



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 06:05 PM UTC

PDB ID : 5DMJ / pdb_00005dmj
Title : Structure of the extracellular domain of the CD40 in complex with 3H56-5 DAB
Authors : Sheriff, S.
Deposited on : 2015-09-08
Resolution : 2.79 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

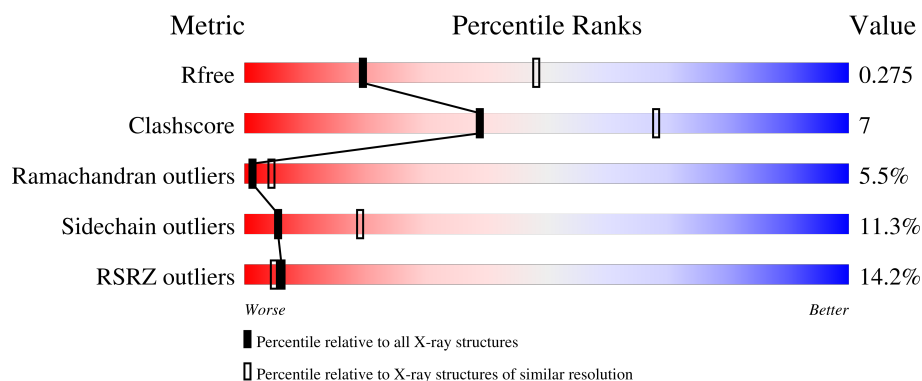
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	183	14% 59% 25% 5% 10%
1	D	183	13% 64% 19% 6% 9%
1	F	183	20% 61% 19% 7% 11%
2	B	121	3% 81% 14% •
2	E	121	4% 74% 17% •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	G	121	20% 81% 13%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6160 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 Tumor necrosis factor receptor superfamily member 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	0	0	0
			1168	710	199	239	20			
1	D	167	Total	C	N	O	S	0	0	0
			1183	723	205	235	20			
1	F	163	Total	C	N	O	S	0	1	0
			1126	687	195	224	20			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	ASP	ASN	SEE REMARK 999	UNP P25942
A	180	ASP	ASN	SEE REMARK 999	UNP P25942
A	194	ASP	-	expression tag	UNP P25942
A	195	PRO	-	expression tag	UNP P25942
A	196	GLY	-	expression tag	UNP P25942
A	197	GLY	-	expression tag	UNP P25942
A	198	GLY	-	expression tag	UNP P25942
A	199	GLY	-	expression tag	UNP P25942
A	200	GLY	-	expression tag	UNP P25942
A	201	ARG	-	expression tag	UNP P25942
A	202	LEU	-	expression tag	UNP P25942
A	203	VAL	-	expression tag	UNP P25942
A	204	PRO	-	expression tag	UNP P25942
A	205	ARG	-	expression tag	UNP P25942
D	153	ASP	ASN	SEE REMARK 999	UNP P25942
D	180	ASP	ASN	SEE REMARK 999	UNP P25942
D	194	ASP	-	expression tag	UNP P25942
D	195	PRO	-	expression tag	UNP P25942
D	196	GLY	-	expression tag	UNP P25942
D	197	GLY	-	expression tag	UNP P25942
D	198	GLY	-	expression tag	UNP P25942
D	199	GLY	-	expression tag	UNP P25942
D	200	GLY	-	expression tag	UNP P25942

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	201	ARG	-	expression tag	UNP P25942
D	202	LEU	-	expression tag	UNP P25942
D	203	VAL	-	expression tag	UNP P25942
D	204	PRO	-	expression tag	UNP P25942
D	205	ARG	-	expression tag	UNP P25942
F	153	ASP	ASN	SEE REMARK 999	UNP P25942
F	180	ASP	ASN	SEE REMARK 999	UNP P25942
F	194	ASP	-	expression tag	UNP P25942
F	195	PRO	-	expression tag	UNP P25942
F	196	GLY	-	expression tag	UNP P25942
F	197	GLY	-	expression tag	UNP P25942
F	198	GLY	-	expression tag	UNP P25942
F	199	GLY	-	expression tag	UNP P25942
F	200	GLY	-	expression tag	UNP P25942
F	201	ARG	-	expression tag	UNP P25942
F	202	LEU	-	expression tag	UNP P25942
F	203	VAL	-	expression tag	UNP P25942
F	204	PRO	-	expression tag	UNP P25942
F	205	ARG	-	expression tag	UNP P25942

- Molecule 2 is a protein called 3H65-5 domain antibody (dAb).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	117	Total	C	N	O	S	0	0	0
			905	569	156	175	5			
2	E	116	Total	C	N	O	S	0	0	0
			884	559	149	171	5			
2	G	116	Total	C	N	O	S	0	0	0
			878	557	147	170	4			

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	K	0	0
			1	1		
3	D	1	Total	K	0	0
			1	1		
3	F	1	Total	K	0	0
			1	1		

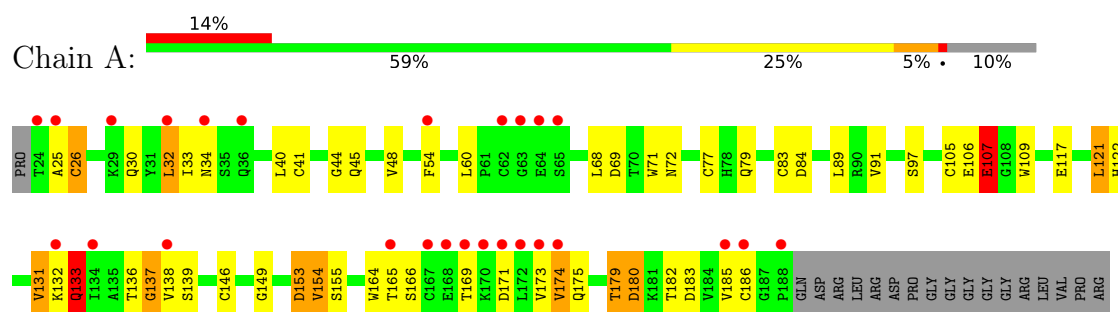
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total 3	O 3	0	0
4	B	1	Total 1	O 1	0	0
4	D	6	Total 6	O 6	0	0
4	E	1	Total 1	O 1	0	0
4	G	2	Total 2	O 2	0	0

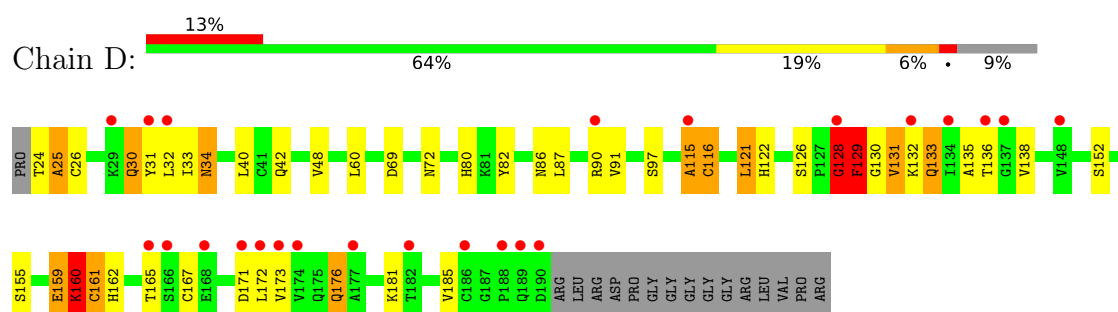
3 Residue-property plots [i](#)

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.

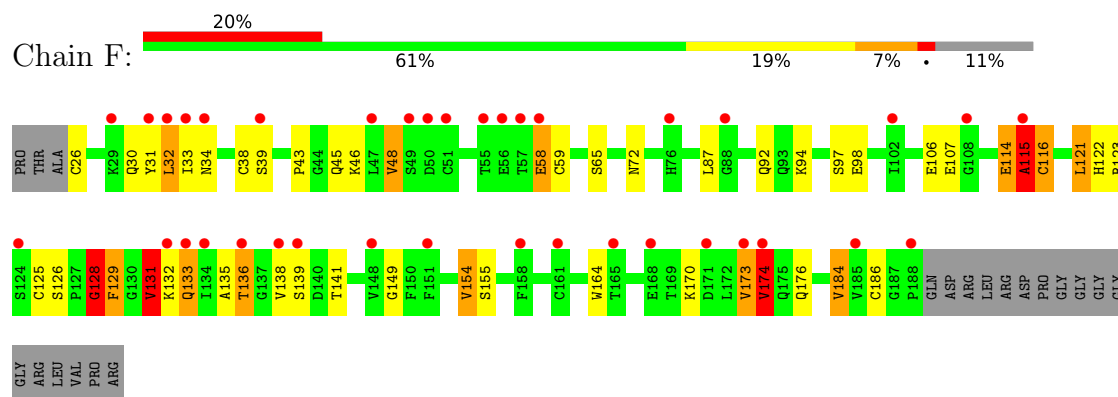
- Molecule 1: Tumor necrosis factor receptor superfamily member 5



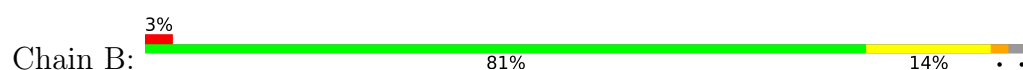
- Molecule 1: Tumor necrosis factor receptor superfamily member 5

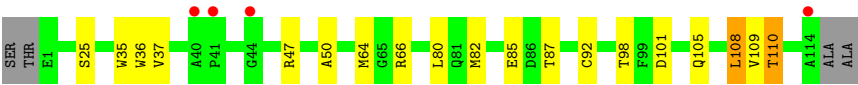


- Molecule 1: Tumor necrosis factor receptor superfamily member 5

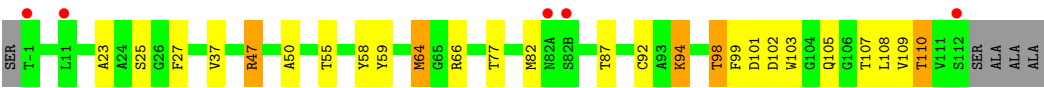
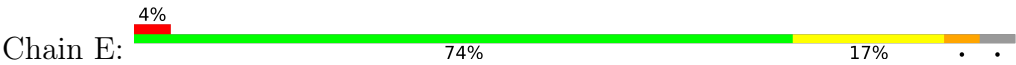


- Molecule 2: 3H65-5 domain antibody (dAb)

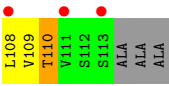
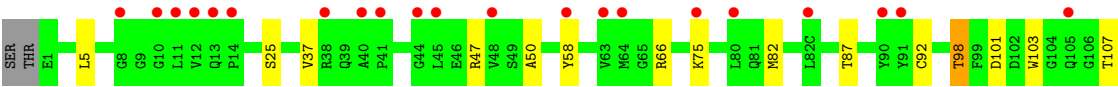
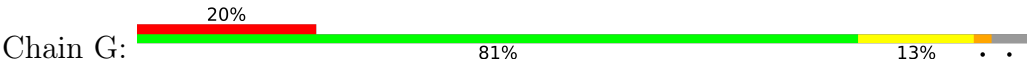




• Molecule 2: 3H65-5 domain antibody (dAb)



• Molecule 2: 3H65-5 domain antibody (dAb)



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	199.30Å 48.70Å 138.80Å 90.00° 118.20° 90.00°	Depositor
Resolution (Å)	46.26 – 2.79 46.26 – 2.79	Depositor EDS
% Data completeness (in resolution range)	98.1 (46.26-2.79) 98.2 (46.26-2.79)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.53 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.229 , 0.258 0.241 , 0.275	Depositor DCC
R_{free} test set	1036 reflections (3.15%)	wwPDB-VP
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 65.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6160	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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 ⓘ

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

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	0.90	2/1193 (0.2%)	1.43	10/1631 (0.6%)
1	D	0.98	2/1209 (0.2%)	1.65	26/1652 (1.6%)
1	F	0.92	2/1155 (0.2%)	1.54	15/1584 (0.9%)
2	B	0.80	0/925	1.15	0/1255
2	E	0.79	0/904	1.15	1/1229 (0.1%)
2	G	0.74	0/898	1.11	1/1221 (0.1%)
All	All	0.87	6/6284 (0.1%)	1.38	53/8572 (0.6%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	132	LYS	CA-C	5.87	1.61	1.52
1	D	132	LYS	CA-C	5.85	1.61	1.52
1	F	136	THR	CA-C	5.46	1.60	1.52
1	D	34	ASN	CA-C	5.25	1.59	1.52
1	A	133	GLN	C-N	5.04	1.39	1.33

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	159	GLU	CA-C-N	11.67	142.71	121.70
1	D	159	GLU	C-N-CA	11.67	142.71	121.70
1	D	128	GLY	CA-C-N	10.92	141.35	121.70
1	D	128	GLY	C-N-CA	10.92	141.35	121.70
1	F	128	GLY	CA-C-N	9.04	137.97	121.70

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	1168	0	971	17	0
1	D	1183	0	992	19	0
1	F	1126	0	917	19	0
2	B	905	0	866	8	0
2	E	884	0	834	13	0
2	G	878	0	826	10	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0
4	D	6	0	0	0	0
4	E	1	0	0	0	0
4	G	2	0	0	0	0
All	All	6160	0	5406	78	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 7.

The worst 5 of 78 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:F:48:VAL:HG13	1:F:58:GLU:HB3	1.77	0.66
1:D:115:ALA:HA	1:D:116:CYS:CB	2.27	0.65
1:D:160:LYS:HB3	1:D:162:HIS:CE1	2.32	0.64
1:D:130:GLY:HA3	1:D:161:CYS:HB2	1.80	0.64
2:B:98:THR:HG22	2:B:101:ASP:H	1.61	0.63

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	163/183 (89%)	131 (80%)	17 (10%)	15 (9%)	0	1
1	D	165/183 (90%)	134 (81%)	16 (10%)	15 (9%)	0	1
1	F	162/183 (88%)	127 (78%)	19 (12%)	16 (10%)	0	1
2	B	115/121 (95%)	113 (98%)	2 (2%)	0	100	100
2	E	114/121 (94%)	111 (97%)	3 (3%)	0	100	100
2	G	114/121 (94%)	112 (98%)	2 (2%)	0	100	100
All	All	833/912 (91%)	728 (87%)	59 (7%)	46 (6%)	1	4

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	LEU
1	A	154	VAL
1	A	165	THR
1	A	173	VAL
1	A	174	VAL

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	122/162 (75%)	106 (87%)	16 (13%)	4	14
1	D	121/162 (75%)	107 (88%)	14 (12%)	5	18
1	F	113/162 (70%)	97 (86%)	16 (14%)	3	12

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	95/98 (97%)	88 (93%)	7 (7%)	13	37
2	E	91/98 (93%)	80 (88%)	11 (12%)	5	16
2	G	89/98 (91%)	82 (92%)	7 (8%)	11	35
All	All	631/780 (81%)	560 (89%)	71 (11%)	5	19

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	97	SER
1	F	125	CYS
2	G	25	SER
1	D	33	ILE
1	D	30	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	82(A)	ASN
2	E	105	GLN
2	G	76	ASN
1	F	86	ASN
1	F	122	HIS

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

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

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 [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	165/183 (90%)	0.74	26 (15%) 5 4	27, 55, 91, 107	0
1	D	167/183 (91%)	0.76	24 (14%) 6 5	17, 47, 86, 96	0
1	F	163/183 (89%)	1.34	37 (22%) 2 1	33, 67, 102, 110	1 (0%)
2	B	117/121 (96%)	0.17	4 (3%) 48 39	18, 36, 68, 79	0
2	E	116/121 (95%)	0.73	5 (4%) 40 31	26, 55, 80, 99	0
2	G	116/121 (95%)	1.34	24 (20%) 2 2	40, 68, 105, 129	0
All	All	844/912 (92%)	0.86	120 (14%) 6 5	17, 56, 97, 129	1 (0%)

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	136	THR	7.7
1	D	31	TYR	5.6
1	F	29	LYS	5.0
2	G	8	GLY	4.6
1	F	56	GLU	4.5

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](#)

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(Å ²)	Q<0.9
3	K	F	301	1/1	0.95	0.05	63,63,63,63	0
3	K	A	301	1/1	0.98	0.04	45,45,45,45	0
3	K	D	301	1/1	0.99	0.03	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.