Full wwPDB X-ray Structure Validation Report ⓘ

Nov 20, 2023 – 06:16 pm GMT

PDB ID	:	8R61
Title	:	Structure of IgE delta epsilon 3-4 in complex with a kappa binding nanobody
Authors	:	Andersen, G.R.; Gandini, R.
Deposited on	:	2023-11-20
Resolution	:	3.10 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:

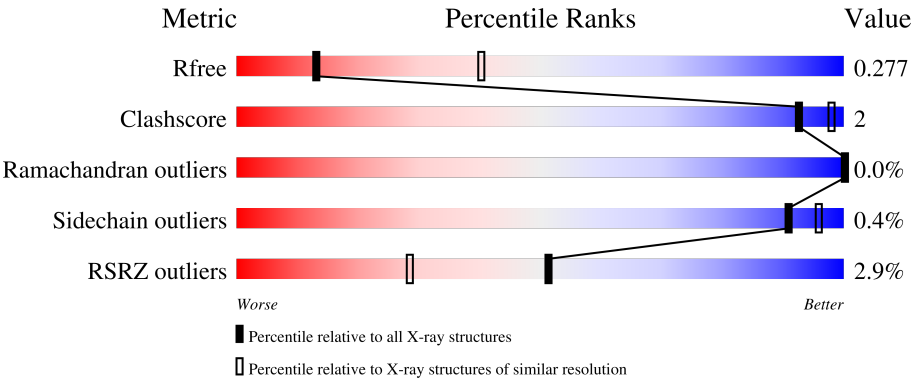
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 <=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	346	2% 62% · 36%
1	D	346	% 62% · 36%
1	G	346	% 61% · 36%
1	J	346	2% 61% · 36%
1	M	346	2% 61% · 36%

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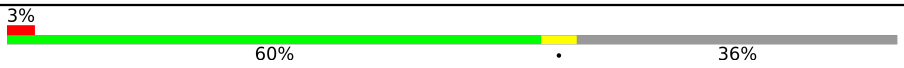
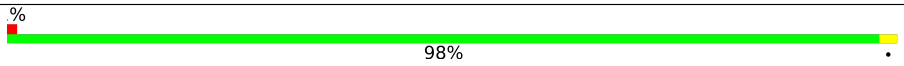
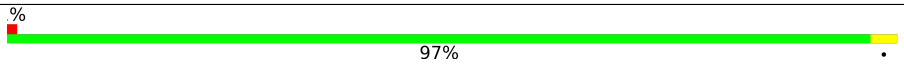
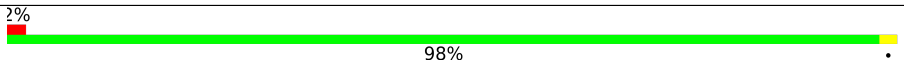
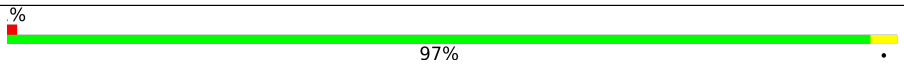
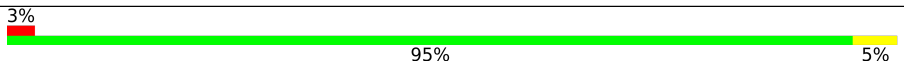
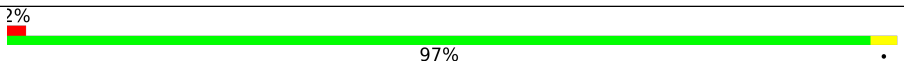
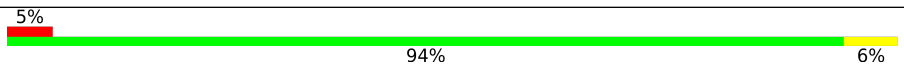
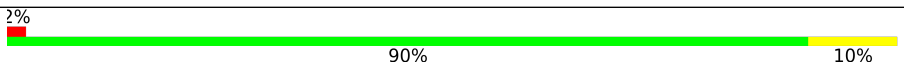
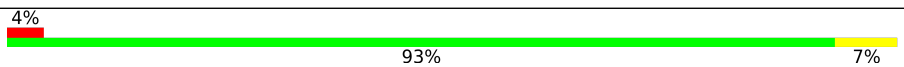
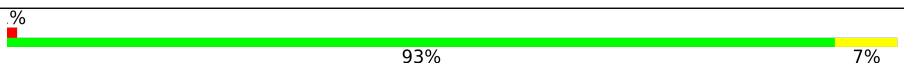
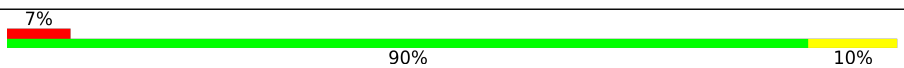
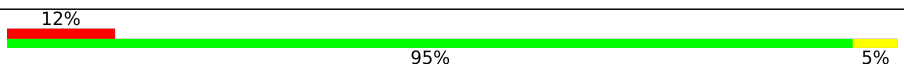
Mol	Chain	Length	Quality of chain
1	P	346	
2	B	217	
2	E	217	
2	H	217	
2	K	217	
2	N	217	
2	Q	217	
3	C	120	
3	F	120	
3	I	120	
3	L	120	
3	O	120	
3	R	120	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 25344 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 Immunoglobulin E VH-Ceps1-Ceps1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1656	1048	272	325	11			
1	D	223	Total	C	N	O	S	0	0	0
			1656	1048	272	325	11			
1	G	223	Total	C	N	O	S	0	0	0
			1656	1048	272	325	11			
1	J	223	Total	C	N	O	S	0	0	0
			1656	1048	272	325	11			
1	M	223	Total	C	N	O	S	0	0	0
			1656	1048	272	325	11			
1	P	223	Total	C	N	O	S	0	0	0
			1656	1048	272	325	11			

- Molecule 2 is a protein called HMM5 IgE light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	217	Total	C	N	O	S	0	0	0
			1643	1025	274	338	6			
2	E	217	Total	C	N	O	S	0	0	0
			1643	1025	274	338	6			
2	H	217	Total	C	N	O	S	0	0	0
			1643	1025	274	338	6			
2	K	217	Total	C	N	O	S	0	0	0
			1643	1025	274	338	6			
2	N	217	Total	C	N	O	S	0	0	0
			1643	1025	274	338	6			
2	Q	217	Total	C	N	O	S	0	0	0
			1643	1025	274	338	6			

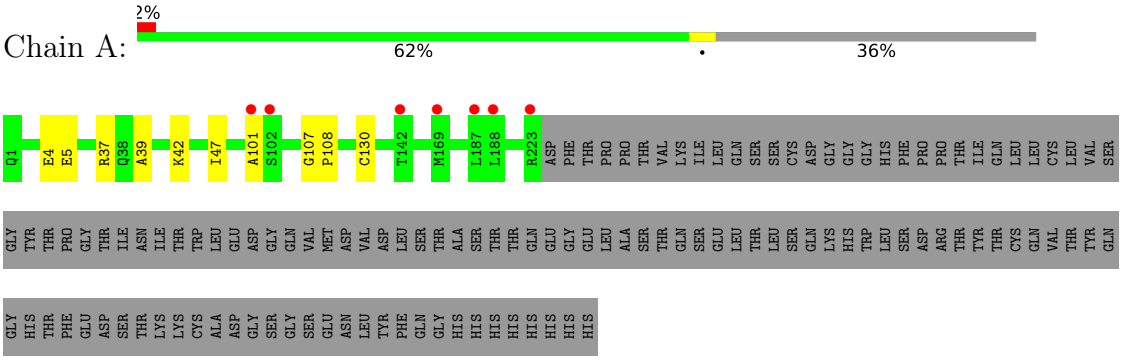
- Molecule 3 is a protein called kappa binding nanobody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	120	Total	C	N	O	S	0	0	0
			925	573	162	186	4			
3	F	120	Total	C	N	O	S	0	0	0
			925	573	162	186	4			
3	I	120	Total	C	N	O	S	0	0	0
			925	573	162	186	4			
3	L	120	Total	C	N	O	S	0	0	0
			925	573	162	186	4			
3	O	120	Total	C	N	O	S	0	0	0
			925	573	162	186	4			
3	R	120	Total	C	N	O	S	0	0	0
			925	573	162	186	4			

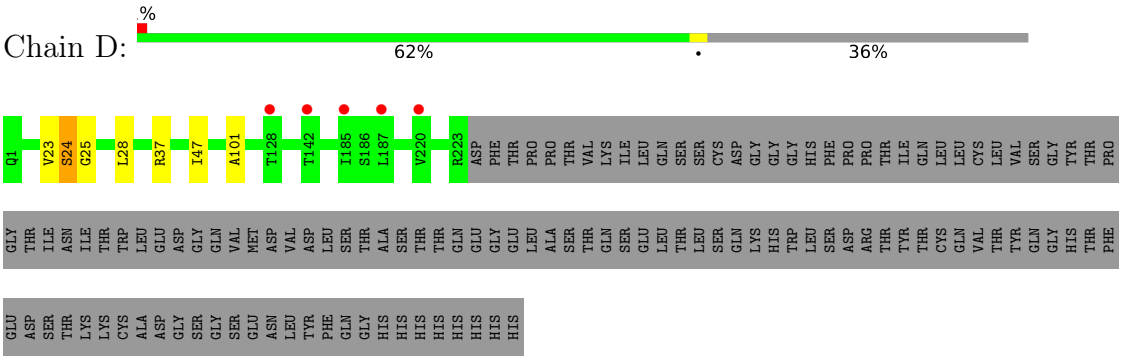
3 Residue-property plots (i)

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.

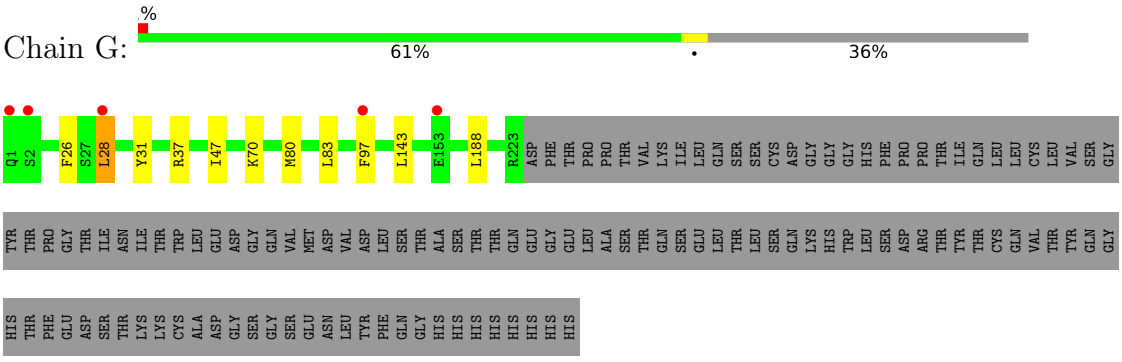
• Molecule 1: Immunoglobulin E VH-Ceps1-Ceps1



• Molecule 1: Immunoglobulin E VH-Ceps1-Ceps1

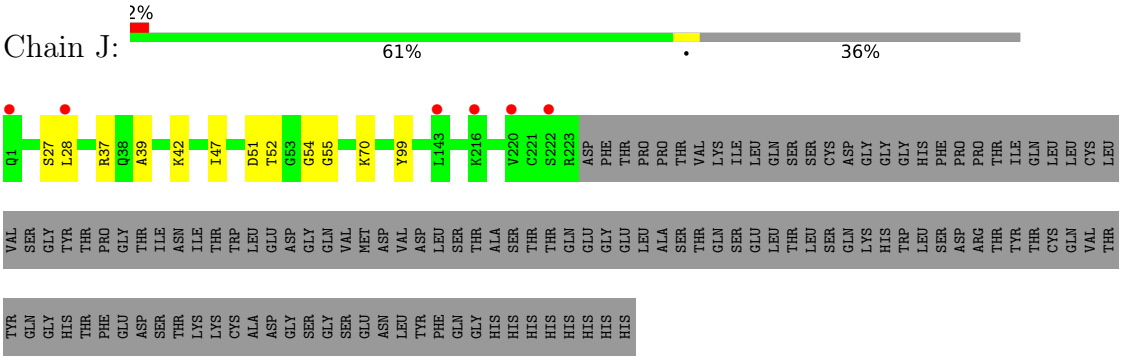


• Molecule 1: Immunoglobulin E VH-Ceps1-Ceps1



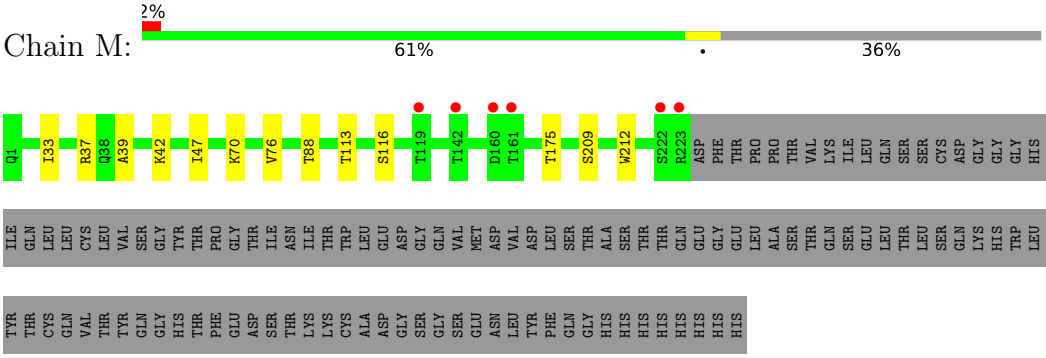
• Molecule 1: Immunoglobulin E VH-Ceps1-Ceps1

Chain J:



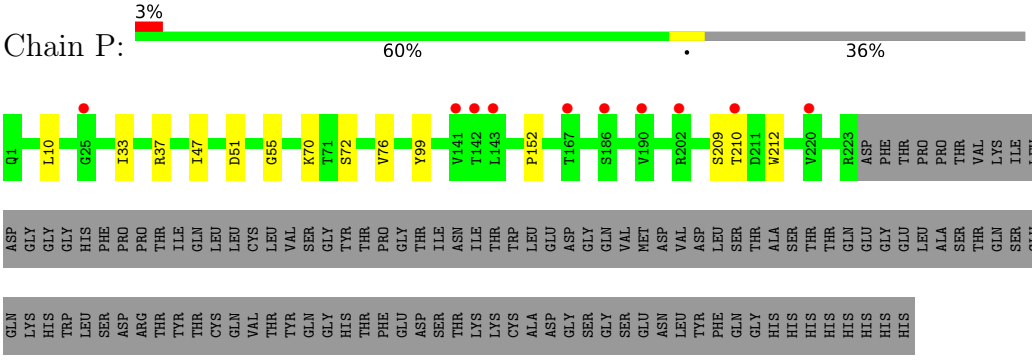
• Molecule 1: Immunoglobulin E VH-Ceps1-Ceps1

Chain M:



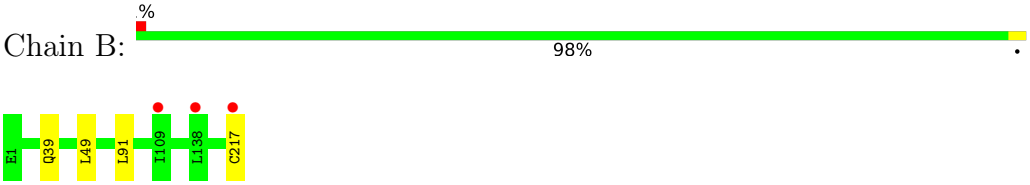
• Molecule 1: Immunoglobulin E VH-Ceps1-Ceps1

Chain P:



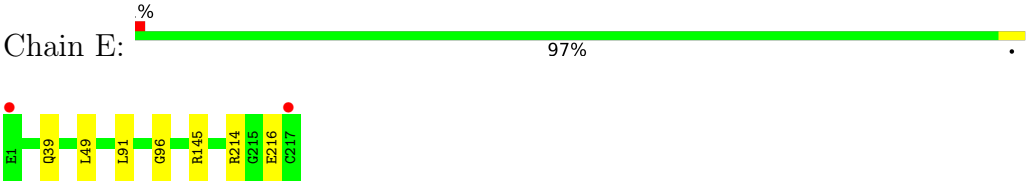
• Molecule 2: HMM5 IgE light chain

Chain B:



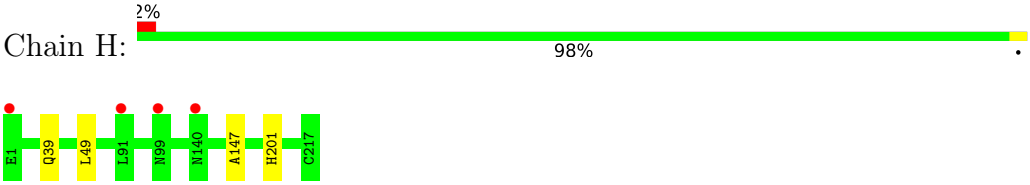
• Molecule 2: HMM5 IgE light chain

Chain E:



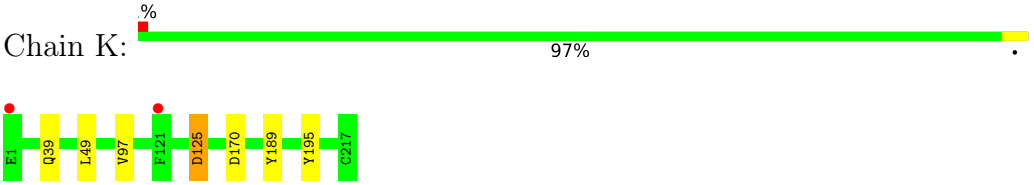
• Molecule 2: HMM5 IgE light chain

Chain H:



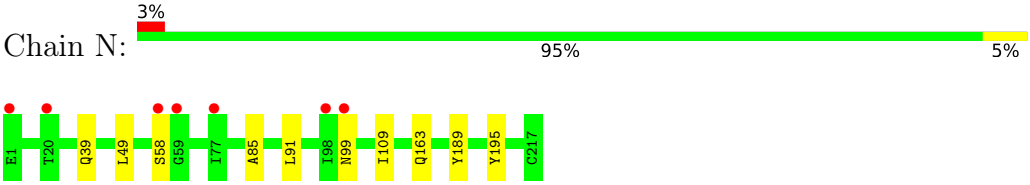
• Molecule 2: HMM5 IgE light chain

Chain K:



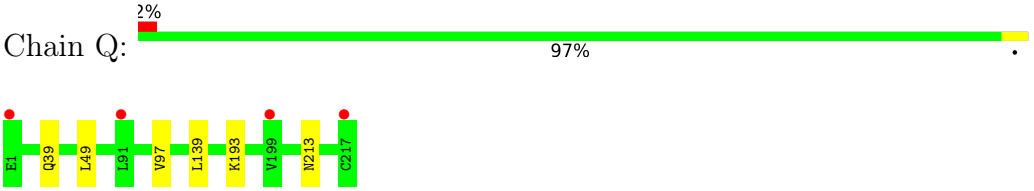
• Molecule 2: HMM5 IgE light chain

Chain N:



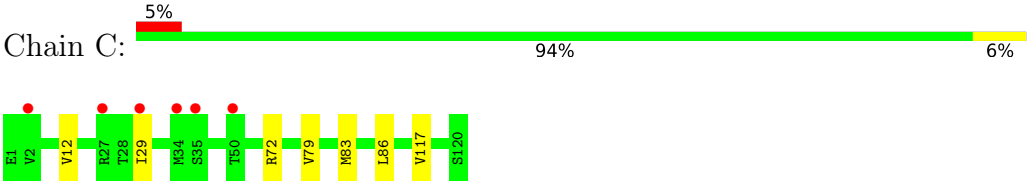
• Molecule 2: HMM5 IgE light chain

Chain Q:



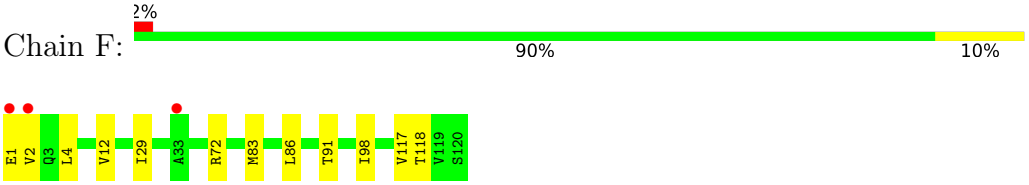
• Molecule 3: kappa binding nanobody

Chain C:



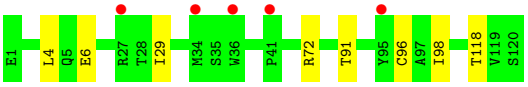
• Molecule 3: kappa binding nanobody

Chain F:



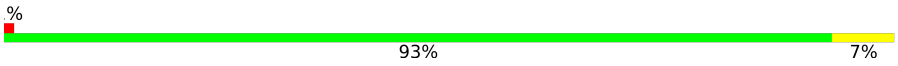
• Molecule 3: kappa binding nanobody

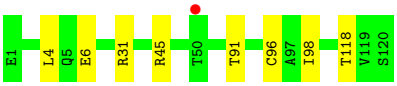
Chain I:



• Molecule 3: kappa binding nanobody

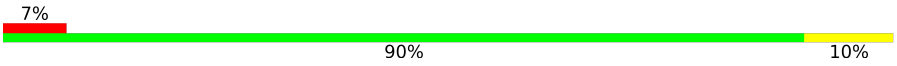
Chain L:

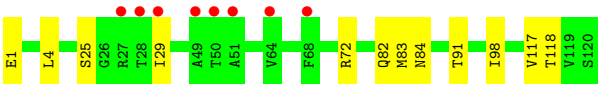




• Molecule 3: kappa binding nanobody

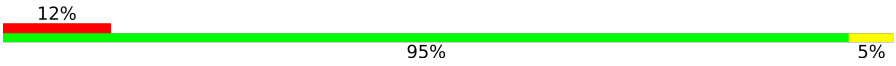
Chain O:

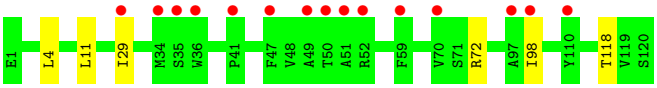




• Molecule 3: kappa binding nanobody

Chain R:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	154.10Å 132.49Å 154.53Å 90.00° 118.84° 90.00°	Depositor
Resolution (Å)	32.46 – 3.10 135.36 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (32.46-3.10) 98.9 (135.36-3.10)	Depositor EDS
R_{merge}	0.31	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.96 (at 3.07Å)	Xtriage
Refinement program	PHENIX 1.21rc1_4903	Depositor
R, R_{free}	0.232 , 0.275 0.236 , 0.277	Depositor DCC
R_{free} test set	2328 reflections (2.36%)	wwPDB-VP
Wilson B-factor (Å^2)	73.8	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 47.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.048 for -h-l,k,h 0.048 for l,k,-h-l 0.048 for h,-k,-h-l 0.049 for -h-l,-k,l 0.176 for l,-k,h	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	25344	wwPDB-VP
Average B, all atoms (Å^2)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.35	0/1698	0.61	0/2325
1	D	0.36	0/1698	0.61	0/2325
1	G	0.36	0/1698	0.62	1/2325 (0.0%)
1	J	0.37	0/1698	0.61	0/2325
1	M	0.33	0/1698	0.59	0/2325
1	P	0.33	0/1698	0.59	0/2325
2	B	0.38	0/1677	0.62	0/2279
2	E	0.39	0/1677	0.63	0/2279
2	H	0.37	0/1677	0.63	0/2279
2	K	0.38	0/1677	0.62	0/2279
2	N	0.37	0/1677	0.62	0/2279
2	Q	0.34	0/1677	0.61	1/2279 (0.0%)
3	C	0.38	0/944	0.64	0/1276
3	F	0.39	0/944	0.66	0/1276
3	I	0.34	0/944	0.61	0/1276
3	L	0.40	0/944	0.65	0/1276
3	O	0.35	0/944	0.61	0/1276
3	R	0.33	0/944	0.60	0/1276
All	All	0.36	0/25914	0.62	2/35280 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	28	LEU	CA-CB-CG	5.76	128.55	115.30
2	Q	139	LEU	CA-CB-CG	5.20	127.25	115.30

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	1656	0	1622	5	0
1	D	1656	0	1622	4	0
1	G	1656	0	1622	6	0
1	J	1656	0	1622	7	0
1	M	1656	0	1622	7	0
1	P	1656	0	1622	7	1
2	B	1643	0	1581	2	0
2	E	1643	0	1581	3	1
2	H	1643	0	1581	2	0
2	K	1643	0	1581	4	0
2	N	1643	0	1581	5	0
2	Q	1643	0	1581	3	0
3	C	925	0	869	4	0
3	F	925	0	869	6	0
3	I	925	0	869	4	0
3	L	925	0	869	4	0
3	O	925	0	869	6	0
3	R	925	0	869	3	0
All	All	25344	0	24432	75	1

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 2.

All (75) 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:M:209:SER:HB3	1:M:212:TRP:HB2	1.80	0.64
2:Q:193:LYS:HE3	2:Q:213:ASN:HB3	1.81	0.62
3:C:29:ILE:O	3:C:72:ARG:NH2	2.39	0.56
2:E:39:GLN:HB2	2:E:49:LEU:HD11	1.90	0.54
2:K:39:GLN:HB2	2:K:49:LEU:HD11	1.90	0.53
2:Q:39:GLN:HB2	2:Q:49:LEU:HD11	1.91	0.53
3:I:6:GLU:OE2	3:I:96:CYS:N	2.43	0.52
1:P:70:LYS:NZ	1:P:72:SER:O	2.42	0.52
3:F:29:ILE:O	3:F:72:ARG:NH2	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:29:ILE:O	3:I:72:ARG:NH2	2.43	0.51
1:M:37:ARG:HB3	1:M:47:ILE:HD11	1.91	0.51
2:N:39:GLN:HB2	2:N:49:LEU:HD11	1.92	0.51
1:P:10:LEU:HB2	1:P:152:PRO:HG3	1.93	0.50
3:O:29:ILE:O	3:O:72:ARG:NH2	2.45	0.49
1:M:33:ILE:HG13	1:M:76:VAL:HG21	1.94	0.49
1:P:37:ARG:HB3	1:P:47:ILE:HD11	1.95	0.49
3:L:91:THR:HG23	3:L:118:THR:HA	1.95	0.49
3:O:82:GLN:NE2	3:O:84:ASN:OD1	2.46	0.49
2:H:39:GLN:HB2	2:H:49:LEU:HD11	1.95	0.49
1:P:51:ASP:OD1	1:P:55:GLY:N	2.45	0.49
2:N:85:ALA:HB2	2:N:109:ILE:HG12	1.95	0.48
1:A:37:ARG:HB3	1:A:47:ILE:HD11	1.95	0.47
1:D:24:SER:OG	1:D:25:GLY:N	2.48	0.47
3:R:4:LEU:HD11	3:R:98:ILE:HG13	1.97	0.47
3:F:4:LEU:HD11	3:F:98:ILE:HG13	1.95	0.47
1:G:37:ARG:HB3	1:G:47:ILE:HD11	1.95	0.47
3:L:4:LEU:HD11	3:L:98:ILE:HG13	1.96	0.46
3:I:4:LEU:HD11	3:I:98:ILE:HG13	1.99	0.45
1:M:88:THR:HG23	1:M:113:THR:HA	1.99	0.45
3:C:12:VAL:HG11	3:C:86:LEU:HD13	1.99	0.45
2:B:39:GLN:HB2	2:B:49:LEU:HD11	1.99	0.45
3:O:4:LEU:HD11	3:O:98:ILE:HG13	1.99	0.45
1:J:37:ARG:HB3	1:J:47:ILE:HD11	1.98	0.45
1:G:143:LEU:HD21	1:G:188:LEU:HD23	1.99	0.45
3:O:83:MET:HE1	3:O:117:VAL:HG21	1.99	0.45
3:R:11:LEU:HD23	3:R:118:THR:HB	1.98	0.44
1:D:37:ARG:HB3	1:D:47:ILE:HD11	1.98	0.44
2:E:96:GLY:HA2	3:L:31:ARG:HB3	2.00	0.44
2:K:189:TYR:O	2:K:195:TYR:OH	2.35	0.44
3:F:12:VAL:HG11	3:F:86:LEU:HD13	1.99	0.44
1:M:70:LYS:HG2	1:M:76:VAL:HG22	1.97	0.44
1:P:33:ILE:HG13	1:P:76:VAL:HG21	2.00	0.44
3:I:91:THR:HG23	3:I:118:THR:HA	2.00	0.44
1:P:209:SER:HB3	1:P:212:TRP:HB2	2.00	0.44
1:A:39:ALA:HB3	1:A:42:LYS:HB2	2.00	0.43
3:F:91:THR:HG23	3:F:118:THR:HA	2.01	0.43
1:J:51:ASP:OD1	1:J:55:GLY:N	2.46	0.43
1:A:4:GLU:HA	1:A:108:PRO:HD2	2.01	0.43
1:G:28:LEU:HD23	1:G:70:LYS:HE3	2.00	0.42
2:H:147:ALA:HB2	2:H:201:HIS:HD2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:91:LEU:HD21	2:N:99:ASN:HB3	2.02	0.42
1:D:101:ALA:HB3	2:E:91:LEU:HD11	2.01	0.42
2:N:189:TYR:O	2:N:195:TYR:OH	2.35	0.42
3:O:91:THR:HG23	3:O:118:THR:HA	2.01	0.42
1:J:28:LEU:HD23	1:J:70:LYS:HE3	2.01	0.41
1:J:39:ALA:HB3	1:J:42:LYS:HB2	2.02	0.41
1:J:51:ASP:OD1	1:J:54:GLY:N	2.53	0.41
1:G:31:TYR:HD1	1:G:97:PHE:HA	1.85	0.41
1:M:175:THR:O	2:N:163:GLN:NE2	2.44	0.41
3:C:83:MET:HE1	3:C:117:VAL:HG21	2.03	0.41
1:G:80:MET:HB3	1:G:83:LEU:HD21	2.02	0.41
2:K:125:ASP:OD1	2:K:125:ASP:N	2.54	0.41
1:D:23:VAL:HG21	1:D:28:LEU:HG	2.02	0.41
3:L:6:GLU:OE2	3:L:96:CYS:N	2.49	0.41
1:G:26:PHE:HD1	1:G:26:PHE:HA	1.77	0.41
1:M:39:ALA:HB3	1:M:42:LYS:HB2	2.01	0.41
3:C:72:ARG:HG2	3:C:79:VAL:HG12	2.02	0.41
1:P:99:TYR:HB3	2:Q:97:VAL:HG13	2.03	0.41
1:A:101:ALA:HB3	2:B:91:LEU:HD11	2.03	0.40
3:F:83:MET:HE1	3:F:117:VAL:HG21	2.04	0.40
1:J:52:THR:HB	3:O:1:GLU:OE2	2.21	0.40
1:J:99:TYR:HB3	2:K:97:VAL:HG13	2.03	0.40
3:R:29:ILE:O	3:R:72:ARG:NH2	2.54	0.40
1:A:5:GLU:OE2	1:A:107:GLY:HA3	2.22	0.40
3:F:1:GLU:HB2	3:F:2:VAL:H	1.55	0.40

All (1) 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)
2:E:216:GLU:OE2	1:P:210:THR:OG1[2_445]	2.04	0.16

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	221/346 (64%)	217 (98%)	4 (2%)	0	100	100
1	D	221/346 (64%)	213 (96%)	7 (3%)	1 (0%)	29	64
1	G	221/346 (64%)	216 (98%)	5 (2%)	0	100	100
1	J	221/346 (64%)	216 (98%)	5 (2%)	0	100	100
1	M	221/346 (64%)	216 (98%)	5 (2%)	0	100	100
1	P	221/346 (64%)	216 (98%)	5 (2%)	0	100	100
2	B	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
2	E	215/217 (99%)	205 (95%)	10 (5%)	0	100	100
2	H	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
2	K	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
2	N	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
2	Q	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
3	C	118/120 (98%)	115 (98%)	3 (2%)	0	100	100
3	F	118/120 (98%)	115 (98%)	3 (2%)	0	100	100
3	I	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
3	L	118/120 (98%)	115 (98%)	3 (2%)	0	100	100
3	O	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
3	R	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
All	All	3324/4098 (81%)	3221 (97%)	102 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	24	SER

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	186/295 (63%)	185 (100%)	1 (0%)	88 94
1	D	186/295 (63%)	186 (100%)	0	100 100
1	G	186/295 (63%)	186 (100%)	0	100 100
1	J	186/295 (63%)	185 (100%)	1 (0%)	88 94
1	M	186/295 (63%)	185 (100%)	1 (0%)	88 94
1	P	186/295 (63%)	186 (100%)	0	100 100
2	B	185/185 (100%)	184 (100%)	1 (0%)	88 94
2	E	185/185 (100%)	183 (99%)	2 (1%)	73 89
2	H	185/185 (100%)	185 (100%)	0	100 100
2	K	185/185 (100%)	183 (99%)	2 (1%)	73 89
2	N	185/185 (100%)	184 (100%)	1 (0%)	88 94
2	Q	185/185 (100%)	185 (100%)	0	100 100
3	C	96/96 (100%)	96 (100%)	0	100 100
3	F	96/96 (100%)	96 (100%)	0	100 100
3	I	96/96 (100%)	96 (100%)	0	100 100
3	L	96/96 (100%)	95 (99%)	1 (1%)	76 90
3	O	96/96 (100%)	95 (99%)	1 (1%)	76 90
3	R	96/96 (100%)	96 (100%)	0	100 100
All	All	2802/3456 (81%)	2791 (100%)	11 (0%)	91 96

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	CYS
2	B	217	CYS
2	E	145	ARG
2	E	214	ARG
1	J	27	SER
2	K	125	ASP
2	K	170	ASP
3	L	45	ARG
1	M	116	SER
2	N	58	SER
3	O	25	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	72	GLN
1	M	181	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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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

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, 95^{th} 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	223/346 (64%)	0.22	7 (3%) 49 26	50, 71, 110, 125	0
1	D	223/346 (64%)	0.26	5 (2%) 62 41	47, 70, 117, 137	0
1	G	223/346 (64%)	0.29	5 (2%) 62 41	44, 71, 109, 134	0
1	J	223/346 (64%)	0.34	6 (2%) 54 31	46, 68, 112, 127	0
1	M	223/346 (64%)	0.29	6 (2%) 54 31	60, 82, 118, 144	0
1	P	223/346 (64%)	0.31	10 (4%) 33 16	55, 84, 131, 170	0
2	B	217/217 (100%)	0.27	3 (1%) 75 56	44, 63, 87, 108	0
2	E	217/217 (100%)	0.20	2 (0%) 84 69	41, 63, 89, 108	0
2	H	217/217 (100%)	0.32	4 (1%) 68 47	44, 63, 95, 116	0
2	K	217/217 (100%)	0.25	2 (0%) 84 69	43, 61, 78, 103	0
2	N	217/217 (100%)	0.37	7 (3%) 47 25	53, 76, 99, 109	0
2	Q	217/217 (100%)	0.38	4 (1%) 68 47	51, 77, 96, 125	0
3	C	120/120 (100%)	0.45	6 (5%) 28 13	51, 66, 87, 105	0
3	F	120/120 (100%)	0.36	3 (2%) 57 34	47, 62, 87, 113	0
3	I	120/120 (100%)	0.44	5 (4%) 36 18	60, 79, 105, 117	0
3	L	120/120 (100%)	0.30	1 (0%) 86 72	49, 68, 95, 113	0
3	O	120/120 (100%)	0.60	8 (6%) 17 7	55, 82, 112, 135	0
3	R	120/120 (100%)	0.63	15 (12%) 3 1	77, 104, 125, 136	0
All	All	3360/4098 (81%)	0.33	99 (2%) 51 28	41, 72, 111, 170	0

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Q	217	CYS	9.0
1	P	142	THR	5.7
1	J	222	SER	4.9

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Mol	Chain	Res	Type	RSRZ
2	N	58	SER	4.8
3	C	35	SER	4.4
1	G	1	GLN	4.4
2	K	1	GLU	4.1
2	E	217	CYS	4.0
1	M	160	ASP	3.9
1	J	1	GLN	3.9
2	N	59	GLY	3.8
3	C	29	ILE	3.6
3	F	1	GLU	3.5
3	R	98	ILE	3.5
3	R	51	ALA	3.5
2	Q	199	VAL	3.3
3	I	27	ARG	3.3
3	F	2	VAL	3.3
2	B	217	CYS	3.3
1	J	143	LEU	3.2
3	C	2	VAL	3.2
2	N	1	GLU	3.2
3	R	36	TRP	3.0
1	P	210	THR	3.0
3	O	27	ARG	2.9
1	D	142	THR	2.9
1	P	186	SER	2.9
3	R	47	PHE	2.9
1	M	161	THR	2.9
3	R	29	ILE	2.9
1	P	141	VAL	2.8
2	N	20	THR	2.8
3	R	52	ARG	2.8
2	Q	1	GLU	2.8
1	J	216	LYS	2.8
1	P	25	GLY	2.7
1	A	187	LEU	2.7
1	M	142	THR	2.7
1	P	202	ARG	2.7
3	R	35	SER	2.6
1	D	128	THR	2.6
3	R	70	VAL	2.6
2	H	1	GLU	2.6
1	P	190	VAL	2.6
3	I	41	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
3	O	29	ILE	2.5
1	G	97	PHE	2.5
1	G	153	GLU	2.5
3	R	34	MET	2.5
1	P	143	LEU	2.5
3	L	50	THR	2.5
3	O	50	THR	2.5
3	F	33	ALA	2.4
3	C	27	ARG	2.4
1	D	187	LEU	2.4
1	P	220	VAL	2.4
2	H	91	LEU	2.4
2	B	138	LEU	2.4
3	R	110	TYR	2.4
1	J	28	LEU	2.3
1	A	188	LEU	2.3
3	R	97	ALA	2.3
1	A	223	ARG	2.3
1	G	2	SER	2.3
1	M	222	SER	2.3
2	N	98	ILE	2.3
3	O	28	THR	2.3
1	A	142	THR	2.3
2	E	1	GLU	2.3
3	I	36	TRP	2.3
3	R	50	THR	2.3
1	D	220	VAL	2.3
3	O	68	PHE	2.3
1	A	169	MET	2.3
1	G	28	LEU	2.3
3	I	34	MET	2.3
3	O	49	ALA	2.2
3	C	34	MET	2.2
1	M	119	THR	2.2
2	Q	91	LEU	2.2
3	R	59	PHE	2.2
1	A	101	ALA	2.2
3	I	95	TYR	2.2
2	K	121	PHE	2.2
2	N	99	ASN	2.2
3	O	64	VAL	2.2
1	D	185	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	102	SER	2.1
3	C	50	THR	2.1
3	O	51	ALA	2.1
3	R	49	ALA	2.1
2	B	109	ILE	2.0
1	P	167	THR	2.0
2	H	140	ASN	2.0
1	J	220	VAL	2.0
1	M	223	ARG	2.0
2	N	77	ILE	2.0
3	R	41	PRO	2.0
2	H	99	ASN	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 monosaccharides 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.