



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:04 PM UTC

PDB ID : 4F37 / pdb_00004f37
Title : Structure of the tethered N-terminus of Alzheimer's disease A peptide
Authors : Nisbet, R.M.; Nuttall, S.D.; Caine, J.M.; Rober, R.; Hittaki, M.; Pearce, L.A.; Davydova, N.; Masters, C.L.; Varghese, J.N.; Streltsov, V.A.
Deposited on : 2012-05-09
Resolution : 2.57 Å (reported)

This is a wwPDB X-ray Structure Validation Summary 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

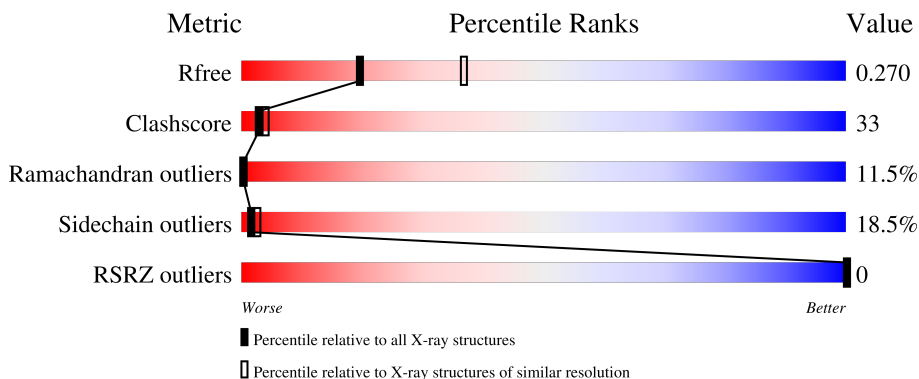
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	124	
1	B	124	
2	F	228	
2	H	228	
3	K	219	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	L	219	 42% 43% 12%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8769 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 Colicin-E7 immunity protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	102	829	520	138	171	0	0	0
1	B	102	829	520	138	171	0	0	0

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ASP	-	expression tag	UNP Q03708
A	2	ALA	-	expression tag	UNP Q03708
A	3	GLU	-	expression tag	UNP Q03708
A	4	PHE	-	expression tag	UNP Q03708
A	5	ARG	-	expression tag	UNP Q03708
A	6	HIS	-	expression tag	UNP Q03708
A	7	ASP	-	expression tag	UNP Q03708
A	8	SER	-	expression tag	UNP Q03708
A	9	GLY	-	expression tag	UNP Q03708
A	10	TYR	-	expression tag	UNP Q03708
A	11	GLU	-	expression tag	UNP Q03708
A	12	VAL	-	expression tag	UNP Q03708
A	13	HIS	-	expression tag	UNP Q03708
A	14	HIS	-	expression tag	UNP Q03708
A	15	GLN	-	expression tag	UNP Q03708
A	16	LYS	-	expression tag	UNP Q03708
A	17	SER	-	expression tag	UNP Q03708
A	104	ALA	-	expression tag	UNP Q03708
A	105	ALA	-	expression tag	UNP Q03708
A	106	ALA	-	expression tag	UNP Q03708
A	107	ASP	-	expression tag	UNP Q03708
A	108	TYR	-	expression tag	UNP Q03708
A	109	LYS	-	expression tag	UNP Q03708
A	110	ASP	-	expression tag	UNP Q03708
A	111	ASP	-	expression tag	UNP Q03708

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	112	ASP	-	expression tag	UNP Q03708
A	113	ASP	-	expression tag	UNP Q03708
A	114	LYS	-	expression tag	UNP Q03708
A	115	ALA	-	expression tag	UNP Q03708
A	116	ALA	-	expression tag	UNP Q03708
A	117	ASP	-	expression tag	UNP Q03708
A	118	TYR	-	expression tag	UNP Q03708
A	119	LYS	-	expression tag	UNP Q03708
A	120	ASP	-	expression tag	UNP Q03708
A	121	ASP	-	expression tag	UNP Q03708
A	122	ASP	-	expression tag	UNP Q03708
A	123	ASP	-	expression tag	UNP Q03708
A	124	LYS	-	expression tag	UNP Q03708
B	1	ASP	-	expression tag	UNP Q03708
B	2	ALA	-	expression tag	UNP Q03708
B	3	GLU	-	expression tag	UNP Q03708
B	4	PHE	-	expression tag	UNP Q03708
B	5	ARG	-	expression tag	UNP Q03708
B	6	HIS	-	expression tag	UNP Q03708
B	7	ASP	-	expression tag	UNP Q03708
B	8	SER	-	expression tag	UNP Q03708
B	9	GLY	-	expression tag	UNP Q03708
B	10	TYR	-	expression tag	UNP Q03708
B	11	GLU	-	expression tag	UNP Q03708
B	12	VAL	-	expression tag	UNP Q03708
B	13	HIS	-	expression tag	UNP Q03708
B	14	HIS	-	expression tag	UNP Q03708
B	15	GLN	-	expression tag	UNP Q03708
B	16	LYS	-	expression tag	UNP Q03708
B	17	SER	-	expression tag	UNP Q03708
B	104	ALA	-	expression tag	UNP Q03708
B	105	ALA	-	expression tag	UNP Q03708
B	106	ALA	-	expression tag	UNP Q03708
B	107	ASP	-	expression tag	UNP Q03708
B	108	TYR	-	expression tag	UNP Q03708
B	109	LYS	-	expression tag	UNP Q03708
B	110	ASP	-	expression tag	UNP Q03708
B	111	ASP	-	expression tag	UNP Q03708
B	112	ASP	-	expression tag	UNP Q03708
B	113	ASP	-	expression tag	UNP Q03708
B	114	LYS	-	expression tag	UNP Q03708
B	115	ALA	-	expression tag	UNP Q03708

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	116	ALA	-	expression tag	UNP Q03708
B	117	ASP	-	expression tag	UNP Q03708
B	118	TYR	-	expression tag	UNP Q03708
B	119	LYS	-	expression tag	UNP Q03708
B	120	ASP	-	expression tag	UNP Q03708
B	121	ASP	-	expression tag	UNP Q03708
B	122	ASP	-	expression tag	UNP Q03708
B	123	ASP	-	expression tag	UNP Q03708
B	124	LYS	-	expression tag	UNP Q03708

- Molecule 2 is a protein called Im7 immunity protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	F	225	Total 1730	C 1094	N 292	O 339	S 5	0	0	0
2	H	225	Total 1730	C 1094	N 292	O 339	S 5	0	0	0

- Molecule 3 is a protein called Fab WO2 anti-amyloid-beta antibody Fab fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	K	218	Total 1693	C 1059	N 287	O 341	S 6	0	0	0
3	L	218	Total 1693	C 1059	N 287	O 341	S 6	0	0	0

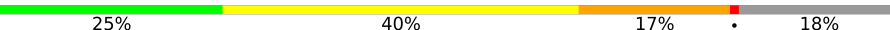
- Molecule 4 is water.

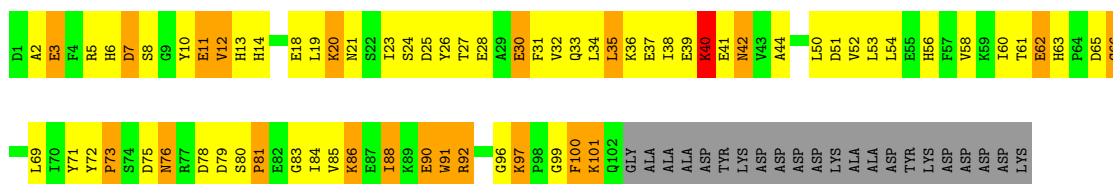
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total 32	O 32	0	0
4	B	34	Total 34	O 34	0	0
4	F	53	Total 53	O 53	0	0
4	H	50	Total 50	O 50	0	0
4	K	42	Total 42	O 42	0	0
4	L	54	Total 54	O 54	0	0

3 Residue-property plots [i](#)

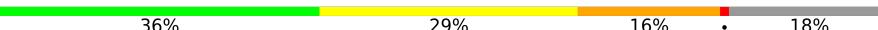
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

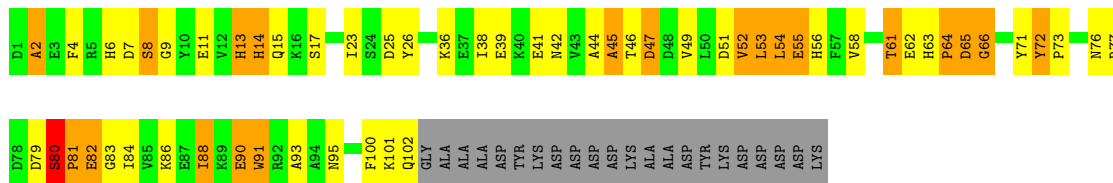
- Molecule 1: Colicin-E7 immunity protein

Chain A: 

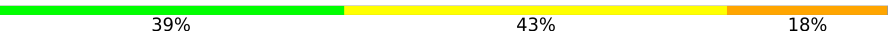


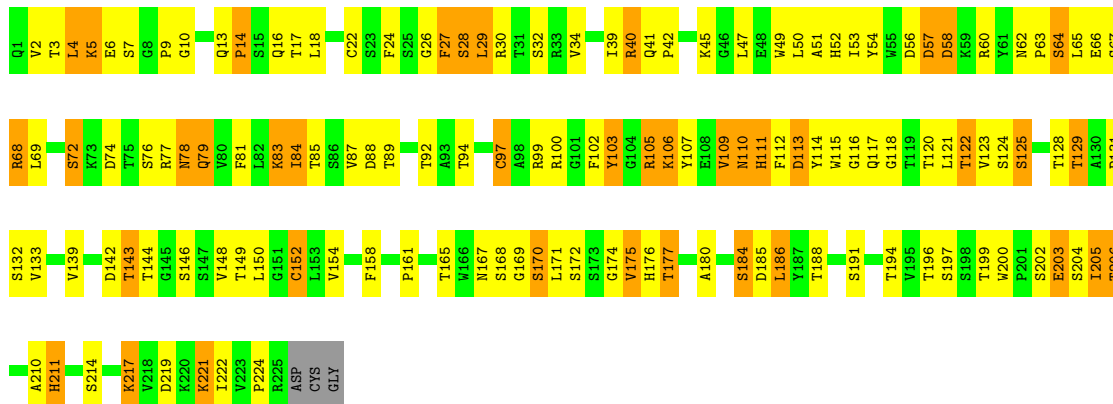
- Molecule 1: Colicin-E7 immunity protein

Chain B: 




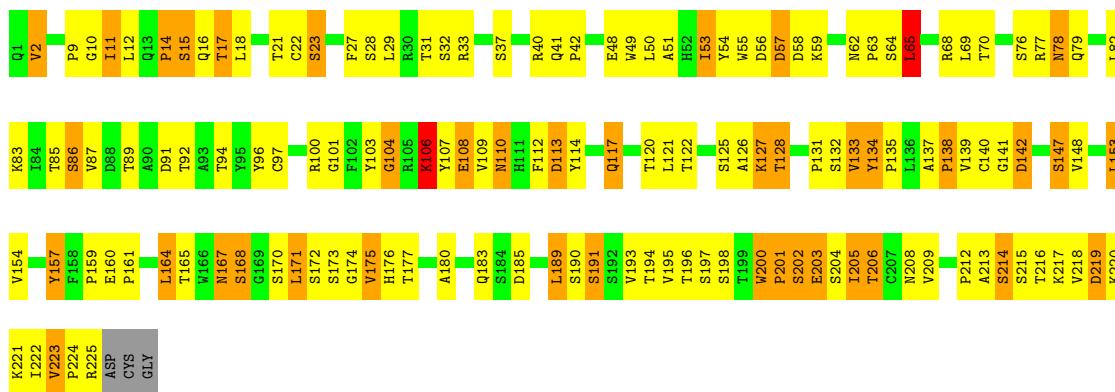
- Molecule 2: Im7 immunity protein

Chain F: 



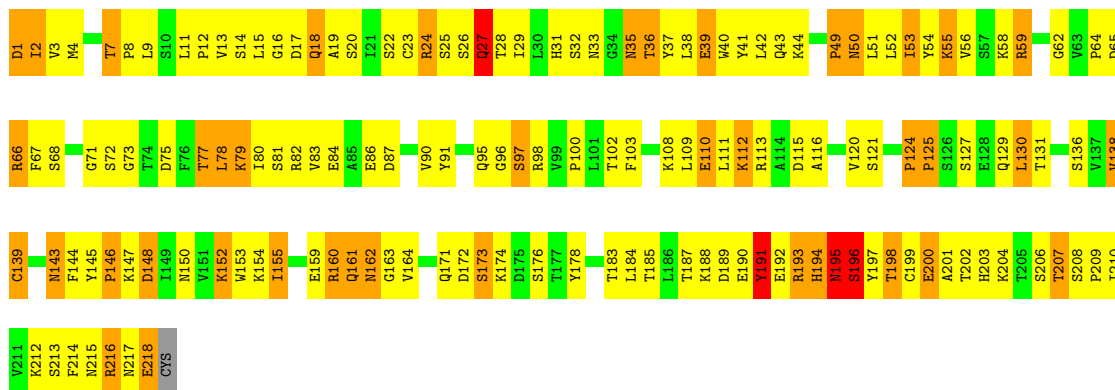
- Molecule 2: Im7 immunity protein

Chain H:  36% 44% 18% ..



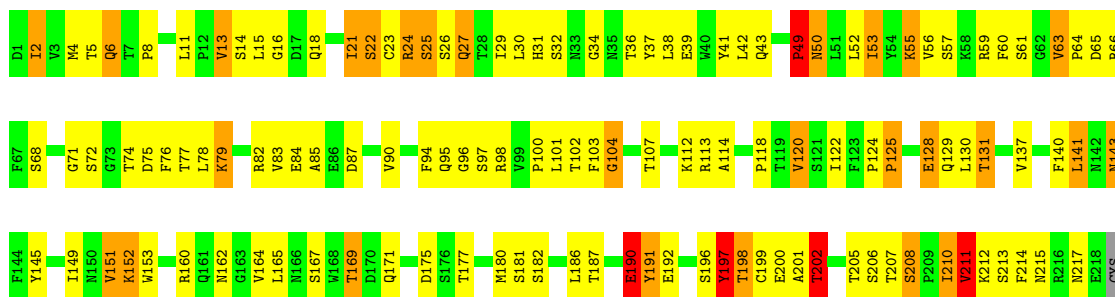
- Molecule 3: Fab WO2 anti-amyloid-beta antibody Fab fragment

Chain K:  30% 49% 19% .



- Molecule 3: Fab WO2 anti-amyloid-beta antibody Fab fragment

Chain L:  42% 43% 12% .



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	36.64Å 82.84Å 89.20Å 90.05° 92.51° 90.00°	Depositor
Resolution (Å)	44.46 – 2.57 44.46 – 2.57	Depositor EDS
% Data completeness (in resolution range)	77.9 (44.46-2.57) 92.5 (44.46-2.57)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.223 , 0.269 (Not available) , 0.270	Depositor DCC
R_{free} test set	6757 reflections (18.58%)	wwPDB-VP
Wilson B-factor (Å ²)	54.0	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-l 0.168 for -h,k,-l 0.000 for -h,-k,l	Xtriage
Reported twinning fraction	0.489 for H, K, L 0.391 for -H, K, -L 0.120 for -h,-k,l	Depositor
Outliers	0 of 31156 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8769	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.36% 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	0.61	0/847	1.07	7/1145 (0.6%)
1	B	0.60	0/847	1.10	6/1145 (0.5%)
2	F	0.69	0/1775	1.03	1/2425 (0.0%)
2	H	0.70	0/1775	1.02	8/2425 (0.3%)
3	K	0.68	0/1730	1.13	13/2347 (0.6%)
3	L	0.70	0/1730	1.08	12/2347 (0.5%)
All	All	0.68	0/8704	1.07	47/11834 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	80	SER	C-N-CD	-9.61	99.45	120.60
3	K	208	SER	CA-C-N	8.60	128.66	119.89
3	K	208	SER	C-N-CA	8.60	128.66	119.89
2	H	167	ASN	N-CA-C	7.57	120.75	108.41
1	B	80	SER	CA-C-N	7.47	144.93	127.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	80	SER	Peptide

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	829	0	782	52	0
1	B	829	0	782	41	1
2	F	1730	0	1699	133	1
2	H	1730	0	1699	119	0
3	K	1693	0	1645	120	0
3	L	1693	0	1645	116	0
4	A	32	0	0	2	0
4	B	34	0	0	1	0
4	F	53	0	0	2	0
4	H	50	0	0	4	0
4	K	42	0	0	1	0
4	L	54	0	0	1	1
All	All	8769	0	8252	546	2

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 33.

The worst 5 of 546 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)
3:L:201:ALA:HB2	3:L:210:ILE:HB	1.28	1.14
2:H:205:ILE:HG23	2:H:221:LYS:HB2	1.16	1.11
2:H:109:VAL:HG23	3:L:55:LYS:HE3	1.24	1.10
2:F:205:ILE:HG21	2:F:222:ILE:HG12	1.32	1.07
2:H:103:TYR:HB2	2:H:109:VAL:HG11	1.36	1.07

All (2) 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)
4:L:321:HOH:O	4:L:354:HOH:O[1_655]	1.90	0.30
1:B:45:ALA:O	2:F:114:TYR:OH[1_655]	2.08	0.12

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	100/124 (81%)	53 (53%)	26 (26%)	21 (21%)	0	0
1	B	100/124 (81%)	62 (62%)	20 (20%)	18 (18%)	0	0
2	F	223/228 (98%)	145 (65%)	55 (25%)	23 (10%)	0	0
2	H	223/228 (98%)	155 (70%)	43 (19%)	25 (11%)	0	0
3	K	216/219 (99%)	153 (71%)	42 (19%)	21 (10%)	0	0
3	L	216/219 (99%)	163 (76%)	37 (17%)	16 (7%)	1	1
All	All	1078/1142 (94%)	731 (68%)	223 (21%)	124 (12%)	0	0

5 of 124 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	GLU
1	A	14	HIS
1	A	40	LYS
1	A	42	ASN
1	A	73	PRO

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	91/107 (85%)	80 (88%)	11 (12%)	5	9
1	B	91/107 (85%)	82 (90%)	9 (10%)	7	15
2	F	199/201 (99%)	165 (83%)	34 (17%)	2	3

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	199/201 (99%)	160 (80%)	39 (20%)	1	2
3	K	195/196 (100%)	151 (77%)	44 (23%)	1	1
3	L	195/196 (100%)	153 (78%)	42 (22%)	1	1
All	All	970/1008 (96%)	791 (82%)	179 (18%)	1	2

5 of 179 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	K	108	LYS
3	L	22	SER
3	K	139	CYS
3	K	196	SER
3	L	55	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	208	ASN
3	L	171	GLN
3	K	35	ASN
3	L	43	GLN
3	K	31	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](#)

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 [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	102/124 (82%)	-1.19	0 100 100	22, 28, 31, 32	0
1	B	102/124 (82%)	-1.19	0 100 100	23, 29, 30, 31	0
2	F	225/228 (98%)	-1.18	0 100 100	18, 22, 29, 34	0
2	H	225/228 (98%)	-1.20	0 100 100	17, 23, 29, 31	0
3	K	218/219 (99%)	-1.22	0 100 100	16, 20, 30, 32	0
3	L	218/219 (99%)	-1.22	0 100 100	14, 18, 30, 33	0
All	All	1090/1142 (95%)	-1.20	0 100 100	14, 24, 30, 34	0

There are no RSRZ outliers to report.

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.