	LEU
1	B	50	ILE
1	B	55	VAL
1	B	70	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	72	VAL
1	B	84	LEU
1	B	88	VAL
1	B	106	GLU
1	B	115	GLU
1	B	129	LEU
1	B	131	GLU
1	B	151	LEU
1	B	157	VAL
1	B	173	CYS
1	B	187	LEU
1	B	191	THR
1	B	195	VAL
1	B	214	THR
1	C	30	LYS
1	C	39	VAL
1	C	46	ASN
1	C	48	LEU
1	C	72	VAL
1	C	106	GLU
1	C	132	ILE
1	C	157	VAL
1	C	191	THR
1	C	192	LEU
1	C	195	VAL
1	C	214	THR
1	C	217	VAL
1	D	4	ILE
1	D	14	LEU
1	D	30	LYS
1	D	39	VAL
1	D	52	LEU
1	D	72	VAL
1	D	83	TRP
1	D	88	VAL
1	D	106	GLU
1	D	107	THR
1	D	109	SER
1	D	132	ILE
1	D	151	LEU
1	D	157	VAL
1	D	160	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	175	VAL
1	D	176	VAL
1	D	191	THR
1	D	195	VAL
1	D	207	LEU
1	D	208	MET
1	D	214	THR
1	D	217	VAL
1	E	1	SER
1	E	7	LEU
1	E	14	LEU
1	E	48	LEU
1	E	52	LEU
1	E	72	VAL
1	E	88	VAL
1	E	106	GLU
1	E	129	LEU
1	E	132	ILE
1	E	137	VAL
1	E	157	VAL
1	E	160	VAL
1	E	175	VAL
1	E	187	LEU
1	E	195	VAL
1	F	9	ARG
1	F	14	LEU
1	F	39	VAL
1	F	72	VAL
1	F	74	VAL
1	F	83	TRP
1	F	106	GLU
1	F	124	HIS
1	F	129	LEU
1	F	143	ILE
1	F	151	LEU
1	F	175	VAL
1	F	176	VAL
1	F	187	LEU
1	F	195	VAL
1	F	197	LYS
1	F	207	LEU
1	F	208	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	141	HIS
1	B	2	ASN
1	B	41	ASN
1	B	124	HIS
1	B	126	HIS
1	C	17	HIS
1	D	75	GLN
1	E	46	ASN
1	E	75	GLN
1	E	124	HIS
1	F	35	HIS
1	F	218	GLN

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](#)

There are no ligands in this entry.

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	219/219 (100%)	0.03	2 (0%) 81 64	87, 101, 122, 154	0
1	B	219/219 (100%)	0.35	6 (2%) 56 36	92, 122, 148, 171	0
1	C	219/219 (100%)	0.27	1 (0%) 87 76	95, 118, 145, 163	0
1	D	209/219 (95%)	0.35	13 (6%) 26 17	85, 102, 127, 148	0
1	E	211/219 (96%)	0.41	9 (4%) 40 24	90, 108, 140, 157	0
1	F	209/219 (95%)	0.33	11 (5%) 32 20	84, 108, 139, 179	0
All	All	1286/1314 (97%)	0.29	42 (3%) 49 30	84, 110, 141, 179	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	135	SER	4.5
1	F	172	ALA	4.2
1	F	137	VAL	4.0
1	D	162	ALA	4.0
1	F	173	CYS	3.7
1	D	62	CYS	3.4
1	B	166	GLY	3.1
1	F	132	ILE	3.1
1	F	52	LEU	3.0
1	D	173	CYS	3.0
1	E	162	ALA	2.8
1	D	52	LEU	2.8
1	D	159	LEU	2.8
1	D	212	ASN	2.7
1	E	159	LEU	2.7
1	F	206	ARG	2.7
1	D	135	SER	2.6
1	F	213	ALA	2.6
1	D	158	ALA	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	158	ALA	2.5
1	F	159	LEU	2.5
1	D	161	GLY	2.5
1	A	214	THR	2.4
1	E	161	GLY	2.4
1	F	156	ALA	2.4
1	B	47	CYS	2.4
1	B	219	GLU	2.4
1	E	137	VAL	2.3
1	B	1	SER	2.3
1	E	214	THR	2.3
1	D	174	SER	2.3
1	E	156	ALA	2.3
1	F	161	GLY	2.3
1	D	156	ALA	2.3
1	B	16	TYR	2.2
1	E	53	GLN	2.2
1	C	52	LEU	2.2
1	B	86	GLU	2.1
1	D	213	ALA	2.1
1	D	137	VAL	2.1
1	A	16	TYR	2.1
1	E	219	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.