



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 05:38 AM GMT

PDB ID : 3UQ7
Title : X-ray structure of a pentameric ligand gated ion channel from *Erwinia chrysanthemi* (ELIC) mutant L240S F247L (L9S F16L) in presence of 10 mM cysteamine
Authors : Gonzalez-Gutierrez, G.; Lukk, T.; Agarwal, V.; Papke, D.; Nair, S.K.; Grosman, C.
Deposited on : 2011-11-19
Resolution : 3.80 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

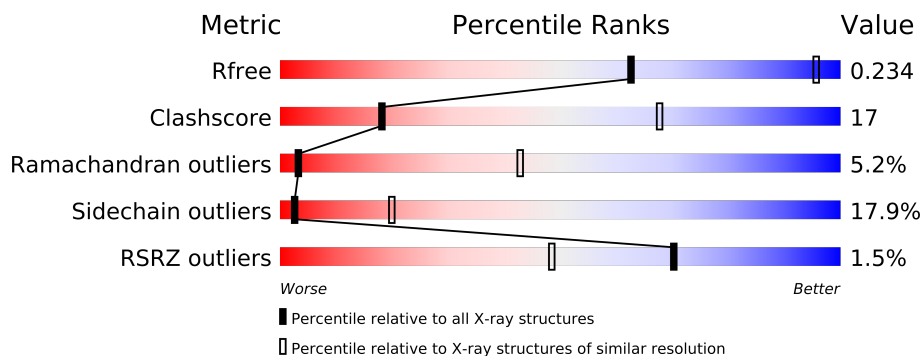
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.80 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}	66092	1162 (4.20-3.40)
Clashscore	79885	1100 (4.10-3.50)
Ramachandran outliers	78287	1050 (4.10-3.50)
Sidechain outliers	78261	1042 (4.10-3.50)
RSRZ outliers	66119	1163 (4.20-3.40)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	324	
1	B	324	
1	C	324	
1	D	324	
1	E	324	
1	F	324	
1	G	324	
1	H	324	
1	I	324	
1	J	324	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25000 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Gamma-aminobutyric-acidreceptor subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	B	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	C	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	D	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	E	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	F	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	G	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	H	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	I	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			
1	J	307	Total	C	N	O	S	0	0	0
			2500	1627	416	451	6			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
A	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
A	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
A	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
B	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
B	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
B	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
B	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
C	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4

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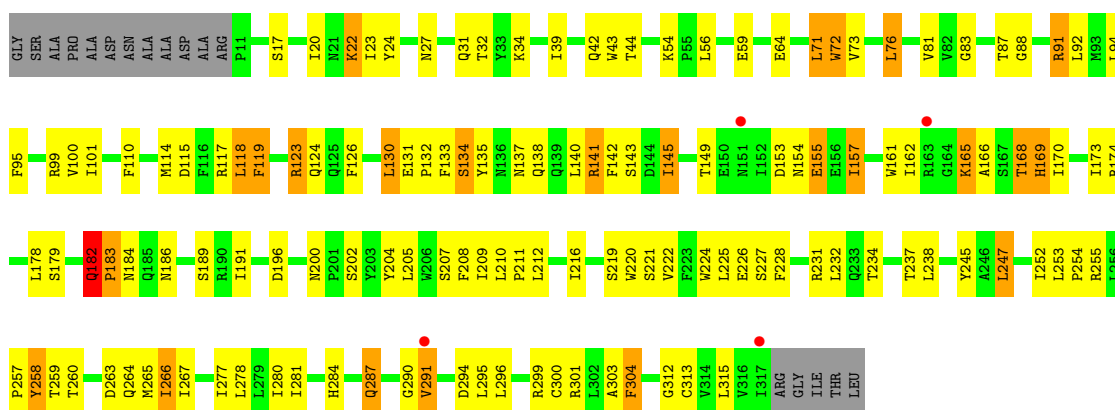
Chain	Residue	Modelled	Actual	Comment	Reference
C	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
C	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
C	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
D	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
D	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
D	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
D	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
E	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
E	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
E	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
E	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
F	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
F	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
F	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
F	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
G	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
G	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
G	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
G	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
H	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
H	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
H	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
H	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
I	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
I	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
I	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
I	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
J	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
J	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
J	240	SER	LEU	ENGINEERED MUTATION	UNP E0SJQ4
J	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

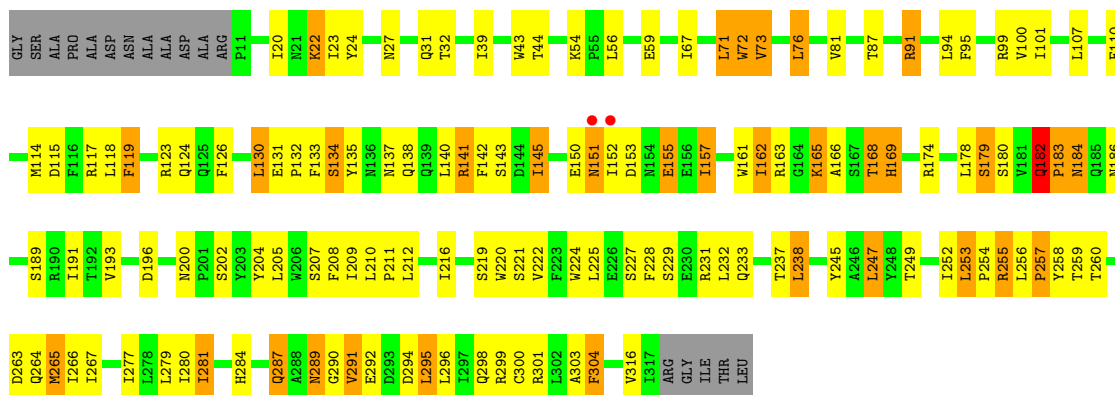
• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

Chain A:



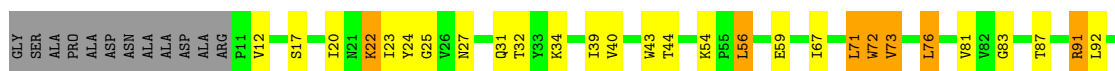
• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

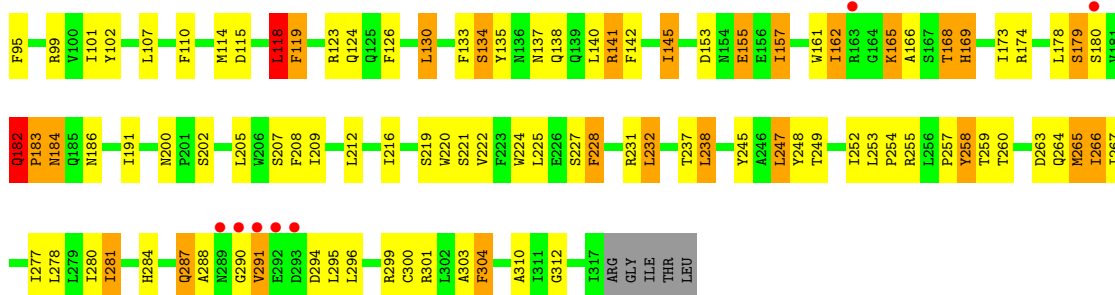
Chain B:



• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

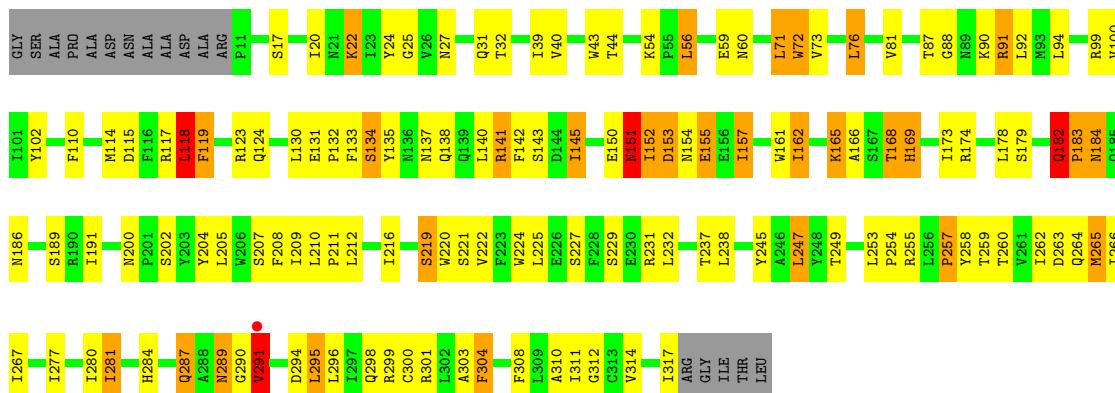
Chain C:





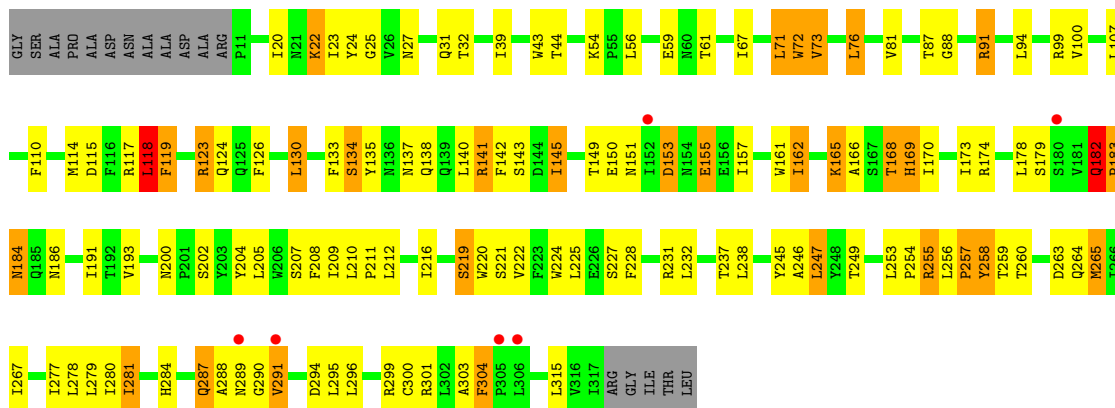
• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

Chain D:



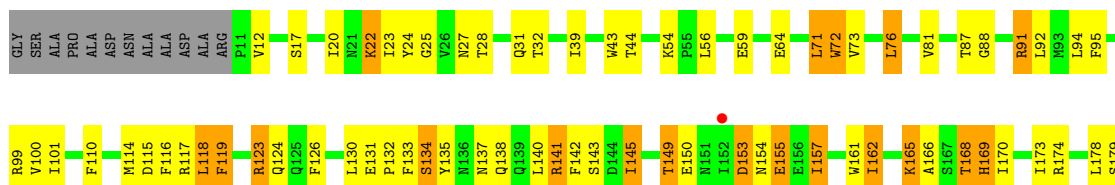
• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

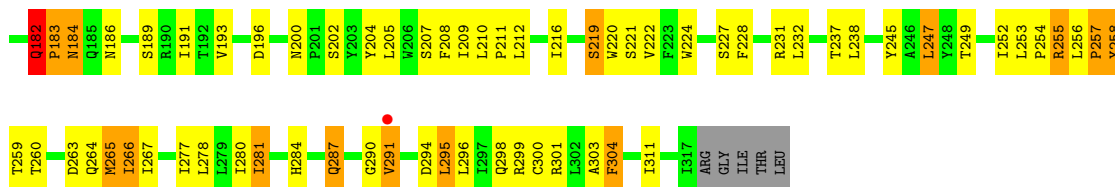
Chain E:



• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

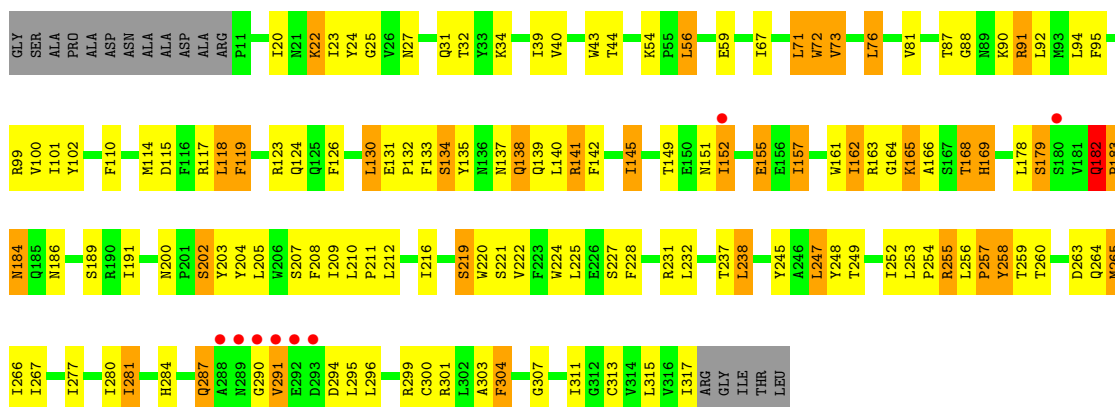
Chain F:





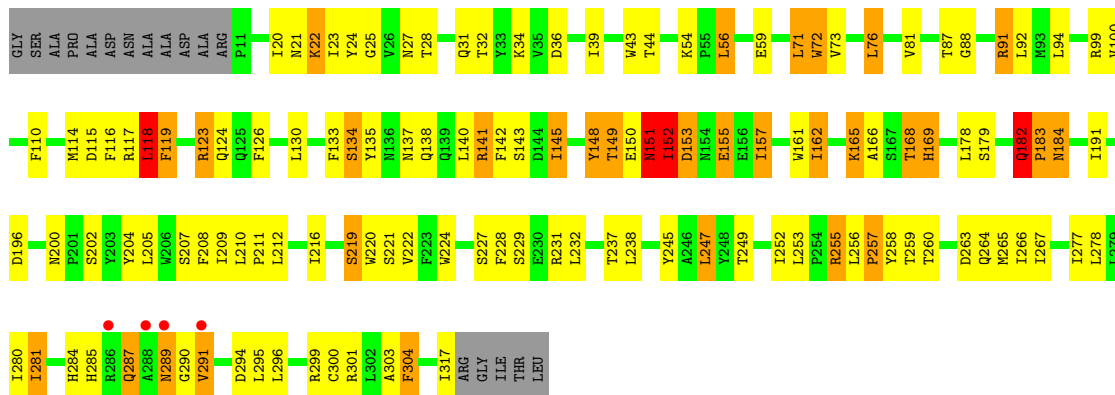
• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

Chain G:



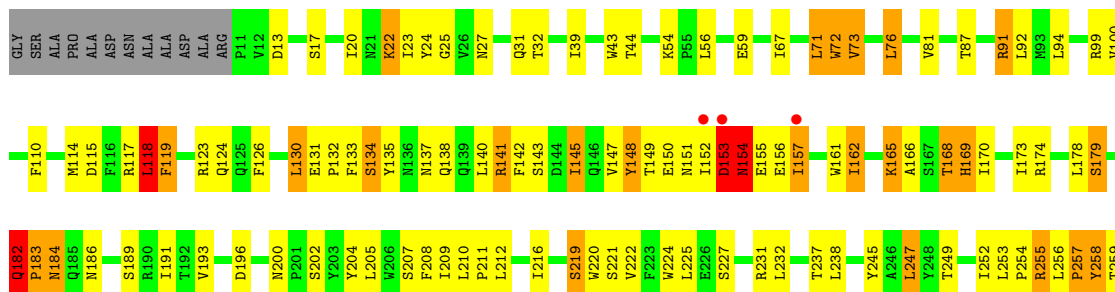
• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

Chain H:



• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

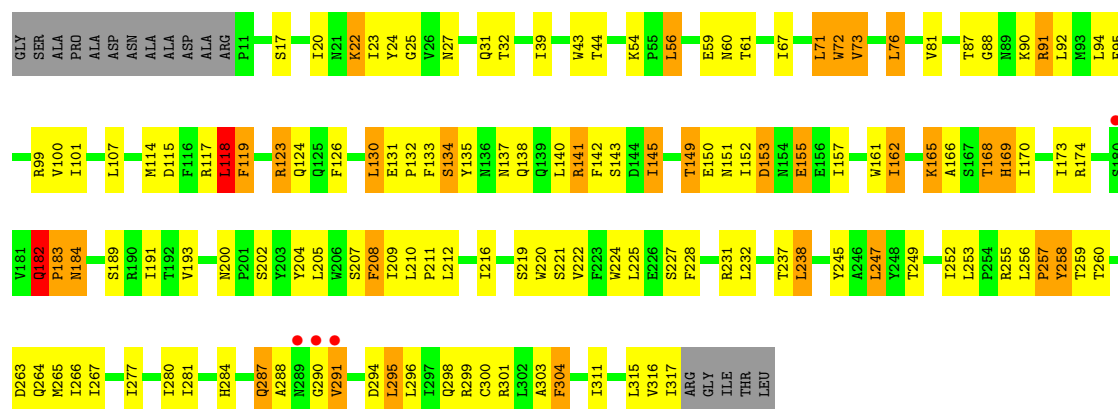
Chain I:





• Molecule 1: Gamma-aminobutyric-acidreceptor subunit beta-1

Chain J: Chain J:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.38Å 266.45Å 110.91Å 90.00° 109.47° 90.00°	Depositor
Resolution (Å)	19.97 – 3.80 19.97 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.97-3.80) 99.9 (19.97-3.80)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.29 (at 3.82Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_897)	Depositor
R, R_{free}	0.215 , 0.244 0.204 , 0.234	Depositor DCC
R_{free} test set	2808 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	110.2	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 62.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	1 of 56196 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	25000	wwPDB-VP
Average B, all atoms (Å ²)	127.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.58	0/2567	0.74	0/3499
1	B	0.60	0/2567	0.77	0/3499
1	C	0.60	0/2567	0.77	0/3499
1	D	0.63	1/2567 (0.0%)	0.77	0/3499
1	E	0.60	0/2567	0.75	0/3499
1	F	0.58	0/2567	0.73	0/3499
1	G	0.63	0/2567	0.79	1/3499 (0.0%)
1	H	0.69	4/2567 (0.2%)	0.83	6/3499 (0.2%)
1	I	0.62	0/2567	0.82	2/3499 (0.1%)
1	J	0.60	0/2567	0.75	1/3499 (0.0%)
All	All	0.62	5/25670 (0.0%)	0.77	10/34990 (0.0%)

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	B	0	2
1	C	0	2
1	D	0	3
1	E	0	2
1	F	0	1
1	G	0	2
1	H	0	3
1	I	0	3
1	J	0	3
All	All	0	23

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	152	ILE	CA-C	6.79	1.70	1.52
1	H	152	ILE	N-CA	6.50	1.59	1.46
1	H	151	ASN	CA-C	5.71	1.67	1.52
1	H	151	ASN	N-CA	5.37	1.57	1.46
1	D	291	VAL	CB-CG2	-5.01	1.42	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	154	ASN	N-CA-C	-12.04	78.50	111.00
1	I	153	ASP	CB-CA-C	11.31	133.02	110.40
1	H	148	TYR	C-N-CA	-7.20	103.69	121.70
1	H	153	ASP	CB-CG-OD2	-7.11	111.90	118.30
1	H	153	ASP	CB-CG-OD1	7.05	124.64	118.30

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	LEU	Peptide
1	A	137	ASN	Peptide
1	B	137	ASN	Peptide
1	B	152	ILE	Peptide
1	C	118	LEU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2500	0	2474	85	0
1	B	2500	0	2474	104	0
1	C	2500	0	2474	89	0
1	D	2500	0	2474	95	0
1	E	2500	0	2474	87	0
1	F	2500	0	2474	89	0
1	G	2500	0	2474	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	2500	0	2474	94	0
1	I	2500	0	2474	115	0
1	J	2500	0	2474	79	0
All	All	25000	0	24740	844	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 17.

The worst 5 of 844 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:289:ASN:ND2	1:B:292:GLU:OE2	1.86	1.07
1:I:154:ASN:HD22	1:I:155:GLU:N	1.52	1.06
1:I:154:ASN:HD22	1:I:155:GLU:H	1.08	1.00
1:H:151:ASN:N	1:H:153:ASP:OD2	1.94	0.99
1:H:152:ILE:N	1:H:153:ASP:OD1	1.99	0.95

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	305/324 (94%)	252 (83%)	41 (13%)	12 (4%)	5	52
1	B	305/324 (94%)	249 (82%)	40 (13%)	16 (5%)	3	43
1	C	305/324 (94%)	247 (81%)	45 (15%)	13 (4%)	4	49
1	D	305/324 (94%)	254 (83%)	34 (11%)	17 (6%)	3	41
1	E	305/324 (94%)	249 (82%)	39 (13%)	17 (6%)	3	41
1	F	305/324 (94%)	253 (83%)	37 (12%)	15 (5%)	3	45
1	G	305/324 (94%)	250 (82%)	40 (13%)	15 (5%)	3	45
1	H	305/324 (94%)	253 (83%)	33 (11%)	19 (6%)	2	38
1	I	305/324 (94%)	254 (83%)	34 (11%)	17 (6%)	3	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	305/324 (94%)	247 (81%)	39 (13%)	19 (6%)	2	38
All	All	3050/3240 (94%)	2508 (82%)	382 (12%)	160 (5%)	3	43

5 of 160 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	PHE
1	A	169	HIS
1	A	182	GLN
1	A	202	SER
1	B	119	PHE

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	275/285 (96%)	226 (82%)	49 (18%)	2	20
1	B	275/285 (96%)	226 (82%)	49 (18%)	2	20
1	C	275/285 (96%)	225 (82%)	50 (18%)	2	19
1	D	275/285 (96%)	224 (82%)	51 (18%)	2	18
1	E	275/285 (96%)	227 (82%)	48 (18%)	3	21
1	F	275/285 (96%)	223 (81%)	52 (19%)	2	17
1	G	275/285 (96%)	224 (82%)	51 (18%)	2	18
1	H	275/285 (96%)	229 (83%)	46 (17%)	3	24
1	I	275/285 (96%)	228 (83%)	47 (17%)	3	23
1	J	275/285 (96%)	226 (82%)	49 (18%)	2	20
All	All	2750/2850 (96%)	2258 (82%)	492 (18%)	2	20

5 of 492 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	162	ILE
1	F	168	THR

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Mol	Chain	Res	Type
1	J	81	VAL
1	E	219	SER
1	F	20	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	124	GLN
1	G	124	GLN
1	I	124	GLN
1	E	124	GLN
1	H	284	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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, 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	307/324 (94%)	-0.13	4 (1%) 74 52	79, 119, 201, 239	0
1	B	307/324 (94%)	-0.14	2 (0%) 84 67	80, 117, 208, 254	0
1	C	307/324 (94%)	-0.05	7 (2%) 57 38	77, 118, 206, 237	0
1	D	307/324 (94%)	-0.10	1 (0%) 91 83	77, 116, 200, 260	0
1	E	307/324 (94%)	-0.11	6 (1%) 62 41	78, 119, 212, 260	0
1	F	307/324 (94%)	-0.14	2 (0%) 84 67	78, 119, 199, 236	0
1	G	307/324 (94%)	-0.12	8 (2%) 53 35	76, 116, 195, 238	0
1	H	307/324 (94%)	-0.17	4 (1%) 74 52	80, 118, 208, 239	0
1	I	307/324 (94%)	-0.09	8 (2%) 53 35	78, 118, 206, 255	0
1	J	307/324 (94%)	-0.14	4 (1%) 74 52	77, 119, 199, 238	0
All	All	3070/3240 (94%)	-0.12	46 (1%) 70 48	76, 118, 207, 260	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	291	VAL	4.8
1	C	292	GLU	4.1
1	G	289	ASN	4.1
1	C	289	ASN	3.9
1	C	180	SER	3.9

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.