



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 09:48 PM UTC

PDB ID : 7P5V / pdb_00007p5v
EMDB ID : EMD-13202
Title : Structure of homomeric LRRC8A Volume-Regulated Anion Channel in complex with synthetic nanobody Sb1
Authors : Deneka, D.; Rutz, S.; Sawicka, M.
Deposited on : 2021-07-15
Resolution : 3.06 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

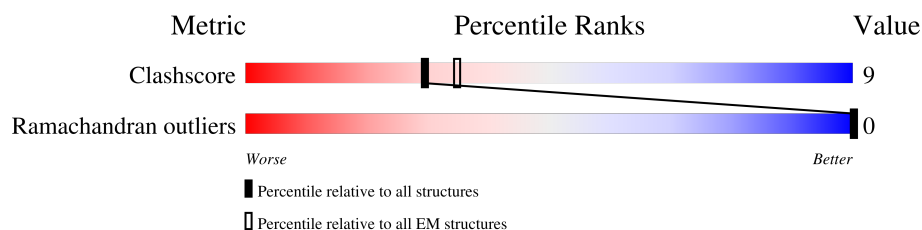
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.06 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	810	 65% 23% 11%
1	B	810	 69% 22% 10%
1	C	810	 67% 21% 11%
1	D	810	 71% 20% 10%
1	E	810	 66% 22% 11%
1	F	810	 69% 21% 10%
2	G	144	 61% 18% 21%
2	H	144	 58% 22% 21%
2	I	144	 61% 18% 21%
2	J	144	 62% 17% 21%

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Mol	Chain	Length	Quality of chain
2	K	144	 56% 23% 21%
2	L	144	 62% 17% 21%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 41274 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Volume-regulated anion channel subunit LRRC8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	718	Total	C	N	O	S	0	0
			5922	3853	997	1047	25		
1	B	732	Total	C	N	O	S	0	0
			6030	3916	1018	1071	25		
1	C	718	Total	C	N	O	S	0	0
			5922	3853	997	1047	25		
1	D	732	Total	C	N	O	S	0	0
			6030	3916	1018	1071	25		
1	E	718	Total	C	N	O	S	0	0
			5922	3853	997	1047	25		
1	F	732	Total	C	N	O	S	0	0
			6030	3916	1018	1071	25		

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q80WG5
A	2	ILE	-	expression tag	UNP Q80WG5
A	3	PRO	-	expression tag	UNP Q80WG5
A	4	VAL	-	expression tag	UNP Q80WG5
A	5	THR	-	expression tag	UNP Q80WG5
A	6	GLU	-	expression tag	UNP Q80WG5
A	7	LEU	-	expression tag	UNP Q80WG5
A	8	ARG	-	expression tag	UNP Q80WG5
A	9	TYR	-	expression tag	UNP Q80WG5
A	10	PHE	-	expression tag	UNP Q80WG5
A	11	ALA	-	expression tag	UNP Q80WG5
A	12	ASP	-	expression tag	UNP Q80WG5
A	13	THR	-	expression tag	UNP Q80WG5
A	14	GLN	-	expression tag	UNP Q80WG5
A	809	GLN	-	expression tag	UNP Q80WG5
A	810	ALA	-	expression tag	UNP Q80WG5
B	1	MET	-	initiating methionine	UNP Q80WG5
B	2	ILE	-	expression tag	UNP Q80WG5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	3	PRO	-	expression tag	UNP Q80WG5
B	4	VAL	-	expression tag	UNP Q80WG5
B	5	THR	-	expression tag	UNP Q80WG5
B	6	GLU	-	expression tag	UNP Q80WG5
B	7	LEU	-	expression tag	UNP Q80WG5
B	8	ARG	-	expression tag	UNP Q80WG5
B	9	TYR	-	expression tag	UNP Q80WG5
B	10	PHE	-	expression tag	UNP Q80WG5
B	11	ALA	-	expression tag	UNP Q80WG5
B	12	ASP	-	expression tag	UNP Q80WG5
B	13	THR	-	expression tag	UNP Q80WG5
B	14	GLN	-	expression tag	UNP Q80WG5
B	809	GLN	-	expression tag	UNP Q80WG5
B	810	ALA	-	expression tag	UNP Q80WG5
C	1	MET	-	initiating methionine	UNP Q80WG5
C	2	ILE	-	expression tag	UNP Q80WG5
C	3	PRO	-	expression tag	UNP Q80WG5
C	4	VAL	-	expression tag	UNP Q80WG5
C	5	THR	-	expression tag	UNP Q80WG5
C	6	GLU	-	expression tag	UNP Q80WG5
C	7	LEU	-	expression tag	UNP Q80WG5
C	8	ARG	-	expression tag	UNP Q80WG5
C	9	TYR	-	expression tag	UNP Q80WG5
C	10	PHE	-	expression tag	UNP Q80WG5
C	11	ALA	-	expression tag	UNP Q80WG5
C	12	ASP	-	expression tag	UNP Q80WG5
C	13	THR	-	expression tag	UNP Q80WG5
C	14	GLN	-	expression tag	UNP Q80WG5
C	809	GLN	-	expression tag	UNP Q80WG5
C	810	ALA	-	expression tag	UNP Q80WG5
D	1	MET	-	initiating methionine	UNP Q80WG5
D	2	ILE	-	expression tag	UNP Q80WG5
D	3	PRO	-	expression tag	UNP Q80WG5
D	4	VAL	-	expression tag	UNP Q80WG5
D	5	THR	-	expression tag	UNP Q80WG5
D	6	GLU	-	expression tag	UNP Q80WG5
D	7	LEU	-	expression tag	UNP Q80WG5
D	8	ARG	-	expression tag	UNP Q80WG5
D	9	TYR	-	expression tag	UNP Q80WG5
D	10	PHE	-	expression tag	UNP Q80WG5
D	11	ALA	-	expression tag	UNP Q80WG5
D	12	ASP	-	expression tag	UNP Q80WG5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	13	THR	-	expression tag	UNP Q80WG5
D	14	GLN	-	expression tag	UNP Q80WG5
D	809	GLN	-	expression tag	UNP Q80WG5
D	810	ALA	-	expression tag	UNP Q80WG5
E	1	MET	-	initiating methionine	UNP Q80WG5
E	2	ILE	-	expression tag	UNP Q80WG5
E	3	PRO	-	expression tag	UNP Q80WG5
E	4	VAL	-	expression tag	UNP Q80WG5
E	5	THR	-	expression tag	UNP Q80WG5
E	6	GLU	-	expression tag	UNP Q80WG5
E	7	LEU	-	expression tag	UNP Q80WG5
E	8	ARG	-	expression tag	UNP Q80WG5
E	9	TYR	-	expression tag	UNP Q80WG5
E	10	PHE	-	expression tag	UNP Q80WG5
E	11	ALA	-	expression tag	UNP Q80WG5
E	12	ASP	-	expression tag	UNP Q80WG5
E	13	THR	-	expression tag	UNP Q80WG5
E	14	GLN	-	expression tag	UNP Q80WG5
E	809	GLN	-	expression tag	UNP Q80WG5
E	810	ALA	-	expression tag	UNP Q80WG5
F	1	MET	-	initiating methionine	UNP Q80WG5
F	2	ILE	-	expression tag	UNP Q80WG5
F	3	PRO	-	expression tag	UNP Q80WG5
F	4	VAL	-	expression tag	UNP Q80WG5
F	5	THR	-	expression tag	UNP Q80WG5
F	6	GLU	-	expression tag	UNP Q80WG5
F	7	LEU	-	expression tag	UNP Q80WG5
F	8	ARG	-	expression tag	UNP Q80WG5
F	9	TYR	-	expression tag	UNP Q80WG5
F	10	PHE	-	expression tag	UNP Q80WG5
F	11	ALA	-	expression tag	UNP Q80WG5
F	12	ASP	-	expression tag	UNP Q80WG5
F	13	THR	-	expression tag	UNP Q80WG5
F	14	GLN	-	expression tag	UNP Q80WG5
F	809	GLN	-	expression tag	UNP Q80WG5
F	810	ALA	-	expression tag	UNP Q80WG5

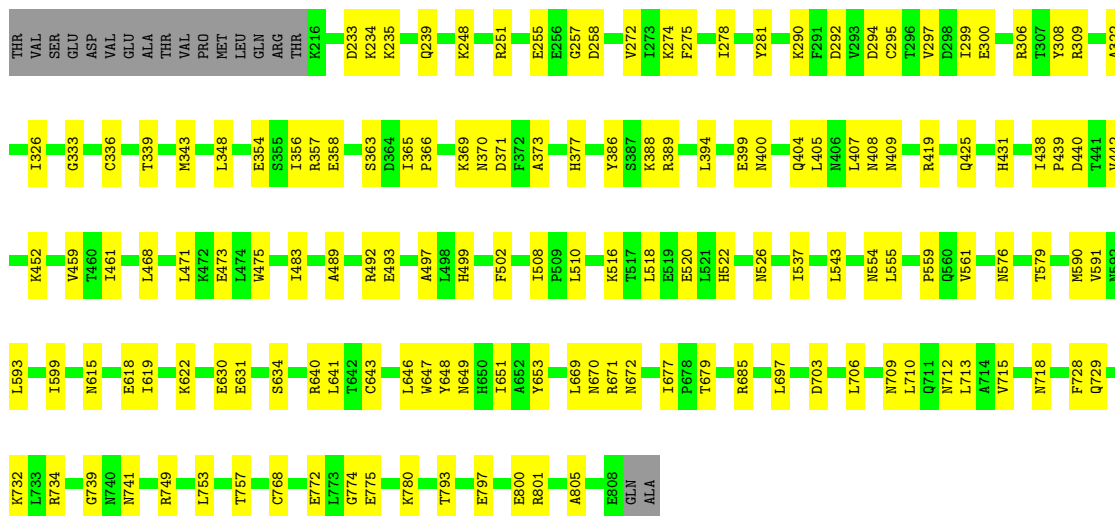
- Molecule 2 is a protein called Synthetic nanobody Sb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	114	Total	C	N	O	S	
			903	575	152	172	4	0

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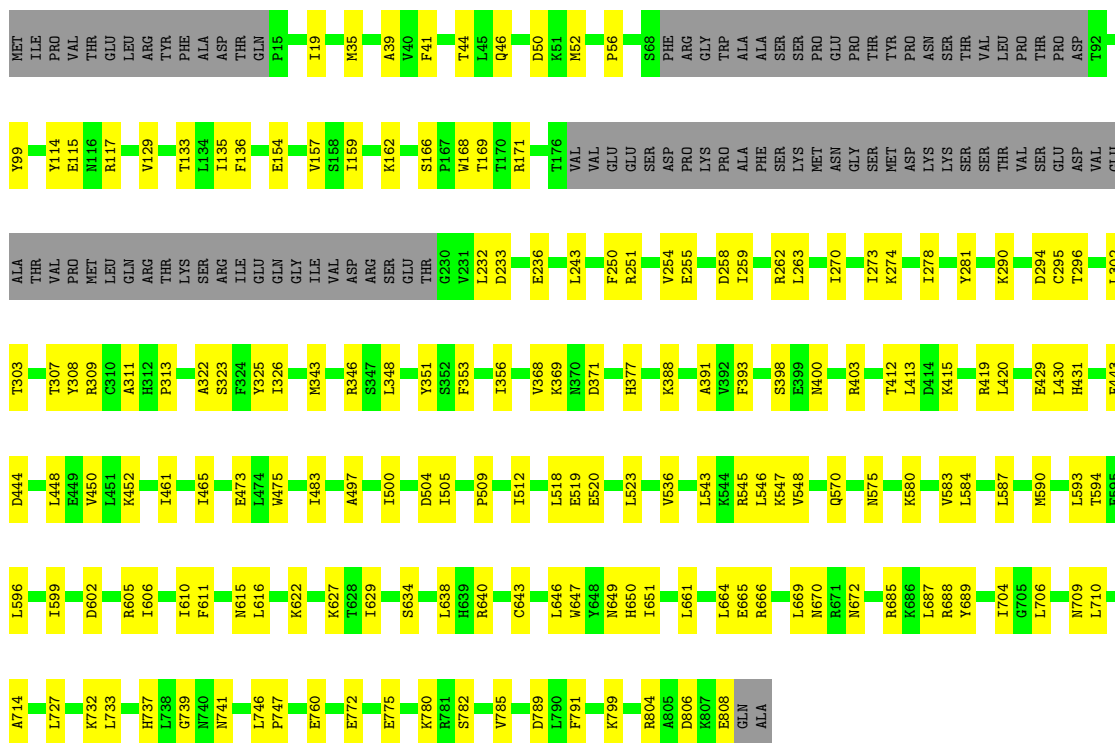
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	114	Total 903	C 575	N 152	O 172	S 4	0	0
2	I	114	Total 903	C 575	N 152	O 172	S 4	0	0
2	J	114	Total 903	C 575	N 152	O 172	S 4	0	0
2	K	114	Total 903	C 575	N 152	O 172	S 4	0	0
2	L	114	Total 903	C 575	N 152	O 172	S 4	0	0



• Molecule 1: Volume-regulated anion channel subunit LRRC8A

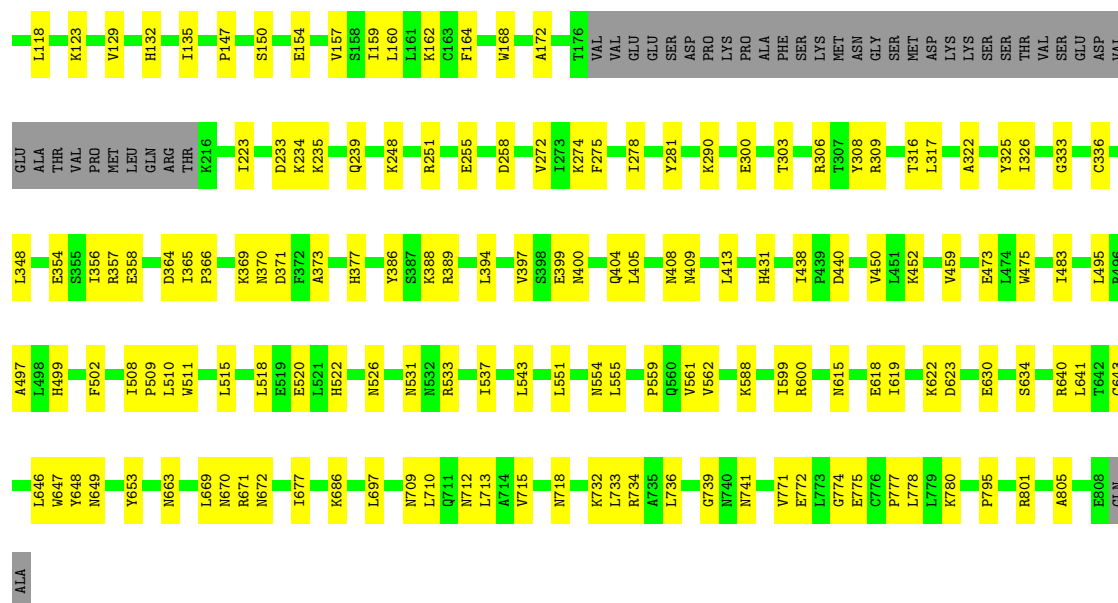
Chain C: 67% 21% 11%



• Molecule 1: Volume-regulated anion channel subunit LRRC8A

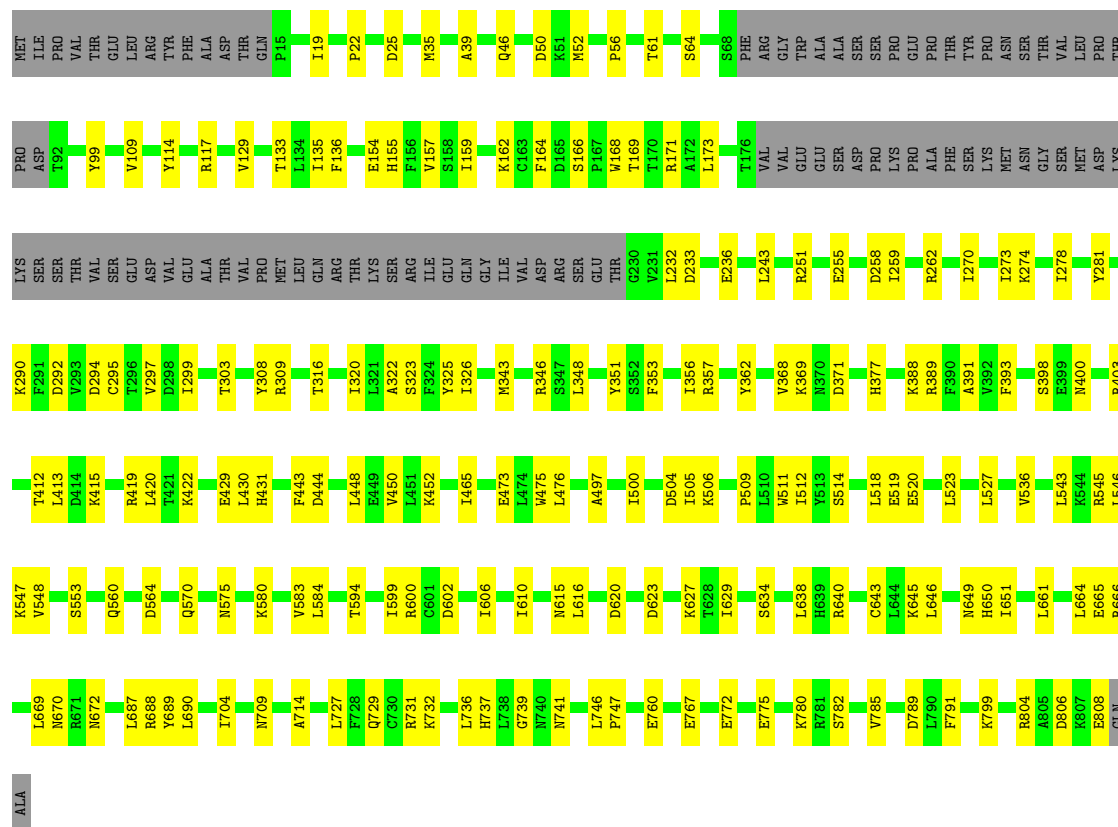
Chain D: 71% 20% 10%





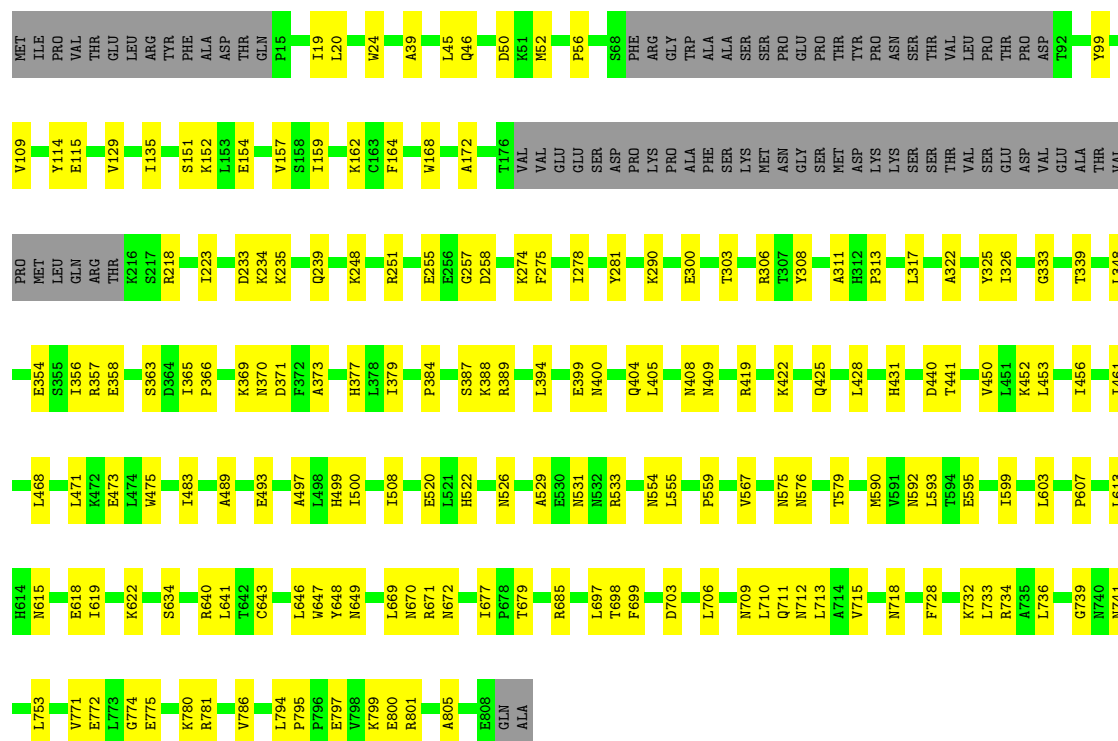
- Molecule 1: Volume-regulated anion channel subunit LRRC8A

Chain E: 66% 22% 11%



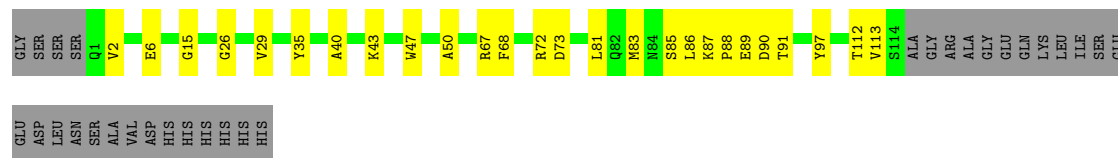
- Molecule 1: Volume-regulated anion channel subunit LRRC8A

Chain F: 69% 21% 10%



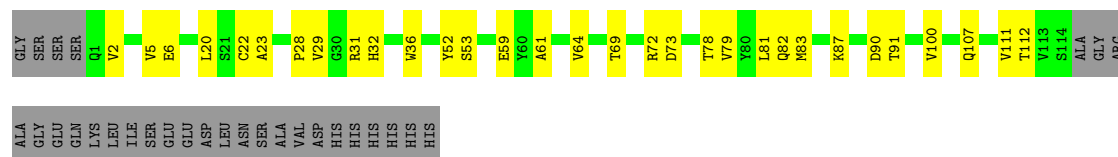
• Molecule 2: Synthetic nanobody Sb1

Chain G: 61% 18% 21%



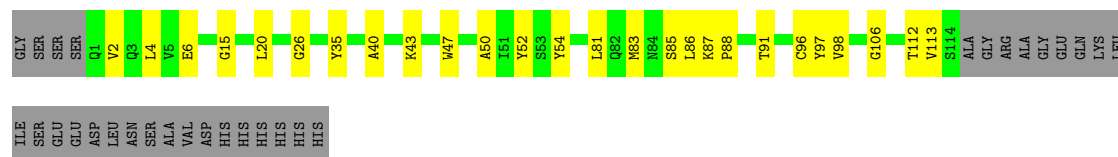
• Molecule 2: Synthetic nanobody Sb1

Chain H: 58% 22% 21%

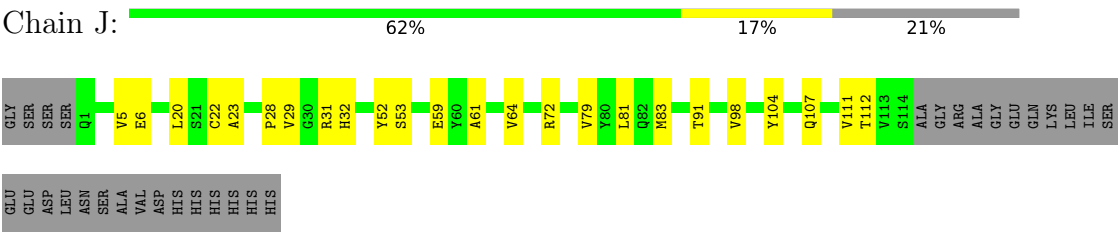


• Molecule 2: Synthetic nanobody Sb1

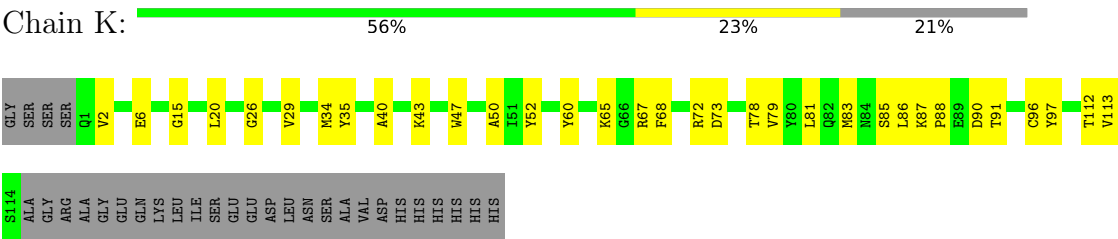
Chain I: 61% 18% 21%



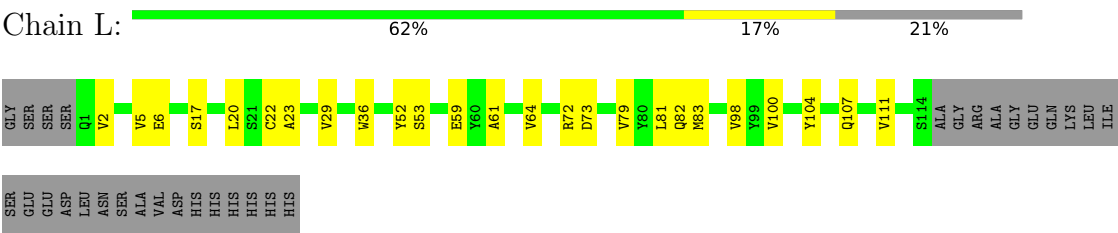
• Molecule 2: Synthetic nanobody Sb1



• Molecule 2: Synthetic nanobody Sb1



• Molecule 2: Synthetic nanobody Sb1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59962	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

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	0.17	0/6055	0.31	0/8207
1	B	0.17	0/6163	0.31	0/8352
1	C	0.17	0/6055	0.30	0/8207
1	D	0.17	0/6163	0.31	0/8352
1	E	0.17	0/6055	0.30	0/8207
1	F	0.17	0/6163	0.30	0/8352
2	G	0.09	0/927	0.24	0/1258
2	H	0.10	0/927	0.25	0/1258
2	I	0.08	0/927	0.23	0/1258
2	J	0.10	0/927	0.25	0/1258
2	K	0.08	0/927	0.23	0/1258
2	L	0.10	0/927	0.26	0/1258
All	All	0.16	0/42216	0.30	0/57225

There are no bond length outliers.

There are no bond angle outliers.

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	5922	0	6081	121	0
1	B	6030	0	6184	112	0
1	C	5922	0	6081	113	0
1	D	6030	0	6184	100	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	5922	0	6081	115	0
1	F	6030	0	6184	111	0
2	G	903	0	852	16	0
2	H	903	0	852	23	0
2	I	903	0	852	16	0
2	J	903	0	852	16	0
2	K	903	0	852	22	0
2	L	903	0	852	18	0
All	All	41274	0	41907	766	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 9.

The worst 5 of 766 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)
2:G:83:MET:HB3	2:G:86:LEU:HD21	1.62	0.81
1:E:634:SER:HG	2:K:52:TYR:HH	1.28	0.81
2:K:83:MET:HB3	2:K:86:LEU:HD21	1.61	0.80
1:C:35:MET:HE2	1:C:133:THR:HG22	1.70	0.74
1:C:351:TYR:HB3	1:C:368:VAL:HG23	1.69	0.73

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 PDB entries followed by that with respect to all EM entries.

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	473/810 (58%)	454 (96%)	19 (4%)	0	100	100
1	B	726/810 (90%)	699 (96%)	27 (4%)	0	100	100
1	C	712/810 (88%)	685 (96%)	27 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	726/810 (90%)	700 (96%)	26 (4%)	0	100	100
1	E	712/810 (88%)	687 (96%)	25 (4%)	0	100	100
1	F	726/810 (90%)	699 (96%)	27 (4%)	0	100	100
2	G	112/144 (78%)	111 (99%)	1 (1%)	0	100	100
2	H	112/144 (78%)	109 (97%)	3 (3%)	0	100	100
2	I	112/144 (78%)	109 (97%)	3 (3%)	0	100	100
2	J	112/144 (78%)	110 (98%)	2 (2%)	0	100	100
2	K	112/144 (78%)	109 (97%)	3 (3%)	0	100	100
2	L	112/144 (78%)	110 (98%)	2 (2%)	0	100	100
All	All	4747/5724 (83%)	4582 (96%)	165 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-13202. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.