



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:13 AM UTC

PDB ID : 9DH2 / pdb_00009dh2
Title : Structure of Fab in complex with NKG2D extracellular domain
Authors : Fallon, D.; Huang, C.S.
Deposited on : 2024-09-03
Resolution : 2.98 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

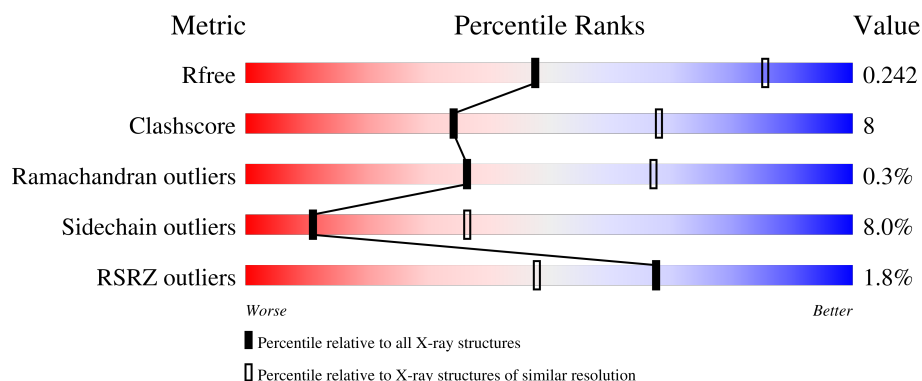
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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	3580 (3.00-2.96)
Clashscore	190562	3904 (3.00-2.96)
Ramachandran outliers	187476	3761 (3.00-2.96)
Sidechain outliers	187428	3764 (3.00-2.96)
RSRZ outliers	180081	3579 (3.00-2.96)

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	220	0% 80% 17% ..
1	G	220	2% 80% 15% ..
1	K	220	4% 76% 20% ..
1	P	220	3% 80% 17% ..
2	D	212	77% 21% .

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Mol	Chain	Length	Quality of chain
2	H	212	80%16%•
2	L	212	81%17%•
2	Q	212	78%20%•
3	M	137	3% 64%22%•10%
3	R	137	66%20%••9%
3	S	137	7% 60%25%5%10%
3	T	137	% 69%20%•9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17120 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 Fab heavy chain.

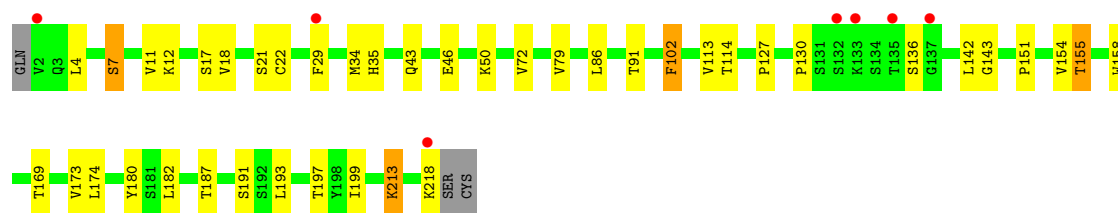
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1646	1043	270	326	7			
1	G	217	Total	C	N	O	S	0	0	0
			1646	1043	270	326	7			
1	K	217	Total	C	N	O	S	0	0	0
			1646	1043	270	326	7			
1	P	217	Total	C	N	O	S	0	0	0
			1646	1043	270	326	7			

- Molecule 2 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	211	Total	C	N	O	S	0	0	0
			1634	1029	271	329	5			
2	H	211	Total	C	N	O	S	0	0	0
			1634	1029	271	329	5			
2	L	211	Total	C	N	O	S	0	0	0
			1634	1029	271	329	5			
2	Q	211	Total	C	N	O	S	0	0	0
			1634	1029	271	329	5			

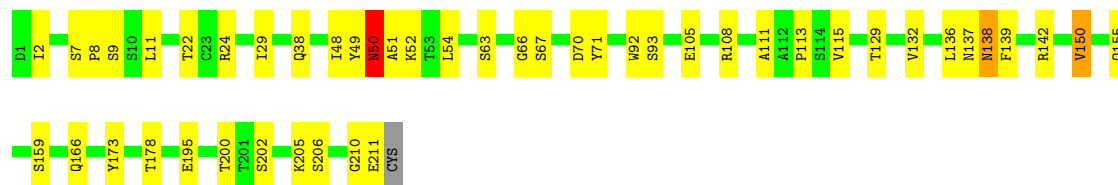
- Molecule 3 is a protein called NKG2-D type II integral membrane protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	123	Total	C	N	O	S	0	0	0
			996	633	160	191	12			
3	R	124	Total	C	N	O	S	0	0	0
			1004	638	161	193	12			
3	S	123	Total	C	N	O	S	0	0	0
			996	633	160	191	12			
3	T	124	Total	C	N	O	S	0	0	0
			1004	638	161	193	12			



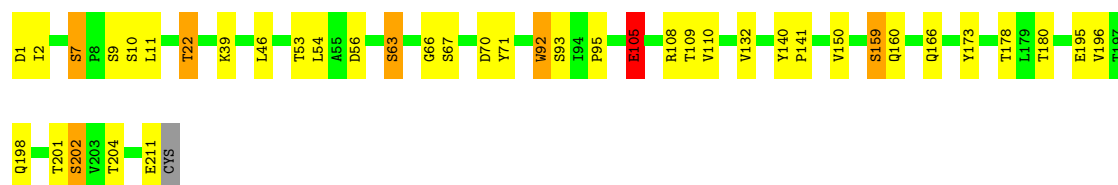
• Molecule 2: Fab light chain

Chain D: 77% 21% .



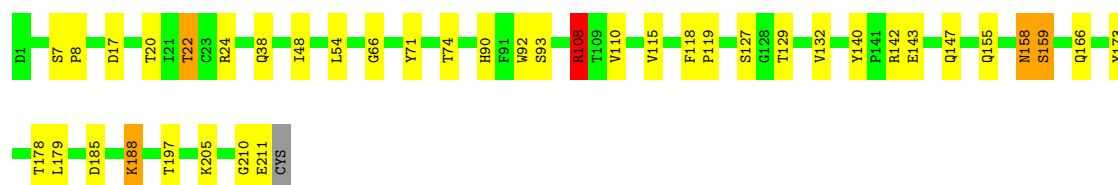
• Molecule 2: Fab light chain

Chain H: 80% 16% .



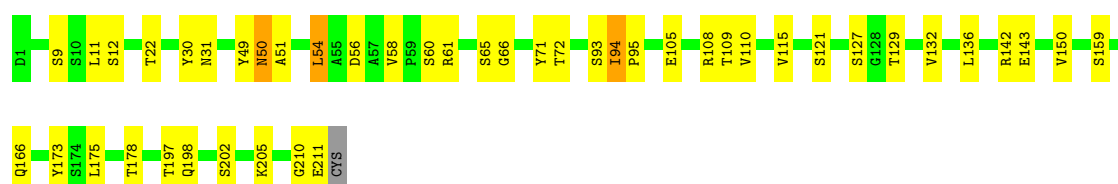
• Molecule 2: Fab light chain

Chain L: 81% 17% .

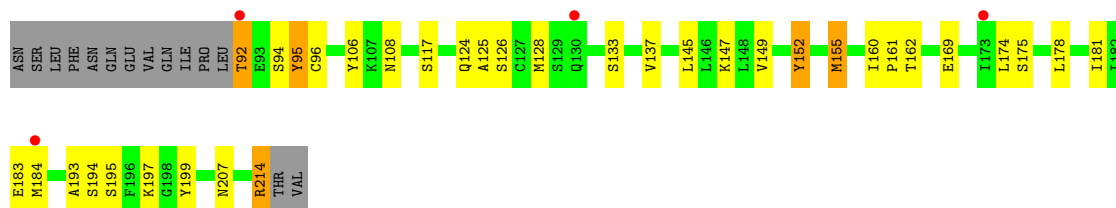


• Molecule 2: Fab light chain

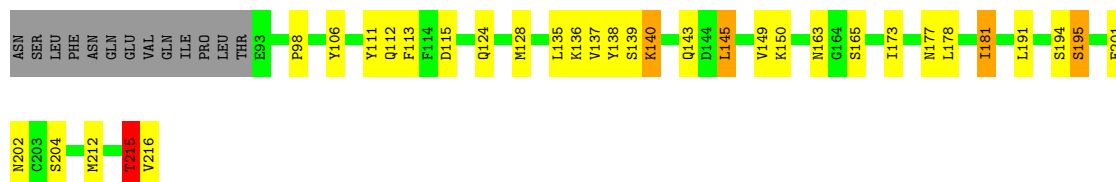
Chain Q: 78% 20% .



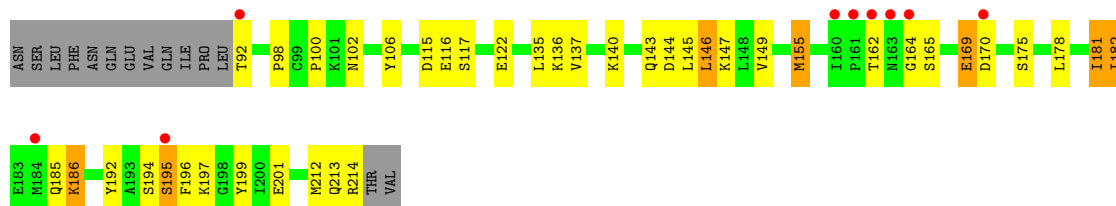
• Molecule 3: NKG2-D type II integral membrane protein



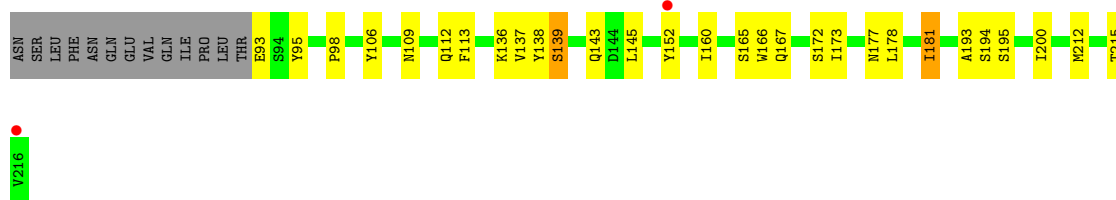
- Molecule 3: NKG2-D type II integral membrane protein



- Molecule 3: NKG2-D type II integral membrane protein



- Molecule 3: NKG2-D type II integral membrane protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	47.06Å 224.43Å 136.30Å 90.00° 91.22° 90.00°	Depositor
Resolution (Å)	136.64 – 2.98 136.27 – 2.98	Depositor EDS
% Data completeness (in resolution range)	97.3 (136.64-2.98) 97.3 (136.27-2.98)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.96Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.197 , 0.243 0.198 , 0.242	Depositor DCC
R_{free} test set	2758 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	45.9	Xtriage
Anisotropy	0.456	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.033 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	17120	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.36% 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

5.1 Standard geometry

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	0.70	1/1688 (0.1%)	1.20	3/2298 (0.1%)
1	G	0.65	0/1688	1.31	12/2298 (0.5%)
1	K	0.65	1/1688 (0.1%)	1.20	7/2298 (0.3%)
1	P	0.66	0/1688	1.18	5/2298 (0.2%)
2	D	0.75	2/1672 (0.1%)	1.18	4/2274 (0.2%)
2	H	0.67	0/1672	1.24	11/2274 (0.5%)
2	L	0.62	0/1672	1.19	5/2274 (0.2%)
2	Q	0.63	0/1672	1.14	3/2274 (0.1%)
3	M	0.61	0/1024	1.16	3/1388 (0.2%)
3	R	0.62	0/1032	1.18	4/1398 (0.3%)
3	S	0.61	0/1024	1.19	5/1388 (0.4%)
3	T	0.65	0/1032	1.14	0/1398
All	All	0.66	4/17552 (0.0%)	1.20	62/23860 (0.3%)

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	A	0	2
1	G	0	2
1	K	0	1
1	P	0	1
3	M	0	2
3	T	0	1
All	All	0	9

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	142	ARG	CD-NE	-12.51	1.28	1.46
1	A	136	SER	CA-CB	-8.30	1.46	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	142	ARG	CG-CD	5.75	1.69	1.52
1	K	165	SER	CA-CB	-5.70	1.45	1.53

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	147	LYS	CA-C-N	-12.14	104.54	123.24
1	G	147	LYS	C-N-CA	-12.14	104.54	123.24
1	G	153	PRO	CB-CA-C	11.17	121.25	111.87
1	A	62	GLN	CB-CG-CD	9.64	128.98	112.60
2	L	158	ASN	CB-CA-C	-9.63	90.01	109.55

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	24	ALA	Peptide
1	A	83	LEU	Peptide
1	G	151	PRO	Peptide
1	G	43	GLN	Peptide
1	K	130	PRO	Peptide

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	1646	0	1601	20	0
1	G	1646	0	1601	26	0
1	K	1646	0	1601	27	0
1	P	1646	0	1601	17	0
2	D	1634	0	1584	23	0
2	H	1634	0	1584	18	0
2	L	1634	0	1584	22	0
2	Q	1634	0	1584	18	0
3	M	996	0	933	22	0
3	R	1004	0	942	29	0
3	S	996	0	933	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	T	1004	0	942	21	0
All	All	17120	0	16490	255	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.

The worst 5 of 255 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:S:155:MET:HE3	3:S:192:TYR:HB2	1.34	1.05
3:S:155:MET:HE3	3:S:192:TYR:CB	1.91	0.99
3:R:135:LEU:HD12	3:R:212:MET:HE3	1.48	0.94
1:G:152:GLU:O	1:G:152:GLU:HG2	1.67	0.94
1:A:39:GLN:HE22	2:D:38:GLN:HE22	1.12	0.92

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	215/220 (98%)	205 (95%)	10 (5%)	0	100	100
1	G	215/220 (98%)	205 (95%)	10 (5%)	0	100	100
1	K	215/220 (98%)	208 (97%)	7 (3%)	0	100	100
1	P	215/220 (98%)	206 (96%)	9 (4%)	0	100	100
2	D	209/212 (99%)	199 (95%)	8 (4%)	2 (1%)	12	42
2	H	209/212 (99%)	197 (94%)	12 (6%)	0	100	100
2	L	209/212 (99%)	201 (96%)	8 (4%)	0	100	100
2	Q	209/212 (99%)	200 (96%)	8 (4%)	1 (0%)	24	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	M	121/137 (88%)	113 (93%)	7 (6%)	1 (1%)	16	47
3	R	122/137 (89%)	115 (94%)	6 (5%)	1 (1%)	16	47
3	S	121/137 (88%)	111 (92%)	9 (7%)	1 (1%)	16	47
3	T	122/137 (89%)	114 (93%)	8 (7%)	0	100	100
All	All	2182/2276 (96%)	2074 (95%)	102 (5%)	6 (0%)	36	67

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	R	195	SER
3	S	195	SER
2	Q	50	ASN
2	D	50	ASN
2	D	138	ASN

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	186/189 (98%)	171 (92%)	15 (8%)	11	36
1	G	186/189 (98%)	173 (93%)	13 (7%)	14	42
1	K	186/189 (98%)	168 (90%)	18 (10%)	8	29
1	P	186/189 (98%)	172 (92%)	14 (8%)	12	39
2	D	184/185 (100%)	169 (92%)	15 (8%)	10	35
2	H	184/185 (100%)	167 (91%)	17 (9%)	8	31
2	L	184/185 (100%)	172 (94%)	12 (6%)	15	45
2	Q	184/185 (100%)	167 (91%)	17 (9%)	8	31
3	M	113/127 (89%)	104 (92%)	9 (8%)	11	36
3	R	114/127 (90%)	106 (93%)	8 (7%)	14	42
3	S	113/127 (89%)	102 (90%)	11 (10%)	8	29
3	T	114/127 (90%)	108 (95%)	6 (5%)	20	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1934/2004 (96%)	1779 (92%)	155 (8%)	11	36

5 of 155 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	Q	12	SER
3	S	162	THR
2	Q	61	ARG
3	R	139	SER
3	T	139	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
2	Q	160	GLN
3	S	130	GLN
3	R	112	GLN
3	R	207	ASN
3	T	112	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	217/220 (98%)	-0.42	3 (1%) 73 55	29, 41, 61, 99	0
1	G	217/220 (98%)	-0.30	5 (2%) 61 42	30, 44, 73, 94	0
1	K	217/220 (98%)	-0.15	9 (4%) 41 25	28, 46, 80, 144	0
1	P	217/220 (98%)	-0.21	7 (3%) 50 33	29, 46, 81, 140	0
2	D	211/212 (99%)	-0.35	0 100 100	31, 47, 65, 80	0
2	H	211/212 (99%)	-0.51	0 100 100	26, 38, 53, 69	0
2	L	211/212 (99%)	-0.40	0 100 100	30, 46, 65, 79	0
2	Q	211/212 (99%)	-0.27	0 100 100	29, 51, 75, 90	0
3	M	123/137 (89%)	0.27	4 (3%) 49 32	46, 65, 95, 130	0
3	R	124/137 (90%)	-0.25	0 100 100	36, 51, 79, 104	0
3	S	123/137 (89%)	0.41	9 (7%) 21 13	47, 69, 96, 111	0
3	T	124/137 (90%)	-0.07	2 (1%) 70 51	39, 55, 87, 104	0
All	All	2206/2276 (96%)	-0.23	39 (1%) 67 48	26, 47, 80, 144	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	2	VAL	5.7
1	P	135	THR	5.3
3	M	92	THR	4.2
1	G	2	VAL	4.0
3	S	92	THR	3.5

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.