



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:03 AM UTC

PDB ID : 7TE6 / pdb_00007te6
Title : Crystal structure of GluN1b-2B ATD complexed to Fab5 anti-GluN2B antibody
Authors : Regan, M.; Tajima, N.; Furukawa, H.
Deposited on : 2022-01-04
Resolution : 4.55 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
Xtrriage (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

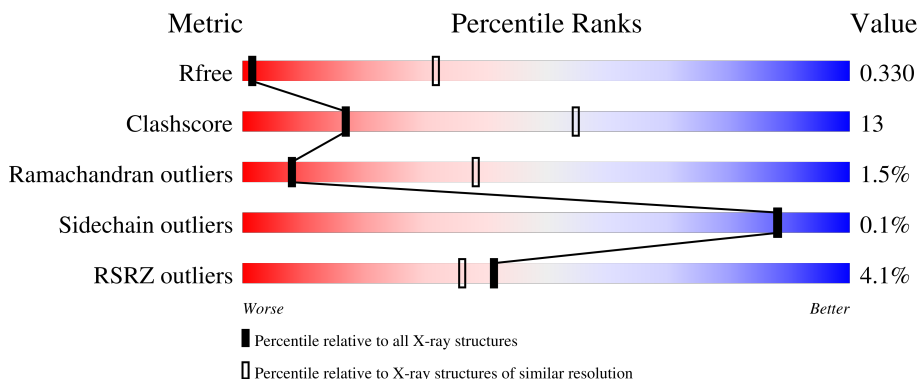
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.55 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.



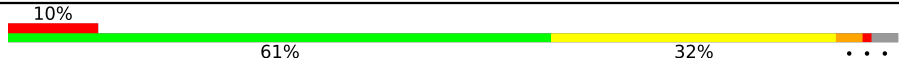

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1000 (5.20-3.92)
Clashscore	190562	1009 (5.14-3.94)
Ramachandran outliers	187476	1067 (5.22-3.90)
Sidechain outliers	187428	1049 (5.22-3.90)
RSRZ outliers	180081	1136 (5.22-3.90)

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	383	 % 69% 20% • 10%
1	E	383	 5% 68% 21% • 10%
2	B	364	 2% 68% 21% • 10%
2	F	364	 5% 64% 23% •• 10%
3	C	221	 3% 67% 27% •••

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Mol	Chain	Length	Quality of chain
3	G	221	
4	D	215	
4	H	215	

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 17193 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 Glutamate receptor ionotropic, NMDA 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	346	2714	1729	472	502	11	0	0	0
1	E	345	2706	1725	470	500	11	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	GLN	ASN	conflict	UNP A0A1L8F5J9
A	371	GLN	ASN	conflict	UNP A0A1L8F5J9
E	61	GLN	ASN	conflict	UNP A0A1L8F5J9
E	371	GLN	ASN	conflict	UNP A0A1L8F5J9

- Molecule 2 is a protein called Glutamate receptor ionotropic, NMDA 2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	329	2584	1653	407	510	14	0	0	0
2	F	327	2571	1645	404	508	14	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	348	ASP	ASN	conflict	UNP Q00960
F	348	ASP	ASN	conflict	UNP Q00960

- Molecule 3 is a protein called Fab5 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	215	1633	1030	269	325	9	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	G	214	Total 1629	C 1028	N 268	O 324	S 9	0	0	0

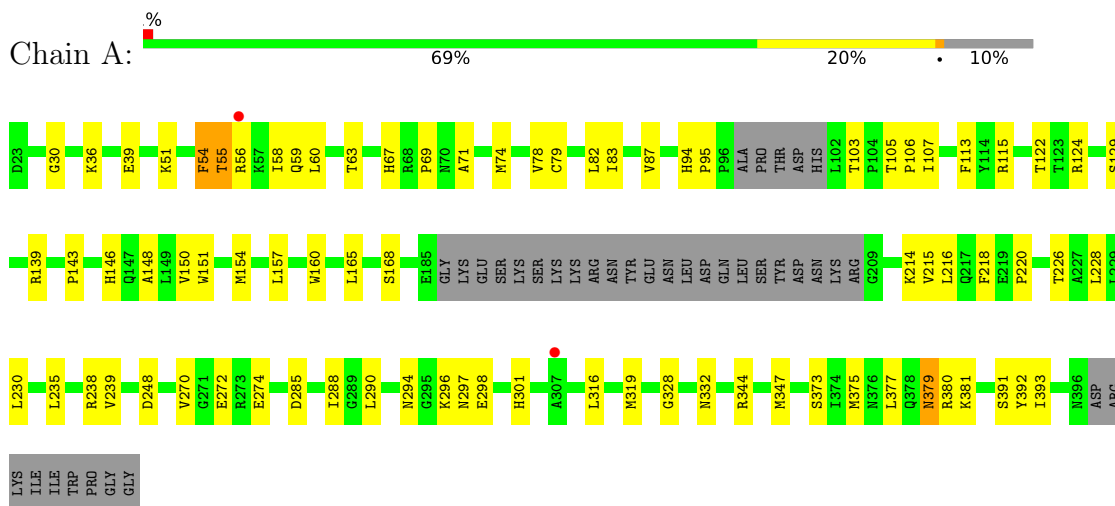
- Molecule 4 is a protein called Fab5 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	215	Total 1678	C 1046	N 287	O 339	S 6	0	0	0
4	H	215	Total 1678	C 1046	N 287	O 339	S 6	0	0	0

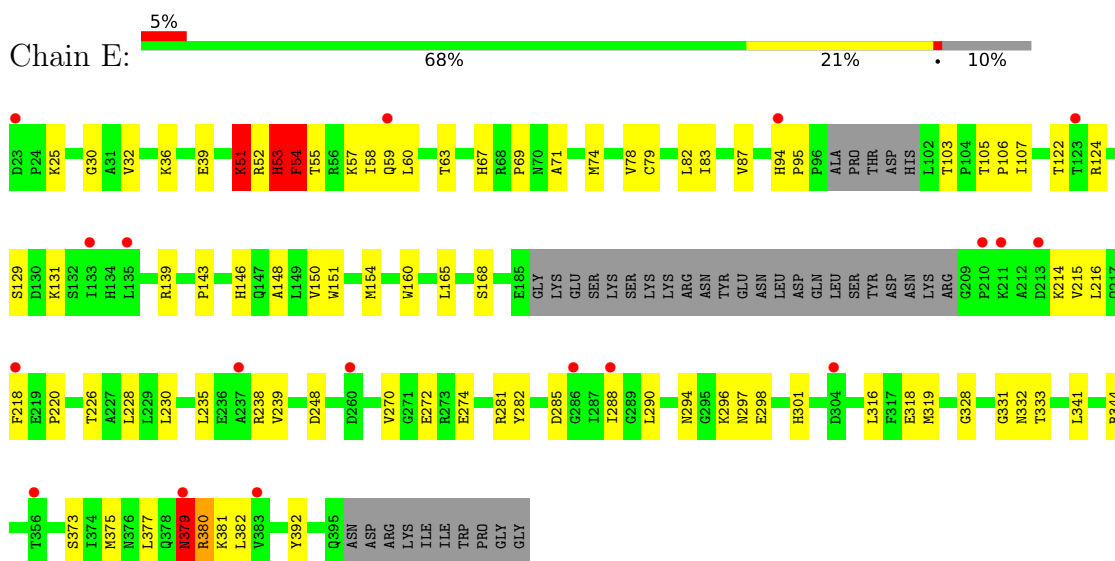
3 Residue-property plots [i](#)

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: Glutamate receptor ionotropic, NMDA 1

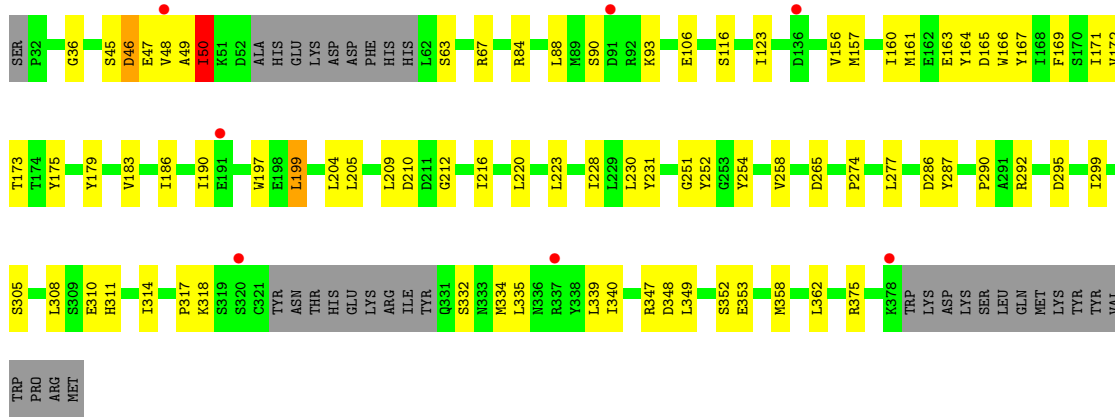


- Molecule 1: Glutamate receptor ionotropic, NMDA 1

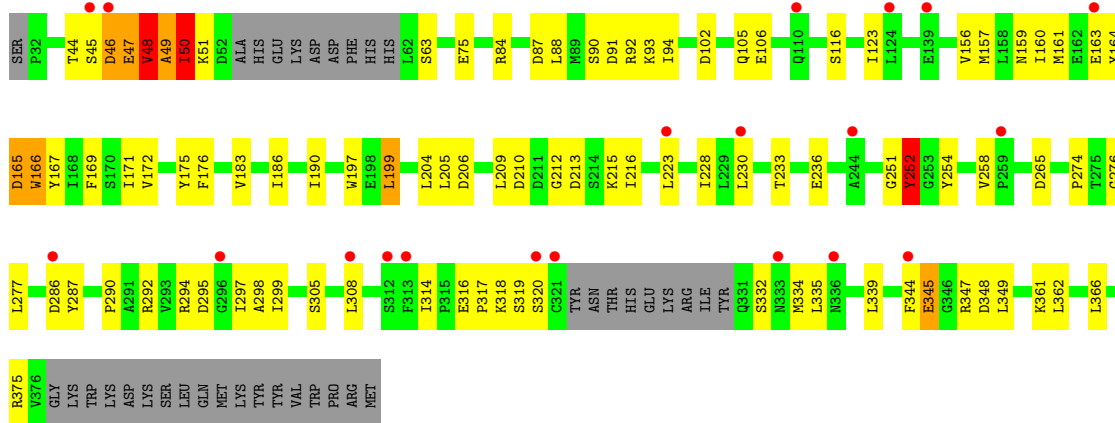


- Molecule 2: Glutamate receptor ionotropic, NMDA 2B

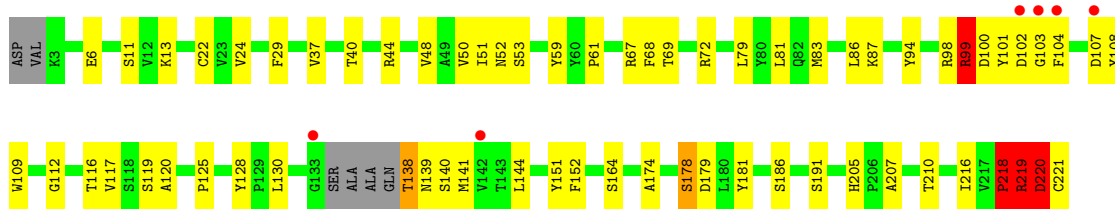




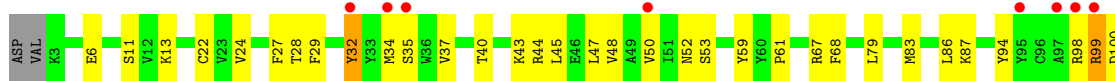
● Molecule 2: Glutamate receptor ionotropic, NMDA 2B

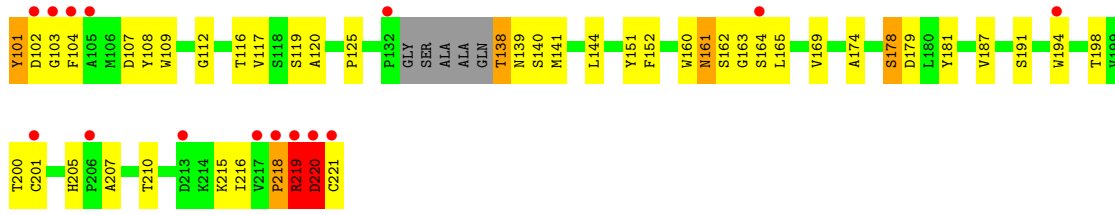


● Molecule 3: Fab5 heavy chain

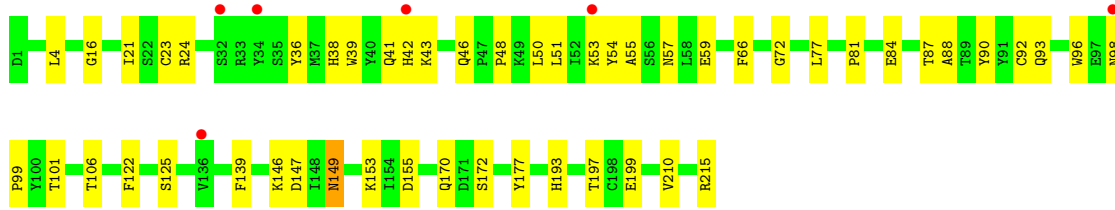
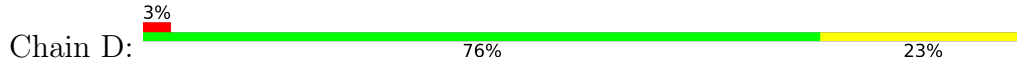


● Molecule 3: Fab5 heavy chain

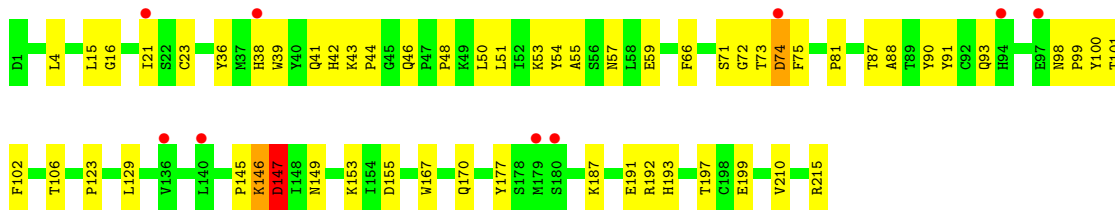
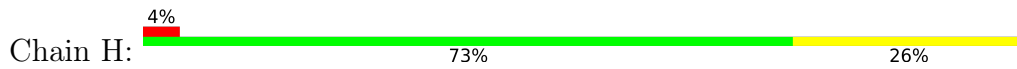




• Molecule 4: Fab5 light chain



• Molecule 4: Fab5 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	124.92Å 124.92Å 407.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.98 – 4.55 24.98 – 4.55	Depositor EDS
% Data completeness (in resolution range)	93.3 (24.98-4.55) 92.6 (24.98-4.55)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 4.62Å)	Xtrriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.282 , 0.324 0.285 , 0.330	Depositor DCC
R_{free} test set	920 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	76.6	Xtrriage
Anisotropy	0.154	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 25.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.81	EDS
Total number of atoms	17193	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.49% 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 [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	0.29	1/2768 (0.0%)	0.58	4/3751 (0.1%)
1	E	0.34	0/2760	0.72	10/3740 (0.3%)
2	B	0.25	0/2635	0.68	7/3576 (0.2%)
2	F	0.35	0/2622	0.77	12/3560 (0.3%)
3	C	0.36	0/1672	0.76	6/2280 (0.3%)
3	G	0.41	1/1668 (0.1%)	0.81	8/2275 (0.4%)
4	D	0.33	1/1721 (0.1%)	0.65	2/2340 (0.1%)
4	H	0.34	1/1721 (0.1%)	0.70	4/2340 (0.2%)
All	All	0.33	4/17567 (0.0%)	0.70	53/23862 (0.2%)

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	E	0	4
2	B	0	3
2	F	0	3
3	C	0	5
3	G	0	5
4	H	0	2
All	All	0	24

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	194	TRP	CB-CG	7.73	1.74	1.50
4	H	149	ASN	CA-CB	5.74	1.64	1.53
4	D	149	ASN	CA-CB	5.71	1.64	1.53
1	A	379	ASN	CB-CG	-5.00	1.39	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	51	LYS	CA-C-N	-9.91	107.77	121.84
1	E	51	LYS	C-N-CA	-9.91	107.77	121.84
2	B	48	VAL	CA-C-N	-9.83	106.81	122.24
2	B	48	VAL	C-N-CA	-9.83	106.81	122.24
2	F	47	GLU	CA-C-N	9.49	139.05	121.97

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	51	LYS	Mainchain
1	A	54	PHE	Mainchain
2	B	252	TYR	Peptide
2	B	46	ASP	Mainchain
2	B	50	ILE	Mainchain

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	2714	0	2744	52	1
1	E	2706	0	2738	59	1
2	B	2584	0	2551	55	0
2	F	2571	0	2535	79	2
3	C	1633	0	1595	52	0
3	G	1629	0	1592	91	0
4	D	1678	0	1600	37	0
4	H	1678	0	1600	47	0
All	All	17193	0	16955	435	2

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 13.

The worst 5 of 435 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)
3:G:161:ASN:HD22	3:G:165:LEU:HD12	1.27	0.97
3:G:198:THR:HG21	3:G:215:LYS:HE3	1.46	0.97
1:E:381:LYS:HG2	1:E:382:LEU:H	1.29	0.96
3:G:219:ARG:H	3:G:220:ASP:HA	1.36	0.90
2:F:46:ASP:C	2:F:48:VAL:H	1.81	0.84

All (2) 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)
1:A:36:LYS:NZ	2:F:102:ASP:O[7_455]	2.19	0.01
1:E:51:LYS:NZ	2:F:276:GLY:O[6_564]	2.19	0.01

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	340/383 (89%)	324 (95%)	14 (4%)	2 (1%)	21 58
1	E	339/383 (88%)	314 (93%)	21 (6%)	4 (1%)	10 43
2	B	323/364 (89%)	297 (92%)	22 (7%)	4 (1%)	10 43
2	F	321/364 (88%)	292 (91%)	21 (6%)	8 (2%)	4 26
3	C	211/221 (96%)	193 (92%)	14 (7%)	4 (2%)	6 32
3	G	210/221 (95%)	191 (91%)	14 (7%)	5 (2%)	4 27
4	D	213/215 (99%)	201 (94%)	10 (5%)	2 (1%)	14 49
4	H	213/215 (99%)	200 (94%)	10 (5%)	3 (1%)	9 39
All	All	2170/2366 (92%)	2012 (93%)	126 (6%)	32 (2%)	8 38

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	99	ARG
3	C	218	PRO
3	C	220	ASP
2	F	49	ALA
2	F	165	ASP

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	296/329 (90%)	296 (100%)	0	100	100
1	E	295/329 (90%)	295 (100%)	0	100	100
2	B	293/327 (90%)	293 (100%)	0	100	100
2	F	292/327 (89%)	291 (100%)	1 (0%)	86	84
3	C	188/192 (98%)	188 (100%)	0	100	100
3	G	188/192 (98%)	188 (100%)	0	100	100
4	D	190/190 (100%)	190 (100%)	0	100	100
4	H	190/190 (100%)	190 (100%)	0	100	100
All	All	1932/2076 (93%)	1931 (100%)	1 (0%)	88	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	366	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
4	H	128	GLN
4	H	41	GLN
1	E	94	HIS
4	H	3	GLN
4	D	194	ASN

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 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	346/383 (90%)	0.27	2 (0%) 85 73	45, 78, 108, 142	0
1	E	345/383 (90%)	0.72	18 (5%) 33 31	57, 91, 123, 158	0
2	B	329/364 (90%)	0.42	7 (2%) 63 50	39, 61, 97, 128	0
2	F	327/364 (89%)	0.72	20 (6%) 27 28	58, 90, 123, 167	0
3	C	215/221 (97%)	0.40	6 (2%) 55 43	54, 85, 141, 179	0
3	G	214/221 (96%)	0.92	23 (10%) 11 15	54, 83, 150, 202	0
4	D	215/215 (100%)	0.39	6 (2%) 55 43	39, 77, 114, 129	0
4	H	215/215 (100%)	0.58	9 (4%) 40 35	50, 78, 103, 123	0
All	All	2206/2366 (93%)	0.55	91 (4%) 41 36	39, 82, 121, 202	0

The worst 5 of 91 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	102	ASP	5.2
1	E	356	THR	4.8
3	G	104	PHE	4.5
3	G	103	GLY	4.3
1	E	135	LEU	4.0

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 oligosaccharides 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.