



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 12:00 AM UTC

PDB ID : 8FQB / pdb_00008fqb
EMDB ID : EMD-29382
Title : GluA2 flip Q isoform of AMPA receptor in complex with gain-of-function TARP gamma2, with 10mM CaCl₂, 140mM NMDG, 330uM CTZ, and 100mM L-glutamate (Open-Ca10)
Authors : Nakagawa, T.
Deposited on : 2023-01-05
Resolution : 2.36 Å(reported)

This is a Full wwPDB EM 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/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

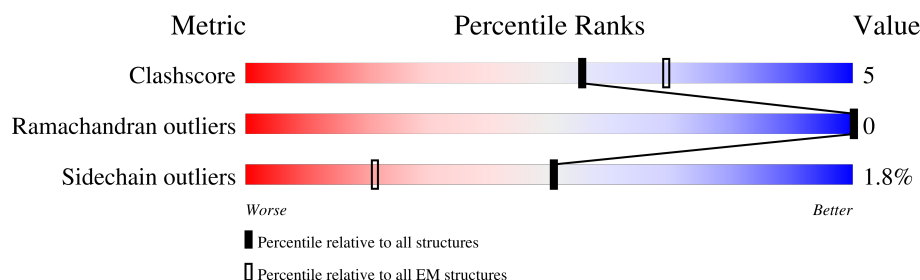
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.36 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
Sidechain outliers	223484	23102

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	889	14% . 83%
1	B	889	16% . 82%
1	C	889	15% . 83%
1	D	889	16% . 82%
2	E	336	46% 9% . 44%
2	F	336	51% 5% 43%
2	G	336	48% 8% . 44%
2	H	336	50% 6% 43%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10823 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 Glutamate receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	149	Total	C	N	O	S	2	0
			1177	783	183	204	7		
1	B	156	Total	C	N	O	S	0	0
			1227	815	193	211	8		
1	C	149	Total	C	N	O	S	2	0
			1177	783	183	204	7		
1	D	156	Total	C	N	O	S	0	0
			1227	815	193	211	8		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	848	ASP	-	insertion	UNP P19491
A	849	TYR	-	insertion	UNP P19491
A	850	LYS	-	insertion	UNP P19491
A	851	ASP	-	insertion	UNP P19491
A	852	ASP	-	insertion	UNP P19491
A	853	ASP	-	insertion	UNP P19491
A	854	ASP	TYR	conflict	UNP P19491
B	848	ASP	-	insertion	UNP P19491
B	849	TYR	-	insertion	UNP P19491
B	850	LYS	-	insertion	UNP P19491
B	851	ASP	-	insertion	UNP P19491
B	852	ASP	-	insertion	UNP P19491
B	853	ASP	-	insertion	UNP P19491
B	854	ASP	TYR	conflict	UNP P19491
C	848	ASP	-	insertion	UNP P19491
C	849	TYR	-	insertion	UNP P19491
C	850	LYS	-	insertion	UNP P19491
C	851	ASP	-	insertion	UNP P19491
C	852	ASP	-	insertion	UNP P19491
C	853	ASP	-	insertion	UNP P19491
C	854	ASP	TYR	conflict	UNP P19491
D	848	ASP	-	insertion	UNP P19491

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	849	TYR	-	insertion	UNP P19491
D	850	LYS	-	insertion	UNP P19491
D	851	ASP	-	insertion	UNP P19491
D	852	ASP	-	insertion	UNP P19491
D	853	ASP	-	insertion	UNP P19491
D	854	ASP	TYR	conflict	UNP P19491

- Molecule 2 is a protein called Voltage-dependent calcium channel gamma-2 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	188	Total	C	N	O	S	0	0
			1451	945	237	258	11		
2	G	188	Total	C	N	O	S	0	0
			1451	945	237	258	11		
2	F	190	Total	C	N	O	S	0	0
			1467	955	240	261	11		
2	H	190	Total	C	N	O	S	0	0
			1467	955	240	261	11		

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	52	GLU	LYS	engineered mutation	UNP O88602
E	53	GLU	LYS	engineered mutation	UNP O88602
E	324	GLY	-	expression tag	UNP O88602
E	325	GLY	-	expression tag	UNP O88602
E	326	ARG	-	expression tag	UNP O88602
E	327	GLY	-	expression tag	UNP O88602
E	328	GLY	-	expression tag	UNP O88602
E	329	THR	-	expression tag	UNP O88602
E	330	GLU	-	expression tag	UNP O88602
E	331	THR	-	expression tag	UNP O88602
E	332	SER	-	expression tag	UNP O88602
E	333	GLN	-	expression tag	UNP O88602
E	334	ALA	-	expression tag	UNP O88602
E	335	PRO	-	expression tag	UNP O88602
E	336	ALA	-	expression tag	UNP O88602
G	52	GLU	LYS	engineered mutation	UNP O88602
G	53	GLU	LYS	engineered mutation	UNP O88602
G	324	GLY	-	expression tag	UNP O88602
G	325	GLY	-	expression tag	UNP O88602
G	326	ARG	-	expression tag	UNP O88602

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	327	GLY	-	expression tag	UNP O88602
G	328	GLY	-	expression tag	UNP O88602
G	329	THR	-	expression tag	UNP O88602
G	330	GLU	-	expression tag	UNP O88602
G	331	THR	-	expression tag	UNP O88602
G	332	SER	-	expression tag	UNP O88602
G	333	GLN	-	expression tag	UNP O88602
G	334	ALA	-	expression tag	UNP O88602
G	335	PRO	-	expression tag	UNP O88602
G	336	ALA	-	expression tag	UNP O88602
F	52	GLU	LYS	engineered mutation	UNP O88602
F	53	GLU	LYS	engineered mutation	UNP O88602
F	324	GLY	-	expression tag	UNP O88602
F	325	GLY	-	expression tag	UNP O88602
F	326	ARG	-	expression tag	UNP O88602
F	327	GLY	-	expression tag	UNP O88602
F	328	GLY	-	expression tag	UNP O88602
F	329	THR	-	expression tag	UNP O88602
F	330	GLU	-	expression tag	UNP O88602
F	331	THR	-	expression tag	UNP O88602
F	332	SER	-	expression tag	UNP O88602
F	333	GLN	-	expression tag	UNP O88602
F	334	ALA	-	expression tag	UNP O88602
F	335	PRO	-	expression tag	UNP O88602
F	336	ALA	-	expression tag	UNP O88602
H	52	GLU	LYS	engineered mutation	UNP O88602
H	53	GLU	LYS	engineered mutation	UNP O88602
H	324	GLY	-	expression tag	UNP O88602
H	325	GLY	-	expression tag	UNP O88602
H	326	ARG	-	expression tag	UNP O88602
H	327	GLY	-	expression tag	UNP O88602
H	328	GLY	-	expression tag	UNP O88602
H	329	THR	-	expression tag	UNP O88602
H	330	GLU	-	expression tag	UNP O88602
H	331	THR	-	expression tag	UNP O88602
H	332	SER	-	expression tag	UNP O88602
H	333	GLN	-	expression tag	UNP O88602
H	334	ALA	-	expression tag	UNP O88602
H	335	PRO	-	expression tag	UNP O88602
H	336	ALA	-	expression tag	UNP O88602

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	C	1	Total 1	Ca 1	0

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	F	1	Total 1	Cl 1	0
4	H	1	Total 1	Cl 1	0

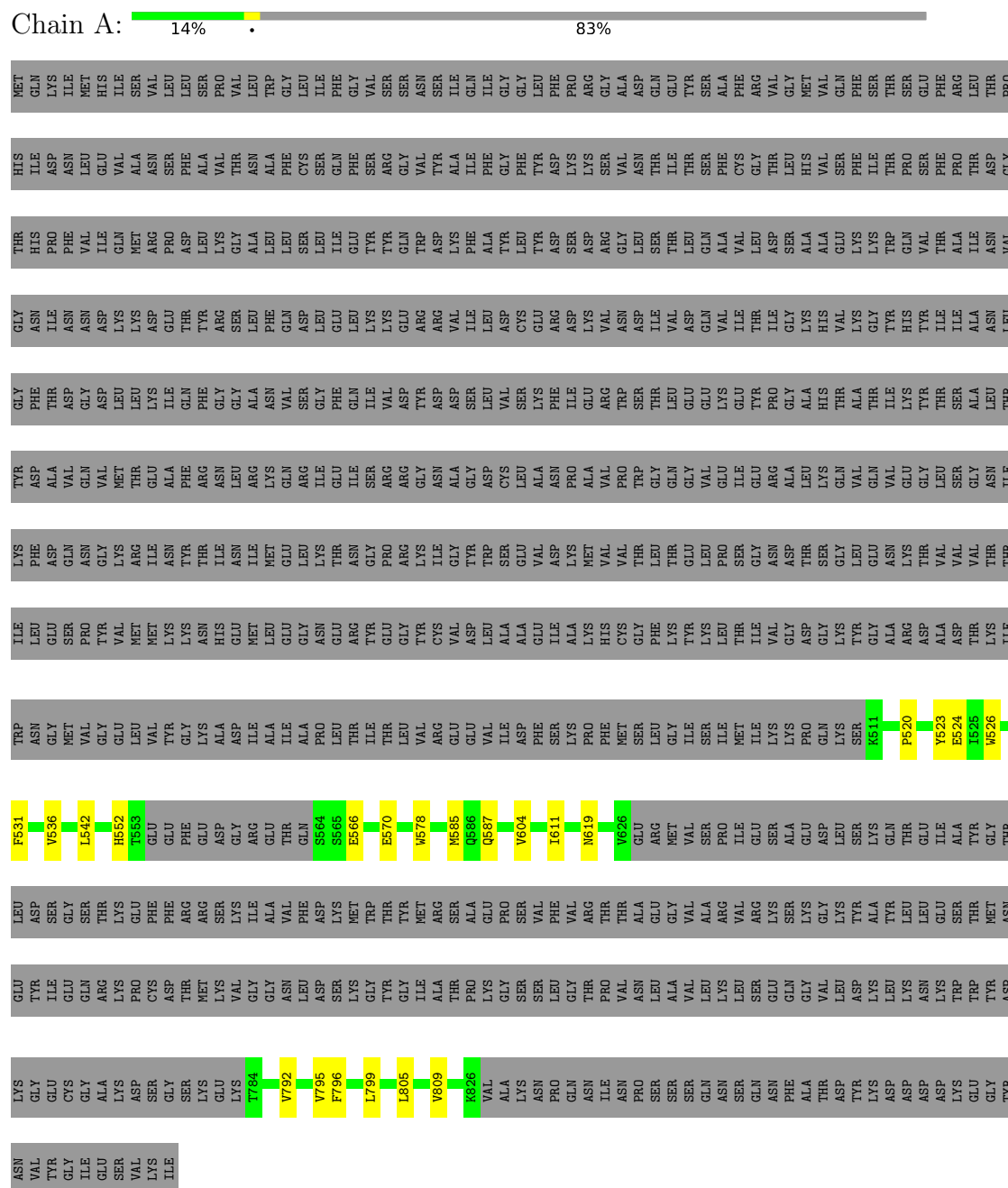
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		AltConf
5	A	30	Total 30	O 30	0
5	B	32	Total 32	O 32	0
5	C	29	Total 29	O 29	0
5	D	31	Total 31	O 31	0
5	E	14	Total 14	O 14	0
5	G	14	Total 14	O 14	0
5	F	13	Total 13	O 13	0
5	H	13	Total 13	O 13	0

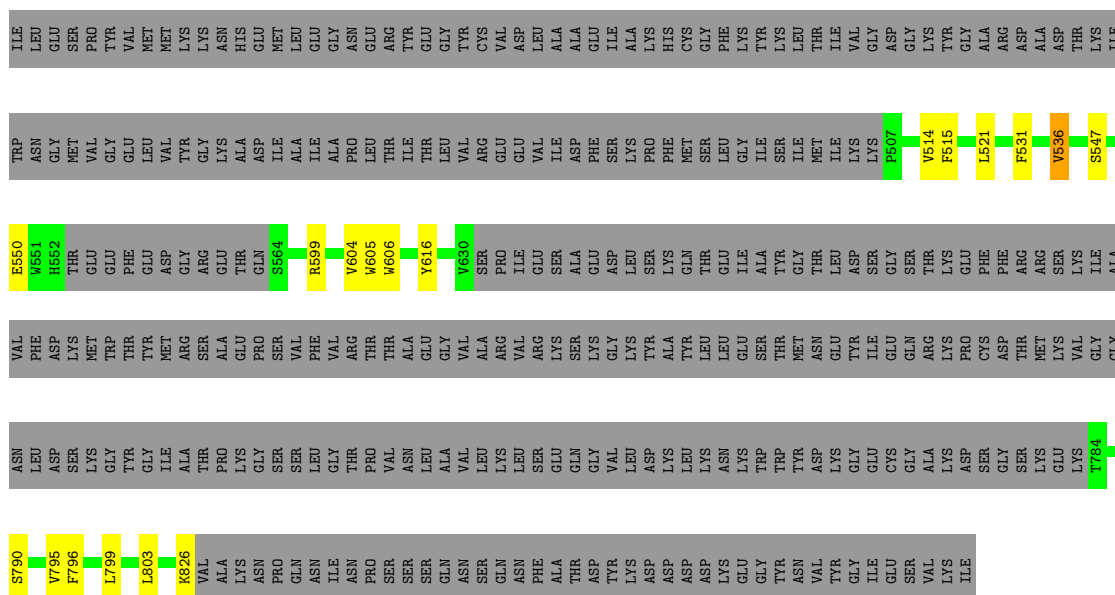
3 Residue-property plots

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. 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. 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.

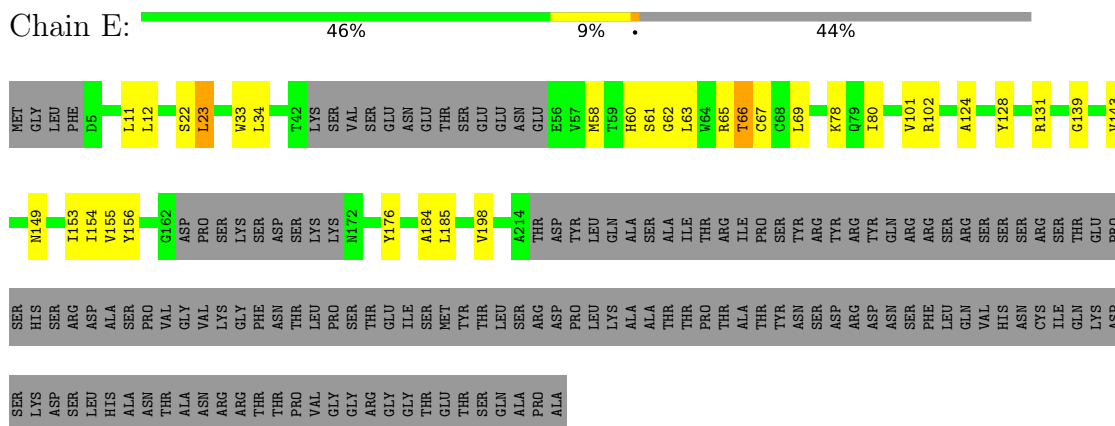
• Molecule 1: Glutamate receptor 2



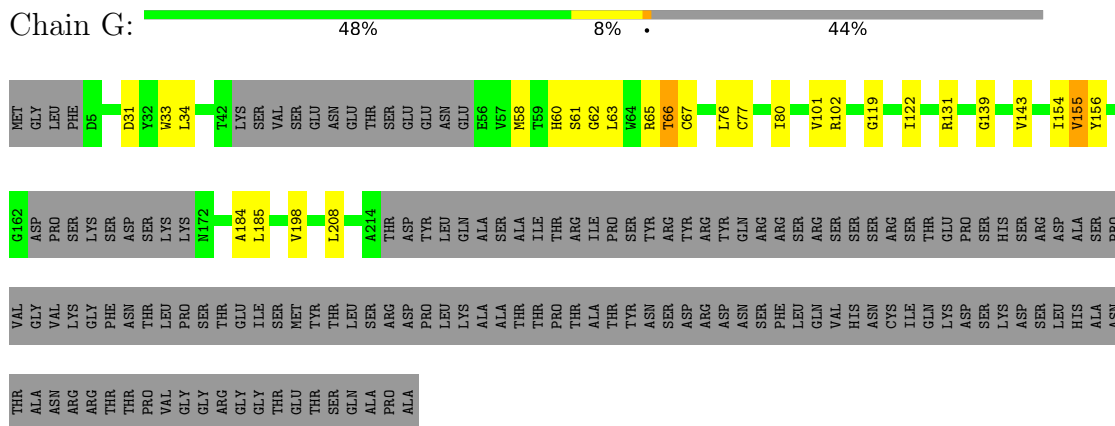




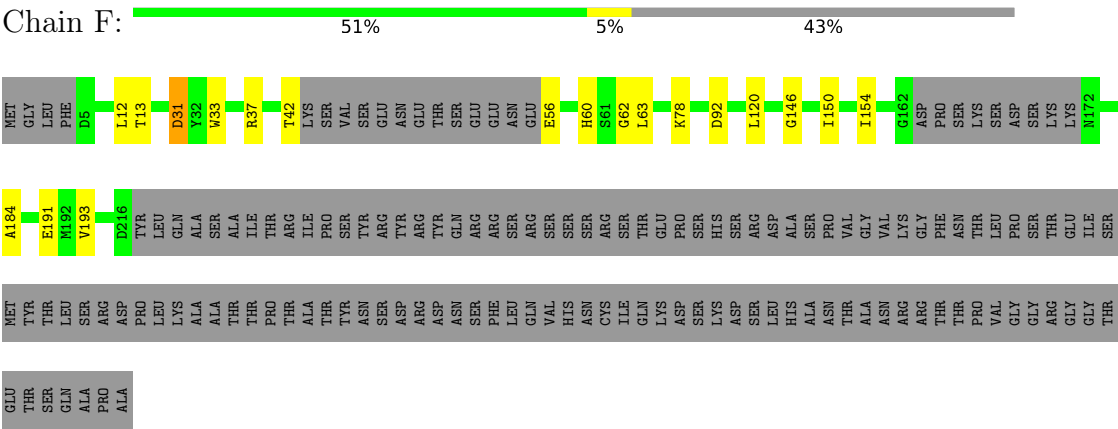
- Molecule 2: Voltage-dependent calcium channel gamma-2 subunit



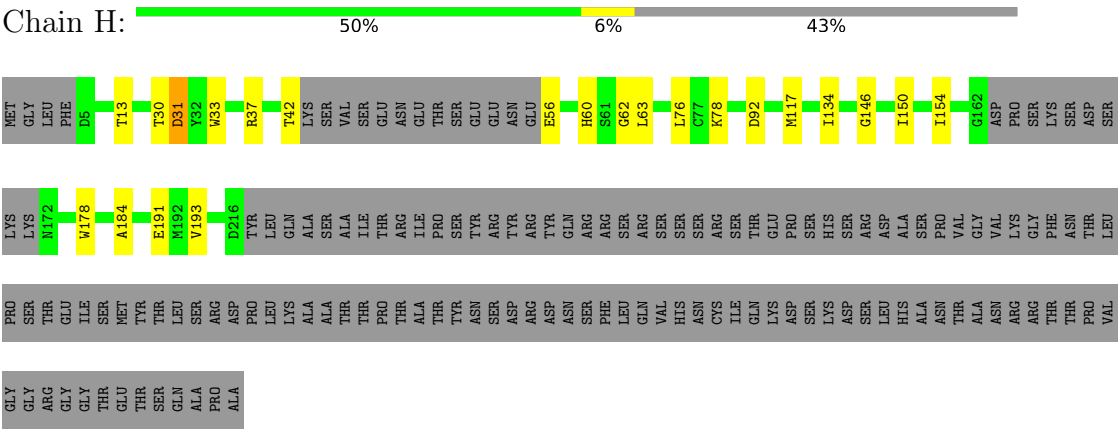
- Molecule 2: Voltage-dependent calcium channel gamma-2 subunit



- Molecule 2: Voltage-dependent calcium channel gamma-2 subunit



● Molecule 2: Voltage-dependent calcium channel gamma-2 subunit



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	986075	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.12	0/1209	0.25	0/1640
1	B	0.13	0/1260	0.29	0/1705
1	C	0.12	0/1209	0.26	0/1640
1	D	0.13	0/1260	0.28	0/1705
2	E	0.10	0/1484	0.25	0/2008
2	F	0.10	0/1500	0.23	0/2029
2	G	0.10	0/1484	0.24	0/2008
2	H	0.10	0/1500	0.23	0/2029
All	All	0.11	0/10906	0.25	0/14764

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	1177	0	1168	17	0
1	B	1227	0	1231	14	0
1	C	1177	0	1168	15	0
1	D	1227	0	1231	14	0
2	E	1451	0	1422	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1467	0	1442	12	0
2	G	1451	0	1422	19	0
2	H	1467	0	1442	15	0
3	C	1	0	0	0	0
4	F	1	0	0	1	0
4	H	1	0	0	1	0
5	A	30	0	0	0	0
5	B	32	0	0	0	0
5	C	29	0	0	0	0
5	D	31	0	0	0	0
5	E	14	0	0	2	0
5	F	13	0	0	0	0
5	G	14	0	0	2	0
5	H	13	0	0	0	0
All	All	10823	0	10526	105	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 5.

All (105) 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:E:102:ARG:NH2	5:E:401:HOH:O	2.23	0.71
1:A:520:PRO:HB3	1:A:619:ASN:HB3	1.73	0.69
1:A:542:LEU:HD12	2:E:198:VAL:HG21	1.75	0.68
1:C:520:PRO:HB3	1:C:619:ASN:HB3	1.75	0.68
2:E:33:TRP:HB2	2:E:62:GLY:HA2	1.78	0.66
1:C:542:LEU:HD12	2:G:198:VAL:HG21	1.78	0.65
2:G:102:ARG:NH2	5:G:402:HOH:O	2.27	0.65
2:F:33:TRP:HB2	2:F:62:GLY:HA2	1.80	0.64
1:C:611:ILE:HG21	1:D:795:VAL:HG11	1.80	0.64
2:H:33:TRP:HB2	2:H:62:GLY:HA2	1.80	0.64
1:C:805:LEU:O	1:C:809:VAL:HG23	1.98	0.63
2:G:33:TRP:HB2	2:G:62:GLY:HA2	1.79	0.63
1:A:805:LEU:O	1:A:809:VAL:HG23	1.98	0.62
1:A:611:ILE:HG21	1:B:795:VAL:HG11	1.81	0.61
1:B:547:SER:HB3	1:B:550:GLU:HG2	1.82	0.60
2:G:65:ARG:NH1	5:G:405:HOH:O	2.33	0.59
1:D:547:SER:HB3	1:D:550:GLU:HG2	1.83	0.59
1:C:585:MET:HA	1:C:585:MET:HE2	1.85	0.58
2:F:37:ARG:HB3	2:F:56:GLU:HG2	1.86	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:524:GLU:OE2	2:E:176:TYR:OH	2.14	0.58
1:A:587:GLN:HG3	1:D:606:TRP:CG	2.40	0.57
1:C:552:HIS:NE2	1:C:566:GLU:OE1	2.36	0.56
1:A:604:VAL:HG13	1:B:799:LEU:HD12	1.88	0.56
1:B:606:TRP:CG	1:C:587:GLN:HG3	2.40	0.56
2:H:37:ARG:HB3	2:H:56:GLU:HG2	1.87	0.55
1:B:604:VAL:HG13	1:C:799:LEU:HD12	1.89	0.55
1:A:585:MET:HE2	1:A:585:MET:HA	1.87	0.55
2:G:66:THR:HG22	2:G:80:ILE:HG12	1.89	0.55
1:D:826:LYS:HD2	1:D:826:LYS:C	2.33	0.54
1:B:826:LYS:HD2	1:B:826:LYS:C	2.33	0.54
1:C:604:VAL:HG13	1:D:799:LEU:HD12	1.88	0.54
1:A:799:LEU:HD12	1:D:604:VAL:HG13	1.89	0.53
2:G:63:LEU:O	2:G:102:ARG:NH2	2.42	0.51
2:H:31:ASP:HA	2:H:62:GLY:HA3	1.92	0.51
2:E:65:ARG:NH1	5:E:404:HOH:O	2.34	0.50
1:A:552:HIS:NE2	1:A:566:GLU:OE2	2.37	0.50
2:F:92:ASP:OD1	2:F:92:ASP:N	2.44	0.50
2:F:31:ASP:HA	2:F:62:GLY:HA3	1.93	0.50
1:D:531:PHE:HZ	2:H:184:ALA:HB1	1.77	0.49
1:B:531:PHE:HZ	2:F:184:ALA:HB1	1.77	0.49
2:G:76:LEU:HD12	2:G:77:CYS:N	2.27	0.49
2:E:149:ASN:O	2:E:153:ILE:HG23	2.13	0.48
2:E:63:LEU:O	2:E:102:ARG:NH2	2.46	0.48
1:A:531:PHE:HZ	2:E:184:ALA:HB1	1.78	0.47
1:D:514:VAL:HG13	1:D:515:PHE:CD1	2.49	0.47
2:G:139:GLY:O	2:G:143:VAL:HG13	2.14	0.47
1:A:587:GLN:HG3	1:D:606:TRP:CD1	2.50	0.47
2:E:139:GLY:O	2:E:143:VAL:HG13	2.15	0.47
2:E:33:TRP:N	2:E:61:SER:O	2.48	0.46
1:B:606:TRP:CD1	1:C:587:GLN:HG3	2.51	0.46
1:D:521:LEU:HG	1:D:616:TYR:HD1	1.80	0.46
2:E:185:LEU:HD23	2:E:185:LEU:HA	1.75	0.46
1:B:521:LEU:HG	1:B:616:TYR:HD1	1.80	0.46
2:E:124:ALA:O	2:E:128:TYR:N	2.48	0.46
2:G:31:ASP:HA	2:G:62:GLY:HA3	1.98	0.46
2:F:37:ARG:NH2	2:F:56:GLU:O	2.35	0.46
1:B:514:VAL:HG13	1:B:515:PHE:CD1	2.51	0.46
1:B:536:VAL:HG21	1:B:605:TRP:CE3	2.51	0.46
1:D:536:VAL:HG21	1:D:605:TRP:CE3	2.51	0.46
2:G:58:MET:SD	2:G:58:MET:N	2.89	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:131:ARG:HA	2:G:131:ARG:HD2	1.75	0.45
2:H:92:ASP:OD1	2:H:92:ASP:N	2.47	0.45
2:E:153:ILE:HG13	2:E:154:ILE:N	2.31	0.45
1:A:523:TYR:HA	1:A:526:TRP:HD1	1.81	0.45
2:E:101:VAL:HG12	2:E:155:VAL:HG11	1.98	0.45
2:G:33:TRP:N	2:G:61:SER:O	2.49	0.45
2:H:60:HIS:O	2:H:60:HIS:HD2	2.00	0.45
1:B:599:ARG:HG2	1:C:578:TRP:CE2	2.52	0.44
2:E:60:HIS:NE2	2:E:67:CYS:HB2	2.33	0.44
2:G:60:HIS:NE2	2:G:67:CYS:HB2	2.32	0.44
2:H:63:LEU:N	4:H:401:CL:CL	2.87	0.44
2:H:13:THR:HG23	2:H:193:VAL:HG13	1.99	0.44
2:F:13:THR:HG23	2:F:193:VAL:HG13	1.98	0.44
2:F:60:HIS:HD2	2:F:60:HIS:O	2.01	0.44
1:A:536:VAL:HG22	1:B:803:LEU:HD21	1.99	0.44
2:E:66:THR:HG22	2:E:80:ILE:HG12	2.00	0.44
1:C:536:VAL:HG22	1:D:803:LEU:HD21	1.99	0.43
2:G:119:GLY:O	2:G:122:ILE:HG22	2.18	0.43
2:H:146:GLY:HA3	2:H:191:GLU:OE1	2.18	0.43
2:H:76:LEU:HD12	2:H:76:LEU:HA	1.84	0.43
1:A:578:TRP:CE2	1:D:599:ARG:HG2	2.54	0.43
2:E:58:MET:N	2:E:58:MET:SD	2.92	0.42
2:E:60:HIS:HD2	2:E:69:LEU:HG	1.85	0.42
2:F:146:GLY:HA3	2:F:191:GLU:OE2	2.19	0.42
1:D:796:PHE:HB3	2:G:154:ILE:HD13	2.01	0.42
2:E:23:LEU:HD12	2:E:23:LEU:HA	1.80	0.42
1:C:531:PHE:HZ	2:G:184:ALA:HB1	1.84	0.42
1:C:792:VAL:O	1:C:795:VAL:HG12	2.20	0.42
2:G:101:VAL:HG12	2:G:155:VAL:HG11	2.02	0.42
2:F:63:LEU:N	4:F:401:CL:CL	2.90	0.42
1:B:796:PHE:HB3	2:E:154:ILE:HD13	2.02	0.42
2:H:134:ILE:H	2:H:134:ILE:HG12	1.67	0.42
2:E:131:ARG:HD2	2:E:131:ARG:HA	1.76	0.41
1:A:796:PHE:HB3	2:H:154:ILE:HD13	2.01	0.41
2:E:78:LYS:HB3	2:E:78:LYS:HE3	1.83	0.41
2:E:12:LEU:HD12	2:E:12:LEU:HA	1.80	0.41
1:C:796:PHE:HB3	2:F:154:ILE:HD13	2.02	0.41
2:G:185:LEU:HD23	2:G:185:LEU:HA	1.76	0.41
2:E:34:LEU:HB2	2:E:156:TYR:OH	2.21	0.41
2:G:34:LEU:HB2	2:G:156:TYR:OH	2.21	0.41
2:F:12:LEU:HD23	2:F:12:LEU:HA	1.92	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:30:THR:HG21	2:H:178:TRP:CH2	2.56	0.41
1:A:792:VAL:O	1:A:795:VAL:HG12	2.21	0.40
2:H:117:MET:HE2	2:H:117:MET:HB3	1.83	0.40
2:H:37:ARG:NH2	2:H:56:GLU:O	2.36	0.40

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	145/889 (16%)	144 (99%)	1 (1%)	0	100	100
1	B	150/889 (17%)	148 (99%)	2 (1%)	0	100	100
1	C	145/889 (16%)	143 (99%)	2 (1%)	0	100	100
1	D	150/889 (17%)	148 (99%)	2 (1%)	0	100	100
2	E	182/336 (54%)	179 (98%)	3 (2%)	0	100	100
2	F	184/336 (55%)	178 (97%)	6 (3%)	0	100	100
2	G	182/336 (54%)	180 (99%)	2 (1%)	0	100	100
2	H	184/336 (55%)	177 (96%)	7 (4%)	0	100	100
All	All	1322/4900 (27%)	1297 (98%)	25 (2%)	0	100	100

There are no Ramachandran outliers to report.

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

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	126/763 (16%)	125 (99%)	1 (1%)	73	84
1	B	132/763 (17%)	131 (99%)	1 (1%)	73	84
1	C	126/763 (16%)	126 (100%)	0	100	100
1	D	132/763 (17%)	130 (98%)	2 (2%)	57	72
2	E	149/282 (53%)	145 (97%)	4 (3%)	39	52
2	F	151/282 (54%)	146 (97%)	5 (3%)	33	44
2	G	149/282 (53%)	146 (98%)	3 (2%)	48	63
2	H	151/282 (54%)	147 (97%)	4 (3%)	40	54
All	All	1116/4180 (27%)	1096 (98%)	20 (2%)	51	66

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	570	GLU
1	B	790	SER
1	D	536	VAL
1	D	790	SER
2	E	11	LEU
2	E	22	SER
2	E	23	LEU
2	E	66	THR
2	G	66	THR
2	G	155	VAL
2	G	208	LEU
2	F	31	ASP
2	F	42	THR
2	F	78	LYS
2	F	120	LEU
2	F	150	ILE
2	H	31	ASP
2	H	42	THR
2	H	78	LYS
2	H	150	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	791	ASN
1	B	619	ASN
1	B	791	ASN
1	C	791	ASN
1	D	619	ASN
1	D	791	ASN
2	E	82	HIS
2	E	132	HIS
2	G	82	HIS
2	G	132	HIS
2	G	149	ASN
2	F	9	GLN
2	H	9	GLN
2	H	82	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](#)

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 [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-29382. 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.