



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:20 am BST

PDB ID : 4WHT
Title : Structure of the Hepatitis C virus envelope glycoprotein E2 antigenic region 412-423 bound to the broadly neutralizing antibody 3/11, P1 crystal form
Authors : Krey, T.; Rey, F.A.
Deposited on : 2014-09-23
Resolution : 2.22 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

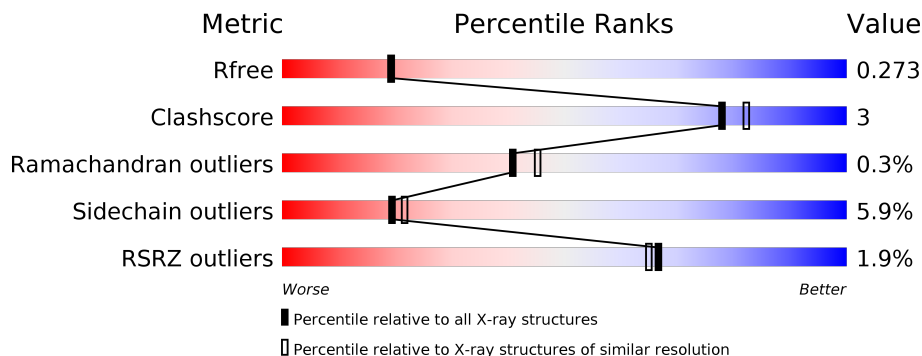
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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.







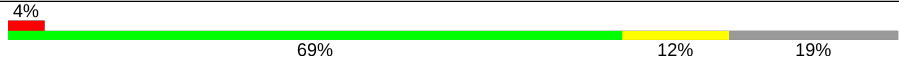
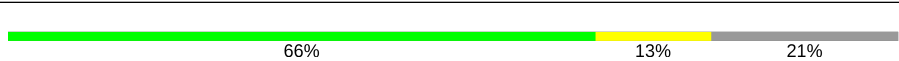
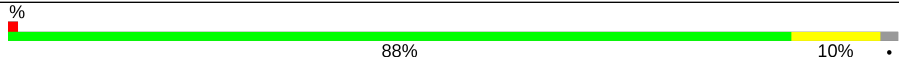
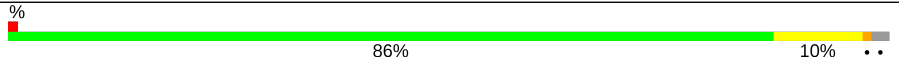
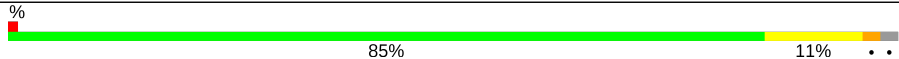
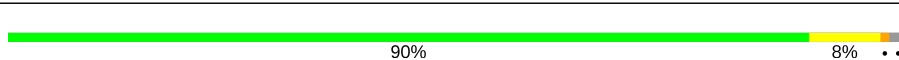
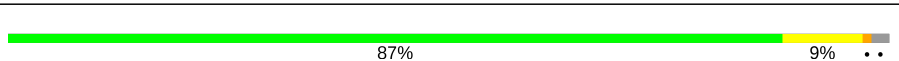

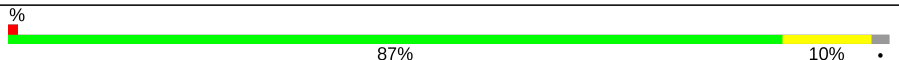
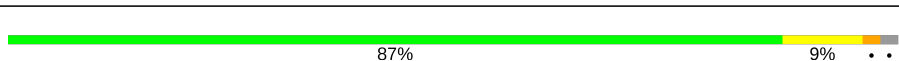


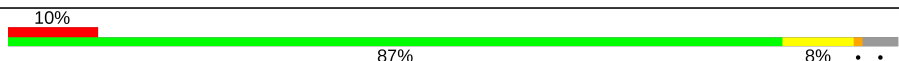
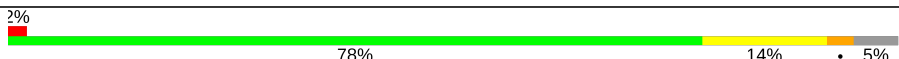
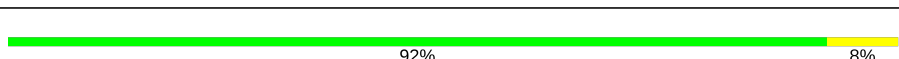
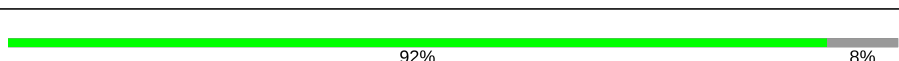
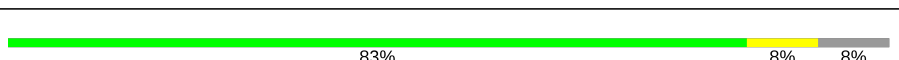
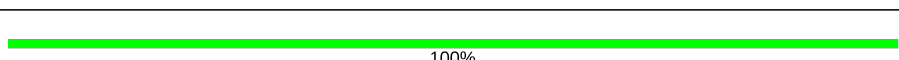
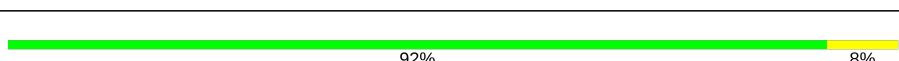
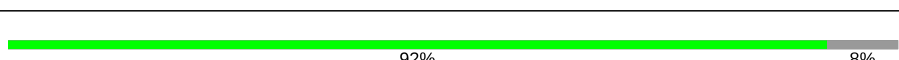
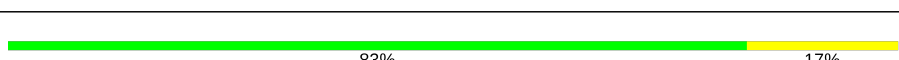
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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 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	252	
1	C	252	
1	E	252	
1	G	252	
1	I	252	
1	K	252	


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Mol	Chain	Length	Quality of chain
1	M	252	
1	O	252	
1	Q	252	
1	S	252	
1	U	252	
1	X	252	
2	B	220	
2	D	220	
2	F	220	
2	H	220	
2	J	220	
2	L	220	
2	N	220	
2	P	220	
2	R	220	
2	T	220	
2	V	220	
2	Y	220	
3	a	12	
3	c	12	
3	e	12	
3	g	12	
3	i	12	
3	k	12	
3	m	12	

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Mol	Chain	Length	Quality of chain
3	o	12	 92% 8%
3	q	12	 83% 17%
3	s	12	 92% 8%
3	u	12	 83% 17%
3	x	12	 92% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 40099 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 Heavy chain of the Fab fragment derived from neutralizing antibody 3/11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	207	1565	988	264	306	7	0	0	0
1	C	205	1554	982	262	303	7	0	0	0
1	E	208	1570	991	265	307	7	0	0	0
1	G	207	1567	989	264	307	7	0	0	0
1	I	205	1550	980	261	302	7	0	0	0
1	K	204	1546	978	260	301	7	0	0	0
1	M	204	1546	978	260	301	7	0	0	0
1	O	205	1550	980	261	302	7	0	0	0
1	Q	206	1557	984	262	304	7	0	0	0
1	S	204	1546	978	260	301	7	0	0	0
1	U	205	1554	982	262	303	7	0	0	0
1	X	199	1495	945	250	293	7	0	0	0

- Molecule 2 is a protein called Light chain of the Fab fragment derived from neutralizing antibody 3/11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	J	215	1634	1014	273	340	7	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	0	0
			1634	1014	273	340	7			
2	D	216	Total	C	N	O	S	0	0	0
			1642	1018	275	342	7			
2	F	215	Total	C	N	O	S	0	0	0
			1634	1014	273	340	7			
2	H	216	Total	C	N	O	S	0	0	0
			1640	1017	274	342	7			
2	L	215	Total	C	N	O	S	0	0	0
			1634	1014	273	340	7			
2	N	215	Total	C	N	O	S	0	0	0
			1634	1014	273	340	7			
2	P	215	Total	C	N	O	S	0	0	0
			1634	1014	273	340	7			
2	R	215	Total	C	N	O	S	0	0	0
			1634	1014	273	340	7			
2	T	215	Total	C	N	O	S	0	0	0
			1634	1014	273	340	7			
2	V	212	Total	C	N	O	S	0	0	0
			1615	1004	270	334	7			
2	Y	210	Total	C	N	O	S	0	0	0
			1591	987	266	331	7			

- Molecule 3 is a protein called Epitope peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	a	12	Total	C	N	O	0	0	0
			97	60	19	18			
3	c	11	Total	C	N	O	0	0	0
			89	56	17	16			
3	e	11	Total	C	N	O	0	0	0
			89	56	17	16			
3	g	12	Total	C	N	O	0	0	0
			97	60	19	18			
3	i	12	Total	C	N	O	0	0	0
			97	60	19	18			
3	k	11	Total	C	N	O	0	0	0
			89	56	17	16			
3	m	12	Total	C	N	O	0	0	0
			97	60	19	18			
3	o	11	Total	C	N	O	0	0	0
			88	55	17	16			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	q	10	Total 80	C 51	N 15	O 14	0	0	0
3	s	11	Total 89	C 56	N 17	O 16	0	0	0
3	u	10	Total 80	C 51	N 15	O 14	0	0	0
3	x	12	Total 97	C 60	N 19	O 18	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	38	Total 38	O 38	0	0
4	C	44	Total 44	O 44	0	0
4	E	34	Total 34	O 34	0	0
4	G	29	Total 29	O 29	0	0
4	I	31	Total 31	O 31	0	0
4	J	55	Total 55	O 55	0	0
4	K	13	Total 13	O 13	0	0
4	M	18	Total 18	O 18	0	0
4	O	26	Total 26	O 26	0	0
4	Q	20	Total 20	O 20	0	0
4	S	27	Total 27	O 27	0	0
4	U	14	Total 14	O 14	0	0
4	X	42	Total 42	O 42	0	0
4	B	47	Total 47	O 47	0	0
4	D	62	Total 62	O 62	0	0

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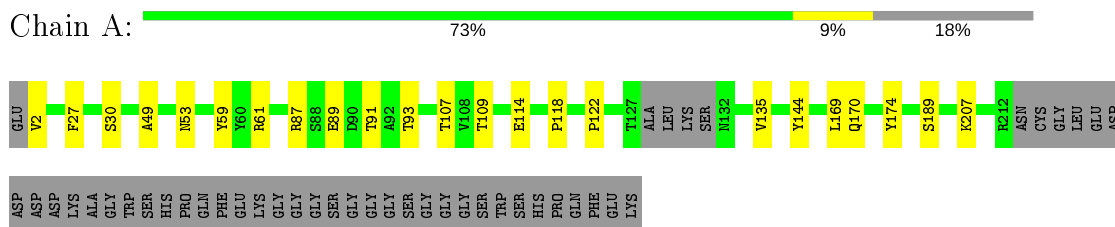
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	48	Total 48	O 48	0	0
4	H	51	Total 51	O 51	0	0
4	L	46	Total 46	O 46	0	0
4	N	24	Total 24	O 24	0	0
4	P	57	Total 57	O 57	0	0
4	R	29	Total 29	O 29	0	0
4	T	32	Total 32	O 32	0	0
4	V	21	Total 21	O 21	0	0
4	Y	40	Total 40	O 40	0	0
4	a	1	Total 1	O 1	0	0
4	s	1	Total 1	O 1	0	0

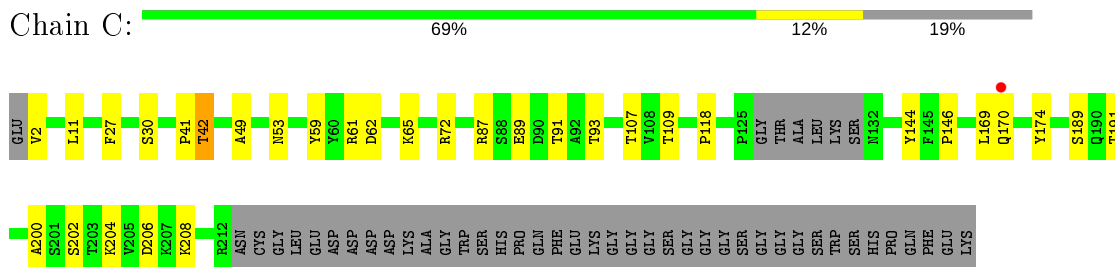
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

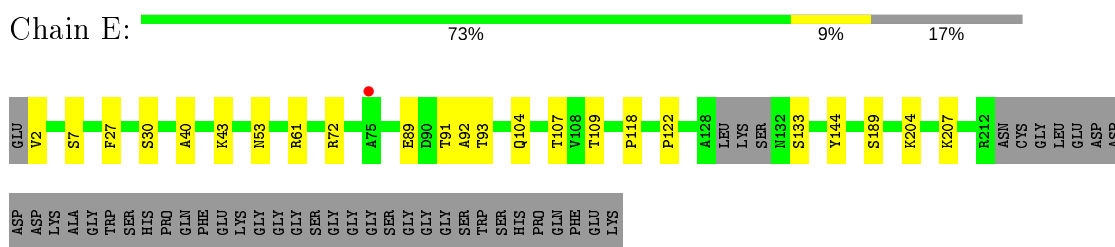
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11



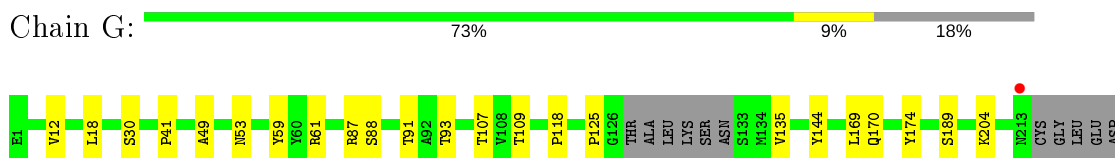
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11



- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11



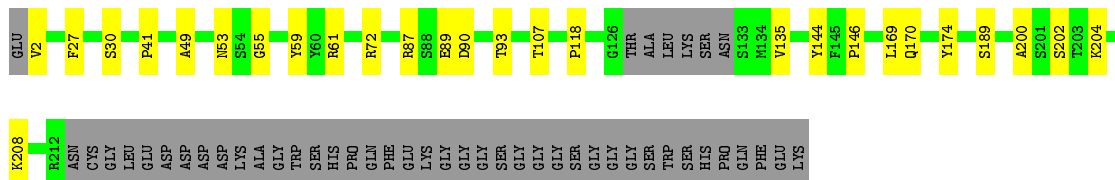
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11



ASP ASP ASP LYS ALA GLY TRP SER HIS ASP GLN PHE GLU LYS GLY GLY SER SER GLY GLY GLY GLY LYS

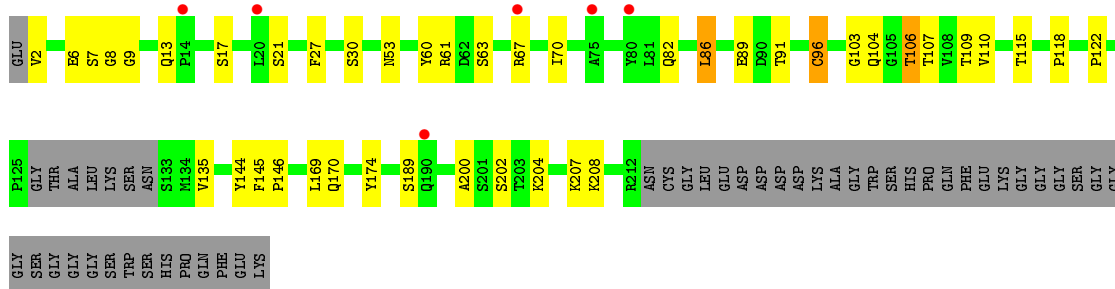
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11

Chain I: 



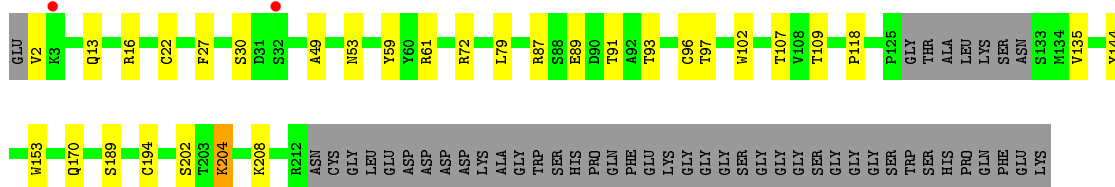
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11

Chain K: 



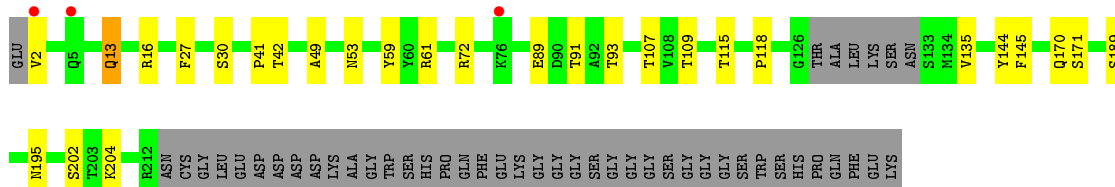
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11

Chain M: 

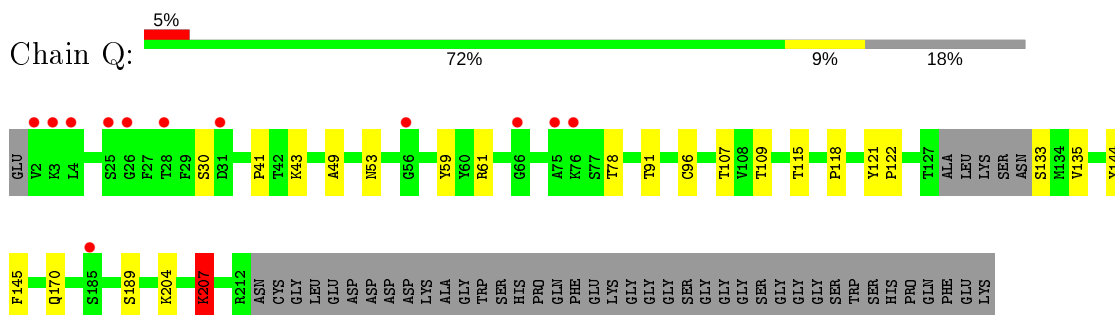


- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11

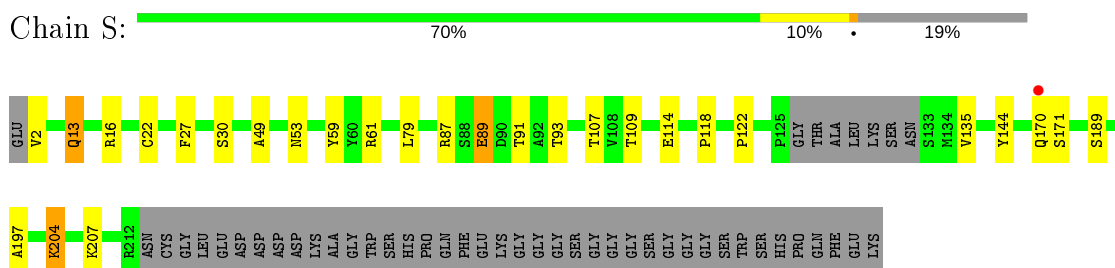
Chain O: 



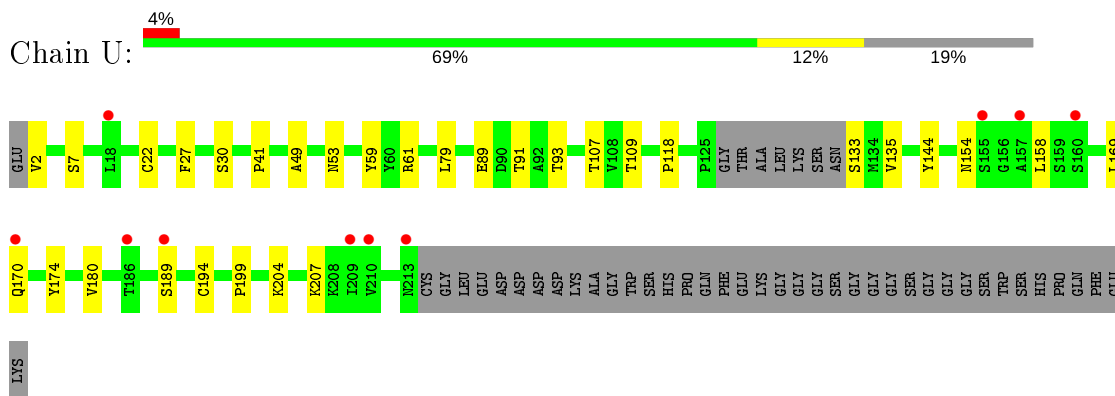
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11



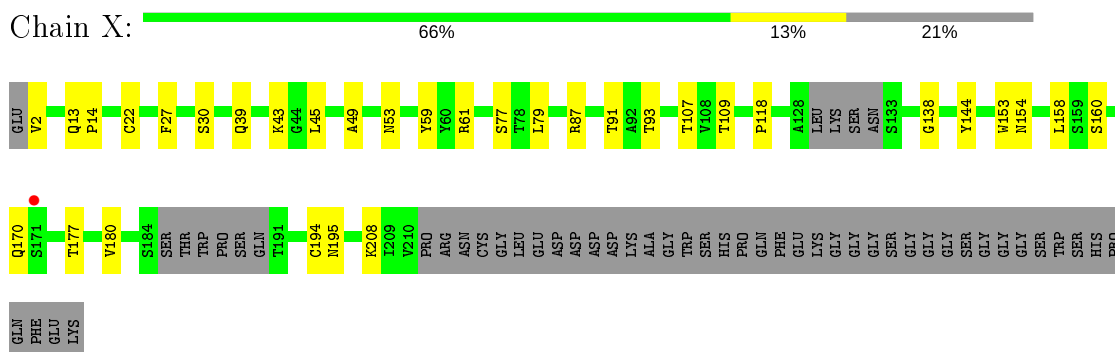
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11



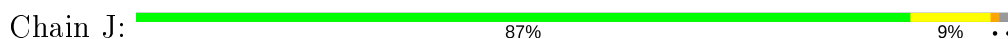
- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11

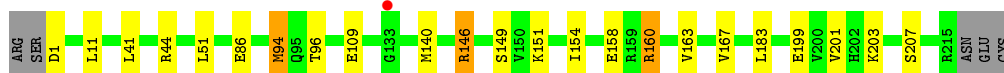


- Molecule 1: Heavy chain of the Fab fragment derived from neutralizing antibody 3/11

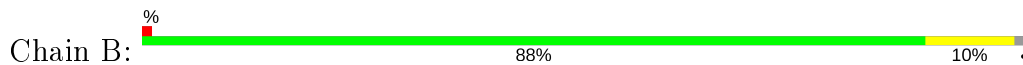


- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11

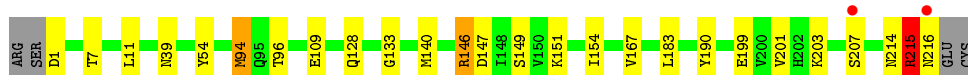
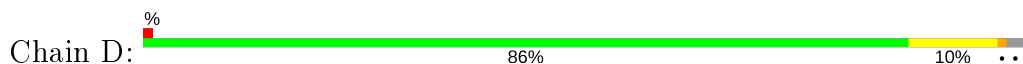




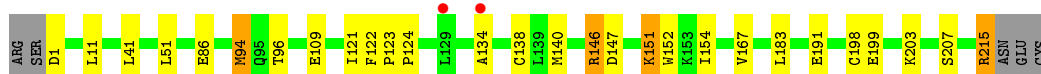
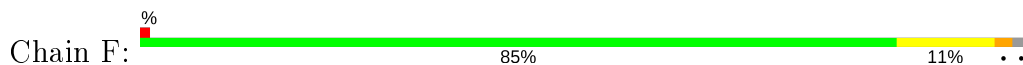
- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11



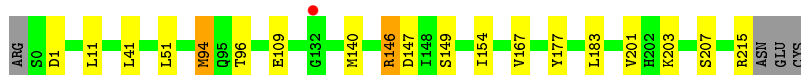
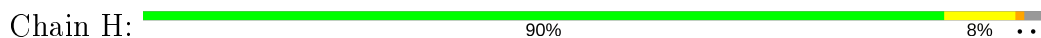
- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11



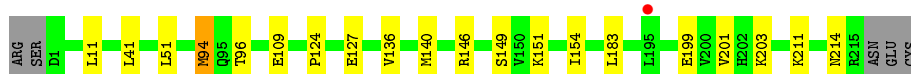
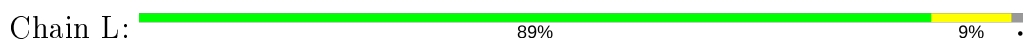
- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11



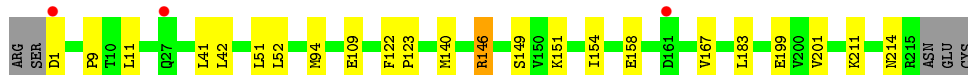
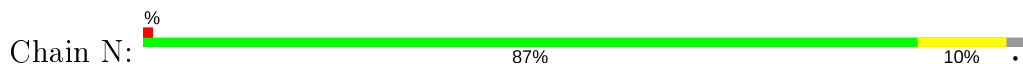
- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11




- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11



- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11




- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11

Chain P:  87% 9%




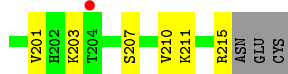
- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11

Chain R:  87% 10%




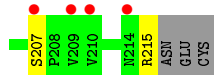
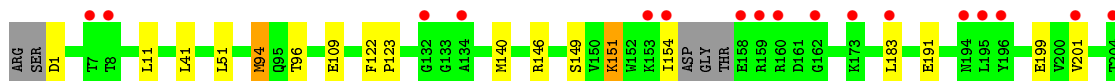
- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11

Chain T:  85% 12%




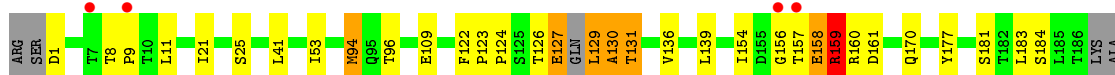
- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11

Chain V:  87% 8%



- Molecule 2: Light chain of the Fab fragment derived from neutralizing antibody 3/11

Chain Y:  78% 14% 5%



- Molecule 3: Epitope peptide

Chain a:  92% 8%




- Molecule 3: Epitope peptide

Chain c:  92% 8%



- Molecule 3: Epitope peptide

Chain e:  83% 8% 8%



- Molecule 3: Epitope peptide

Chain g:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: Epitope peptide

Chain i:  92% 8%




- Molecule 3: Epitope peptide

Chain k:  92% 8%



- Molecule 3: Epitope peptide

Chain m:  83% 17%

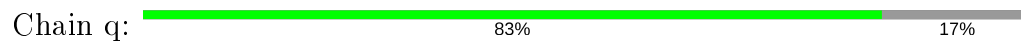


- Molecule 3: Epitope peptide

Chain o:  92% 8%



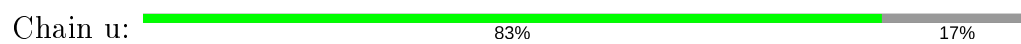
- Molecule 3: Epitope peptide



- Molecule 3: Epitope peptide



- Molecule 3: Epitope peptide



- Molecule 3: Epitope peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	64.79Å 128.22Å 163.63Å 88.79° 94.36° 96.15°	Depositor
Resolution (Å)	32.50 – 2.22 48.74 – 2.22	Depositor EDS
% Data completeness (in resolution range)	95.4 (32.50-2.22) 95.4 (48.74-2.22)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 2.22Å)	Xtrriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.209 , 0.243 0.233 , 0.273	Depositor DCC
R_{free} test set	12380 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	33.1	Xtrriage
Anisotropy	0.254	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	40099	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.77% 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	0.51	0/1603	0.76	0/2188
1	C	0.52	0/1592	0.75	0/2173
1	E	0.51	0/1608	0.74	0/2195
1	G	0.50	0/1605	0.75	0/2190
1	I	0.50	0/1588	0.75	1/2167 (0.0%)
1	K	0.51	0/1584	0.74	0/2162
1	M	0.47	0/1584	0.73	0/2162
1	O	0.49	0/1588	0.74	0/2167
1	Q	0.48	0/1595	0.73	1/2177 (0.0%)
1	S	0.53	0/1584	0.75	0/2162
1	U	0.49	0/1592	0.75	0/2173
1	X	0.56	0/1528	0.82	0/2082
2	B	0.53	0/1664	0.74	0/2264
2	D	0.52	0/1672	0.74	0/2275
2	F	0.51	0/1664	0.72	0/2264
2	H	0.51	0/1670	0.73	0/2272
2	J	0.51	0/1664	0.73	0/2264
2	L	0.51	0/1664	0.72	0/2264
2	N	0.44	0/1664	0.71	0/2264
2	P	0.48	0/1664	0.73	1/2264 (0.0%)
2	R	0.45	0/1664	0.71	0/2264
2	T	0.50	0/1664	0.73	0/2264
2	V	0.47	0/1644	0.69	0/2235
2	Y	0.61	0/1618	0.88	2/2199 (0.1%)
3	a	0.51	0/99	0.67	0/135
3	c	0.48	0/91	0.71	0/124
3	e	0.57	0/91	0.71	0/124
3	g	0.56	0/99	0.70	0/135
3	i	0.50	0/99	0.75	0/135
3	k	0.55	0/91	0.78	0/124
3	m	0.45	0/99	0.75	0/135
3	o	0.45	0/90	0.64	0/123
3	q	0.46	0/82	0.73	0/112
3	s	0.52	0/91	0.74	0/124

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	u	0.49	0/82	0.73	0/112
3	x	0.67	0/99	0.82	0/135
All	All	0.51	0/40080	0.74	5/54609 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	130	ALA	C-N-CA	5.87	136.37	121.70
2	P	94	MET	N-CA-CB	-5.52	100.66	110.60
1	I	55	GLY	N-CA-C	5.43	126.67	113.10
1	Q	207	LYS	CG-CD-CE	-5.22	96.25	111.90
2	Y	158	GLU	C-N-CA	5.04	134.30	121.70

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	1565	0	1536	7	0
1	C	1554	0	1526	14	0
1	E	1570	0	1541	7	0
1	G	1567	0	1538	6	0
1	I	1550	0	1523	10	0
1	K	1546	0	1520	18	0
1	M	1546	0	1520	12	0
1	O	1550	0	1523	9	0
1	Q	1557	0	1530	7	0
1	S	1546	0	1520	12	0
1	U	1554	0	1526	10	0
1	X	1495	0	1472	13	0
2	B	1634	0	1593	6	0
2	D	1642	0	1599	15	0
2	F	1634	0	1593	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	1640	0	1598	6	0
2	J	1634	0	1593	10	0
2	L	1634	0	1593	7	0
2	N	1634	0	1593	8	0
2	P	1634	0	1593	10	0
2	R	1634	0	1593	8	0
2	T	1634	0	1593	9	0
2	V	1615	0	1578	8	0
2	Y	1591	0	1552	11	0
3	a	97	0	88	0	0
3	c	89	0	82	0	0
3	e	89	0	82	0	0
3	g	97	0	88	0	0
3	i	97	0	88	0	0
3	k	89	0	82	0	0
3	m	97	0	88	0	0
3	o	88	0	80	0	0
3	q	80	0	74	0	0
3	s	89	0	82	0	0
3	u	80	0	74	0	0
3	x	97	0	88	0	0
4	A	38	0	0	0	0
4	B	47	0	0	0	0
4	C	44	0	0	2	0
4	D	62	0	0	1	0
4	E	34	0	0	0	0
4	F	48	0	0	0	0
4	G	29	0	0	0	0
4	H	51	0	0	0	0
4	I	31	0	0	0	0
4	J	55	0	0	0	0
4	K	13	0	0	0	0
4	L	46	0	0	0	0
4	M	18	0	0	1	0
4	N	24	0	0	0	0
4	O	26	0	0	0	0
4	P	57	0	0	0	0
4	Q	20	0	0	0	0
4	R	29	0	0	1	0
4	S	27	0	0	1	0
4	T	32	0	0	1	0
4	U	14	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	V	21	0	0	0	0
4	X	42	0	0	0	0
4	Y	40	0	0	0	0
4	a	1	0	0	0	0
4	s	1	0	0	0	0
All	All	40099	0	38342	223	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 3.

All (223) 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:97:THR:HG21	1:M:102:TRP:CE3	2.13	0.83
1:C:202:SER:HB3	1:I:208:LYS:HB3	1.65	0.76
2:J:44:ARG:NH1	2:J:86:GLU:O	2.23	0.71
1:K:208:LYS:HB3	1:M:202:SER:HB3	1.75	0.66
2:D:214:ASN:O	2:D:215:ARG:HB2	1.95	0.66
2:L:154:ILE:HD11	2:L:183:LEU:HD21	1.78	0.66
2:J:160:ARG:HH21	2:J:163:VAL:HG11	1.62	0.65
2:F:191:GLU:HA	2:F:215:ARG:HH22	1.62	0.65
2:V:191:GLU:HA	2:V:215:ARG:HH22	1.62	0.64
2:Y:127:GLU:O	2:Y:129:LEU:N	2.31	0.63
1:G:30:SER:O	1:G:53:ASN:HB2	2.00	0.62
1:U:118:PRO:HB3	1:U:144:TYR:HB3	1.83	0.61
1:M:97:THR:HG21	1:M:102:TRP:CD2	2.37	0.60
1:G:118:PRO:HB3	1:G:144:TYR:HB3	1.84	0.59
1:I:118:PRO:HB3	1:I:144:TYR:HB3	1.84	0.59
1:S:118:PRO:HB3	1:S:144:TYR:HB3	1.83	0.59
1:S:171:SER:HB3	2:Y:159:ARG:HG3	1.84	0.58
1:Q:30:SER:O	1:Q:53:ASN:HB2	2.04	0.57
1:M:30:SER:O	1:M:53:ASN:HB2	2.04	0.57
1:O:30:SER:O	1:O:53:ASN:HB2	2.03	0.57
1:Q:118:PRO:HB3	1:Q:144:TYR:HB3	1.87	0.57
1:X:118:PRO:HB3	1:X:144:TYR:HB3	1.86	0.56
2:T:197:THR:HG23	2:T:210:VAL:HG13	1.88	0.56
2:N:154:ILE:HD11	2:N:183:LEU:HD21	1.88	0.56
1:U:30:SER:O	1:U:53:ASN:HB2	2.06	0.56
1:A:118:PRO:HB3	1:A:144:TYR:HB3	1.88	0.55
1:O:118:PRO:HB3	1:O:144:TYR:HB3	1.88	0.55
1:S:30:SER:O	1:S:53:ASN:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:118:PRO:HB3	1:K:144:TYR:HB3	1.89	0.55
1:C:208:LYS:HB3	1:I:202:SER:HB3	1.88	0.55
1:I:30:SER:O	1:I:53:ASN:HB2	2.06	0.55
1:E:118:PRO:HB3	1:E:144:TYR:HB3	1.87	0.55
1:X:30:SER:O	1:X:53:ASN:HB2	2.06	0.55
1:X:22:CYS:HB3	1:X:79:LEU:HB3	1.89	0.54
2:B:146:ARG:HD3	2:B:167:VAL:HG11	1.90	0.54
2:N:146:ARG:HD3	2:N:167:VAL:HG11	1.89	0.54
1:C:206:ASP:HB2	1:I:204:LYS:HB2	1.88	0.54
1:O:202:SER:HB3	1:X:208:LYS:HB3	1.89	0.54
1:C:118:PRO:HB3	1:C:144:TYR:HB3	1.89	0.54
2:D:154:ILE:HD11	2:D:183:LEU:HD21	1.89	0.54
2:D:94:MET:CE	2:D:96:THR:HG23	2.38	0.54
2:T:55:SER:O	2:T:56:VAL:HG12	2.07	0.54
1:A:30:SER:O	1:A:53:ASN:HB2	2.07	0.53
2:D:190:TYR:CE2	2:D:216:ASN:CB	2.91	0.53
2:R:197:THR:HG23	2:R:210:VAL:HG13	1.91	0.53
2:D:190:TYR:CE2	2:D:216:ASN:HB3	2.44	0.53
1:K:146:PRO:HD2	1:K:200:ALA:CB	2.39	0.53
1:M:118:PRO:HB3	1:M:144:TYR:HB3	1.89	0.53
2:R:146:ARG:HD3	2:R:167:VAL:HG11	1.90	0.52
1:U:22:CYS:HB3	1:U:79:LEU:HB3	1.92	0.52
2:H:146:ARG:HG2	2:H:177:TYR:CE1	2.45	0.52
2:J:146:ARG:HD3	2:J:167:VAL:HG11	1.92	0.52
2:F:121:ILE:HD12	2:F:198:CYS:HB2	1.90	0.52
2:T:111:LYS:HA	2:T:144:TYR:OH	2.10	0.52
2:Y:124:PRO:HD3	2:Y:136:VAL:HG22	1.92	0.52
2:D:146:ARG:HD3	2:D:167:VAL:HG11	1.91	0.51
2:P:154:ILE:HD11	2:P:183:LEU:HD21	1.92	0.51
1:Q:122:PRO:HD3	1:Q:207:LYS:HE3	1.92	0.51
1:S:13:GLN:HG2	1:S:16:ARG:HD3	1.92	0.51
2:D:39:ASN:OD1	2:D:54:TYR:HA	2.09	0.51
2:H:154:ILE:HD11	2:H:183:LEU:HD21	1.92	0.51
1:K:6:GLU:OE1	1:K:103:GLY:HA3	2.10	0.51
1:X:177:THR:HG21	2:Y:139:LEU:HD21	1.93	0.51
1:U:158:LEU:HD23	1:U:180:VAL:HG21	1.93	0.51
2:B:154:ILE:HD11	2:B:183:LEU:HD21	1.93	0.51
1:S:87:ARG:HG3	1:S:89:GLU:HB3	1.93	0.51
2:V:151:LYS:HB3	2:V:199:GLU:HB3	1.93	0.51
1:A:91:THR:HG23	1:A:109:THR:HA	1.91	0.51
1:X:154:ASN:HB2	1:X:158:LEU:HD13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:151:LYS:HB3	2:F:199:GLU:HB3	1.91	0.50
2:R:154:ILE:HD11	2:R:183:LEU:HD21	1.93	0.50
2:L:124:PRO:HD3	2:L:136:VAL:HG22	1.94	0.50
2:N:42:LEU:HB2	2:N:52:LEU:HD11	1.94	0.50
1:C:30:SER:O	1:C:53:ASN:HB2	2.11	0.50
1:K:2:VAL:HG13	1:K:27:PHE:CD1	2.48	0.49
2:R:16:GLY:HA2	4:R:320:HOH:O	2.12	0.49
1:X:39:GLN:HB2	1:X:45:LEU:HD23	1.95	0.49
1:O:13:GLN:HG3	1:O:16:ARG:HD3	1.95	0.49
2:F:154:ILE:HD11	2:F:183:LEU:HD21	1.95	0.49
1:O:41:PRO:O	1:O:42:THR:HB	2.13	0.48
2:D:190:TYR:CE2	2:D:216:ASN:HB2	2.49	0.48
2:V:154:ILE:HD11	2:V:183:LEU:HD21	1.95	0.48
2:J:154:ILE:HD11	2:J:183:LEU:HD21	1.95	0.48
1:K:63:SER:O	1:K:67:ARG:NH2	2.46	0.48
1:S:22:CYS:HB3	1:S:79:LEU:HB3	1.95	0.48
1:U:2:VAL:HG13	1:U:27:PHE:CD1	2.49	0.48
2:T:35:ASN:HB3	4:T:327:HOH:O	2.14	0.48
2:D:94:MET:HE3	2:D:96:THR:HG23	1.96	0.47
1:E:91:THR:HG23	1:E:109:THR:HA	1.97	0.47
1:E:2:VAL:HG13	1:E:27:PHE:CD1	2.49	0.47
1:K:30:SER:O	1:K:53:ASN:HB2	2.14	0.47
1:S:2:VAL:HG13	1:S:27:PHE:CD1	2.49	0.47
2:D:151:LYS:HB3	2:D:199:GLU:HB3	1.96	0.47
1:K:115:THR:HA	1:K:145:PHE:O	2.14	0.47
1:E:30:SER:O	1:E:53:ASN:HB2	2.13	0.47
2:F:146:ARG:HD3	2:F:167:VAL:HG11	1.95	0.47
1:I:2:VAL:HG13	1:I:27:PHE:CD1	2.49	0.47
2:J:151:LYS:HB3	2:J:199:GLU:HB3	1.96	0.47
1:X:91:THR:HG23	1:X:109:THR:HA	1.97	0.47
1:A:2:VAL:HG13	1:A:27:PHE:CD1	2.50	0.47
1:X:2:VAL:HG13	1:X:27:PHE:CD1	2.50	0.46
1:A:49:ALA:HA	1:A:59:TYR:O	2.15	0.46
1:O:2:VAL:HG13	1:O:27:PHE:CD1	2.51	0.46
1:E:122:PRO:HD3	1:E:207:LYS:HE3	1.98	0.46
2:L:149:SER:HB3	2:L:201:VAL:HB	1.97	0.46
2:L:151:LYS:HB3	2:L:199:GLU:HB3	1.97	0.46
1:C:49:ALA:HA	1:C:59:TYR:O	2.16	0.46
1:G:49:ALA:HA	1:G:59:TYR:O	2.15	0.46
1:M:2:VAL:HG13	1:M:27:PHE:CD1	2.50	0.46
1:U:199:PRO:HD2	4:U:306:HOH:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:147:ASP:O	2:P:202:HIS:CD2	2.68	0.46
1:U:91:THR:HG23	1:U:109:THR:HA	1.97	0.45
1:C:91:THR:HG23	1:C:109:THR:HA	1.98	0.45
2:R:41:LEU:HD23	2:R:51:LEU:HA	1.98	0.45
1:S:91:THR:HG23	1:S:109:THR:HA	1.98	0.45
1:X:49:ALA:HA	1:X:59:TYR:O	2.17	0.45
2:Y:170:GLN:HB2	2:Y:177:TYR:CZ	2.52	0.45
2:H:146:ARG:HD3	2:H:167:VAL:HG11	1.97	0.45
1:K:91:THR:HG23	1:K:109:THR:HA	1.98	0.45
1:Q:49:ALA:HA	1:Q:59:TYR:O	2.17	0.45
1:M:204:LYS:HG2	4:M:303:HOH:O	2.16	0.45
1:O:91:THR:HG23	1:O:109:THR:HA	1.99	0.45
1:G:91:THR:HG23	1:G:109:THR:HA	1.98	0.45
2:P:214:ASN:O	2:P:215:ARG:HB2	2.17	0.45
1:Q:91:THR:HG23	1:Q:109:THR:HA	1.98	0.45
1:K:9:GLY:HA3	1:K:106:THR:HG23	1.98	0.45
2:P:147:ASP:O	2:P:202:HIS:HD2	2.00	0.45
1:K:122:PRO:HD3	1:K:207:LYS:HE3	1.99	0.45
2:Y:94:MET:CE	2:Y:96:THR:HG23	2.47	0.45
1:C:11:LEU:HD11	4:C:325:HOH:O	2.17	0.45
1:I:49:ALA:HA	1:I:59:TYR:O	2.17	0.45
2:P:149:SER:HB3	2:P:201:VAL:HB	1.99	0.45
2:T:96:THR:HG23	2:T:100:PRO:HG3	1.99	0.45
2:N:151:LYS:HB3	2:N:199:GLU:HB3	1.99	0.44
1:X:138:GLY:HA2	1:X:153:TRP:CH2	2.53	0.44
2:L:94:MET:HE3	2:L:96:THR:HG23	1.99	0.44
1:M:91:THR:HG23	1:M:109:THR:HA	2.00	0.44
2:B:194:ASN:O	2:B:214:ASN:HA	2.17	0.44
1:C:2:VAL:HG13	1:C:27:PHE:CD1	2.53	0.44
2:P:151:LYS:HB3	2:P:199:GLU:HB3	2.00	0.44
2:B:149:SER:HB3	2:B:201:VAL:HB	1.99	0.44
2:N:151:LYS:HG2	2:N:158:GLU:HG3	2.00	0.44
1:M:49:ALA:HA	1:M:59:TYR:O	2.18	0.44
1:X:13:GLN:HG3	1:X:14:PRO:HD2	2.00	0.44
2:Y:122:PHE:HA	2:Y:123:PRO:HD3	1.92	0.43
1:C:41:PRO:O	1:C:42:THR:HG22	2.18	0.43
1:K:86:LEU:HG	1:K:110:VAL:HG21	2.00	0.43
2:V:149:SER:HB3	2:V:201:VAL:HB	2.01	0.43
2:B:151:LYS:HB3	2:B:199:GLU:HB3	2.00	0.43
1:I:87:ARG:O	1:I:90:ASP:HB2	2.19	0.43
1:K:60:TYR:CE1	1:K:70:ILE:HG22	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:149:SER:HB3	2:H:201:VAL:HB	2.00	0.43
2:F:124:PRO:HG3	2:F:134:ALA:HB1	2.01	0.43
1:O:49:ALA:HA	1:O:59:TYR:O	2.19	0.43
1:Q:121:TYR:CD2	2:R:128:GLN:HG3	2.54	0.43
1:C:146:PRO:HD2	1:C:200:ALA:CB	2.49	0.43
1:E:40:ALA:HB3	1:E:43:LYS:HB2	2.00	0.43
2:N:41:LEU:HD23	2:N:51:LEU:HA	2.00	0.43
1:S:197:ALA:HB2	1:S:204:LYS:HE2	2.01	0.43
1:U:49:ALA:HA	1:U:59:TYR:O	2.19	0.43
2:V:94:MET:CE	2:V:96:THR:HG23	2.48	0.43
2:J:94:MET:CE	2:J:96:THR:HG23	2.49	0.43
2:P:197:THR:HG1	2:P:212:SER:HG	1.67	0.43
2:B:41:LEU:HD23	2:B:51:LEU:HA	2.00	0.42
2:D:149:SER:HB3	2:D:201:VAL:HB	2.00	0.42
1:X:153:TRP:CZ3	1:X:194:CYS:HB3	2.53	0.42
2:J:151:LYS:HG2	2:J:158:GLU:HG3	2.01	0.42
2:D:146:ARG:HB2	4:D:340:HOH:O	2.19	0.42
2:T:41:LEU:HD23	2:T:51:LEU:HA	2.02	0.42
2:T:146:ARG:HD3	2:T:167:VAL:HG11	2.02	0.42
2:D:94:MET:HE1	2:D:96:THR:HG23	2.01	0.42
1:K:202:SER:HB3	1:M:208:LYS:HB3	2.00	0.42
2:L:94:MET:CE	2:L:96:THR:HG23	2.49	0.42
1:A:122:PRO:HD3	1:A:207:LYS:HE3	2.02	0.42
1:K:7:SER:OG	1:K:8:GLY:N	2.53	0.42
1:G:12:VAL:CG2	1:G:18:LEU:HD13	2.48	0.42
2:J:94:MET:HE2	2:J:96:THR:HG23	2.02	0.42
2:J:41:LEU:HD23	2:J:51:LEU:HA	2.00	0.42
1:S:49:ALA:HA	1:S:59:TYR:O	2.20	0.42
2:V:41:LEU:HD23	2:V:51:LEU:HA	2.02	0.42
2:F:94:MET:CE	2:F:96:THR:HG23	2.48	0.42
2:P:107:LYS:HE3	2:P:109:GLU:HB3	2.02	0.42
2:P:41:LEU:HD23	2:P:51:LEU:HA	2.01	0.42
2:R:66:ARG:NE	2:R:87:ASP:OD2	2.46	0.42
2:T:149:SER:HB3	2:T:201:VAL:HB	2.02	0.42
1:U:154:ASN:HB2	1:U:158:LEU:HD13	2.02	0.42
1:A:169:LEU:HG	1:A:174:TYR:CE1	2.54	0.41
1:C:62:ASP:HA	1:C:65:LYS:HD2	2.00	0.41
1:K:169:LEU:HG	1:K:174:TYR:CE1	2.55	0.41
4:S:304:HOH:O	2:T:127:GLU:HG3	2.19	0.41
1:C:169:LEU:HG	1:C:174:TYR:CE1	2.55	0.41
2:N:149:SER:HB3	2:N:201:VAL:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:115:THR:HA	1:O:145:PHE:O	2.20	0.41
2:L:41:LEU:HD23	2:L:51:LEU:HA	2.02	0.41
1:G:169:LEU:HG	1:G:174:TYR:CE1	2.55	0.41
2:H:94:MET:CE	2:H:96:THR:HG23	2.51	0.41
2:Y:154:ILE:HD11	2:Y:183:LEU:HD21	2.01	0.41
1:E:91:THR:O	1:E:92:ALA:HB2	2.21	0.41
1:K:6:GLU:HG3	1:K:96:CYS:HB3	2.03	0.41
2:P:151:LYS:HG2	2:P:158:GLU:HG3	2.02	0.41
2:Y:129:LEU:O	2:Y:131:THR:N	2.53	0.41
2:R:149:SER:HB3	2:R:201:VAL:HB	2.03	0.41
2:D:190:TYR:HE2	2:D:216:ASN:HB3	1.86	0.41
2:F:122:PHE:HA	2:F:123:PRO:HD3	1.97	0.41
2:J:149:SER:HB3	2:J:201:VAL:HB	2.02	0.41
2:H:41:LEU:HD23	2:H:51:LEU:HA	2.02	0.41
1:S:122:PRO:HD3	1:S:207:LYS:HE3	2.03	0.41
2:V:94:MET:HE3	2:V:96:THR:HG23	2.03	0.41
1:U:169:LEU:HG	1:U:174:TYR:CE1	2.56	0.40
1:C:191:THR:HA	4:C:327:HOH:O	2.21	0.40
2:D:128:GLN:HG2	2:D:133:GLY:O	2.21	0.40
2:F:138:CYS:HB2	2:F:152:TRP:CH2	2.56	0.40
1:I:146:PRO:HD2	1:I:200:ALA:CB	2.51	0.40
1:M:153:TRP:CH2	1:M:194:CYS:HB3	2.56	0.40
1:M:22:CYS:HB3	1:M:79:LEU:HB3	2.03	0.40
2:V:122:PHE:HA	2:V:123:PRO:HD3	1.98	0.40
2:N:122:PHE:HA	2:N:123:PRO:HD3	2.00	0.40
2:F:41:LEU:HD23	2:F:51:LEU:HA	2.03	0.40
1:I:169:LEU:HG	1:I:174:TYR:CE1	2.56	0.40
1:K:17:SER:HB3	1:K:82:GLN:HE22	1.87	0.40
1:Q:115:THR:HA	1:Q:145:PHE:O	2.22	0.40
1:S:171:SER:CB	2:Y:159:ARG:HG3	2.51	0.40
2:Y:94:MET:HE2	2:Y:96:THR:HG23	2.04	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 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	203/252 (81%)	195 (96%)	8 (4%)	0	100	100
1	C	201/252 (80%)	195 (97%)	6 (3%)	0	100	100
1	E	204/252 (81%)	197 (97%)	7 (3%)	0	100	100
1	G	203/252 (81%)	197 (97%)	4 (2%)	2 (1%)	15	13
1	I	201/252 (80%)	197 (98%)	3 (2%)	1 (0%)	29	30
1	K	200/252 (79%)	194 (97%)	6 (3%)	0	100	100
1	M	200/252 (79%)	196 (98%)	4 (2%)	0	100	100
1	O	201/252 (80%)	196 (98%)	5 (2%)	0	100	100
1	Q	202/252 (80%)	199 (98%)	2 (1%)	1 (0%)	29	30
1	S	200/252 (79%)	196 (98%)	4 (2%)	0	100	100
1	U	201/252 (80%)	197 (98%)	3 (2%)	1 (0%)	29	30
1	X	193/252 (77%)	189 (98%)	2 (1%)	2 (1%)	15	13
2	B	213/220 (97%)	208 (98%)	5 (2%)	0	100	100
2	D	214/220 (97%)	208 (97%)	4 (2%)	2 (1%)	17	15
2	F	213/220 (97%)	208 (98%)	5 (2%)	0	100	100
2	H	214/220 (97%)	212 (99%)	2 (1%)	0	100	100
2	J	213/220 (97%)	208 (98%)	5 (2%)	0	100	100
2	L	213/220 (97%)	210 (99%)	3 (1%)	0	100	100
2	N	213/220 (97%)	208 (98%)	5 (2%)	0	100	100
2	P	213/220 (97%)	206 (97%)	7 (3%)	0	100	100
2	R	213/220 (97%)	206 (97%)	7 (3%)	0	100	100
2	T	213/220 (97%)	207 (97%)	6 (3%)	0	100	100
2	V	208/220 (94%)	203 (98%)	5 (2%)	0	100	100
2	Y	204/220 (93%)	186 (91%)	12 (6%)	6 (3%)	4	2
3	a	10/12 (83%)	10 (100%)	0	0	100	100
3	c	9/12 (75%)	9 (100%)	0	0	100	100
3	e	9/12 (75%)	9 (100%)	0	0	100	100
3	g	10/12 (83%)	10 (100%)	0	0	100	100
3	i	10/12 (83%)	10 (100%)	0	0	100	100
3	k	9/12 (75%)	8 (89%)	1 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	m	10/12 (83%)	10 (100%)	0	0	100	100
3	o	9/12 (75%)	8 (89%)	1 (11%)	0	100	100
3	q	8/12 (67%)	7 (88%)	1 (12%)	0	100	100
3	s	9/12 (75%)	9 (100%)	0	0	100	100
3	u	8/12 (67%)	8 (100%)	0	0	100	100
3	x	10/12 (83%)	10 (100%)	0	0	100	100
All	All	5064/5808 (87%)	4926 (97%)	123 (2%)	15 (0%)	41	45

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	7	THR
2	D	215	ARG
2	Y	159	ARG
1	G	125	PRO
1	X	160	SER
2	Y	156	GLY
1	X	43	LYS
2	Y	130	ALA
2	Y	131	THR
2	Y	184	SER
2	Y	9	PRO
1	I	41	PRO
1	U	41	PRO
1	G	41	PRO
1	Q	41	PRO

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	176/208 (85%)	167 (95%)	9 (5%)	24	27
1	C	175/208 (84%)	165 (94%)	10 (6%)	20	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	176/208 (85%)	166 (94%)	10 (6%)	20	23
1	G	176/208 (85%)	167 (95%)	9 (5%)	24	27
1	I	174/208 (84%)	166 (95%)	8 (5%)	27	32
1	K	174/208 (84%)	161 (92%)	13 (8%)	13	13
1	M	174/208 (84%)	161 (92%)	13 (8%)	13	13
1	O	174/208 (84%)	162 (93%)	12 (7%)	15	15
1	Q	175/208 (84%)	164 (94%)	11 (6%)	18	19
1	S	174/208 (84%)	164 (94%)	10 (6%)	20	23
1	U	175/208 (84%)	163 (93%)	12 (7%)	15	15
1	X	167/208 (80%)	159 (95%)	8 (5%)	25	30
2	B	191/196 (97%)	180 (94%)	11 (6%)	20	22
2	D	192/196 (98%)	182 (95%)	10 (5%)	23	27
2	F	191/196 (97%)	179 (94%)	12 (6%)	18	19
2	H	192/196 (98%)	182 (95%)	10 (5%)	23	27
2	J	191/196 (97%)	182 (95%)	9 (5%)	26	31
2	L	191/196 (97%)	182 (95%)	9 (5%)	26	31
2	N	191/196 (97%)	182 (95%)	9 (5%)	26	31
2	P	191/196 (97%)	181 (95%)	10 (5%)	23	27
2	R	191/196 (97%)	181 (95%)	10 (5%)	23	27
2	T	191/196 (97%)	178 (93%)	13 (7%)	16	16
2	V	189/196 (96%)	181 (96%)	8 (4%)	30	36
2	Y	187/196 (95%)	164 (88%)	23 (12%)	4	3
3	a	11/11 (100%)	10 (91%)	1 (9%)	9	8
3	c	10/11 (91%)	10 (100%)	0	100	100
3	e	10/11 (91%)	9 (90%)	1 (10%)	7	6
3	g	11/11 (100%)	11 (100%)	0	100	100
3	i	11/11 (100%)	10 (91%)	1 (9%)	9	8
3	k	10/11 (91%)	10 (100%)	0	100	100
3	m	11/11 (100%)	9 (82%)	2 (18%)	1	1
3	o	10/11 (91%)	10 (100%)	0	100	100
3	q	9/11 (82%)	9 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	s	10/11 (91%)	10 (100%)	0	100	100
3	u	9/11 (82%)	9 (100%)	0	100	100
3	x	11/11 (100%)	10 (91%)	1 (9%)	9	8
All	All	4501/4980 (90%)	4236 (94%)	265 (6%)	19	22

All (265) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	ARG
1	A	87	ARG
1	A	89	GLU
1	A	93	THR
1	A	107	THR
1	A	114	GLU
1	A	135	VAL
1	A	170	GLN
1	A	189	SER
1	C	42	THR
1	C	61	ARG
1	C	72	ARG
1	C	87	ARG
1	C	89	GLU
1	C	93	THR
1	C	107	THR
1	C	170	GLN
1	C	189	SER
1	C	204	LYS
1	E	7	SER
1	E	61	ARG
1	E	72	ARG
1	E	89	GLU
1	E	93	THR
1	E	104	GLN
1	E	107	THR
1	E	133	SER
1	E	189	SER
1	E	204	LYS
1	G	61	ARG
1	G	87	ARG
1	G	88	SER
1	G	93	THR

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Mol	Chain	Res	Type
1	G	107	THR
1	G	135	VAL
1	G	170	GLN
1	G	189	SER
1	G	204	LYS
1	I	61	ARG
1	I	72	ARG
1	I	89	GLU
1	I	93	THR
1	I	107	THR
1	I	135	VAL
1	I	170	GLN
1	I	189	SER
2	J	1	ASP
2	J	11	LEU
2	J	94	MET
2	J	109	GLU
2	J	140	MET
2	J	146	ARG
2	J	160	ARG
2	J	203	LYS
2	J	207	SER
1	K	13	GLN
1	K	21	SER
1	K	61	ARG
1	K	86	LEU
1	K	89	GLU
1	K	96	CYS
1	K	104	GLN
1	K	106	THR
1	K	107	THR
1	K	135	VAL
1	K	170	GLN
1	K	189	SER
1	K	204	LYS
1	M	13	GLN
1	M	16	ARG
1	M	61	ARG
1	M	72	ARG
1	M	87	ARG
1	M	89	GLU
1	M	93	THR

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Mol	Chain	Res	Type
1	M	96	CYS
1	M	107	THR
1	M	135	VAL
1	M	170	GLN
1	M	189	SER
1	M	204	LYS
1	O	13	GLN
1	O	61	ARG
1	O	72	ARG
1	O	89	GLU
1	O	93	THR
1	O	107	THR
1	O	135	VAL
1	O	170	GLN
1	O	171	SER
1	O	189	SER
1	O	195	ASN
1	O	204	LYS
1	Q	43	LYS
1	Q	61	ARG
1	Q	78	THR
1	Q	96	CYS
1	Q	107	THR
1	Q	133	SER
1	Q	135	VAL
1	Q	170	GLN
1	Q	189	SER
1	Q	204	LYS
1	Q	207	LYS
1	S	13	GLN
1	S	61	ARG
1	S	89	GLU
1	S	93	THR
1	S	107	THR
1	S	114	GLU
1	S	135	VAL
1	S	170	GLN
1	S	189	SER
1	S	204	LYS
1	U	7	SER
1	U	61	ARG
1	U	89	GLU

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Mol	Chain	Res	Type
1	U	93	THR
1	U	107	THR
1	U	133	SER
1	U	135	VAL
1	U	170	GLN
1	U	189	SER
1	U	194	CYS
1	U	204	LYS
1	U	207	LYS
1	X	61	ARG
1	X	77	SER
1	X	87	ARG
1	X	93	THR
1	X	107	THR
1	X	170	GLN
1	X	180	VAL
1	X	195	ASN
2	B	1	ASP
2	B	7	THR
2	B	11	LEU
2	B	94	MET
2	B	109	GLU
2	B	140	MET
2	B	146	ARG
2	B	147	ASP
2	B	161	ASP
2	B	203	LYS
2	B	207	SER
2	D	1	ASP
2	D	11	LEU
2	D	94	MET
2	D	109	GLU
2	D	140	MET
2	D	146	ARG
2	D	147	ASP
2	D	203	LYS
2	D	207	SER
2	D	215	ARG
2	F	1	ASP
2	F	11	LEU
2	F	86	GLU
2	F	94	MET

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Mol	Chain	Res	Type
2	F	109	GLU
2	F	140	MET
2	F	146	ARG
2	F	147	ASP
2	F	151	LYS
2	F	203	LYS
2	F	207	SER
2	F	215	ARG
2	H	1	ASP
2	H	11	LEU
2	H	94	MET
2	H	109	GLU
2	H	140	MET
2	H	146	ARG
2	H	147	ASP
2	H	203	LYS
2	H	207	SER
2	H	215	ARG
2	L	11	LEU
2	L	94	MET
2	L	109	GLU
2	L	127	GLU
2	L	140	MET
2	L	146	ARG
2	L	203	LYS
2	L	211	LYS
2	L	214	ASN
2	N	1	ASP
2	N	9	PRO
2	N	11	LEU
2	N	94	MET
2	N	109	GLU
2	N	140	MET
2	N	146	ARG
2	N	211	LYS
2	N	214	ASN
2	P	1	ASP
2	P	11	LEU
2	P	94	MET
2	P	109	GLU
2	P	140	MET
2	P	146	ARG

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Mol	Chain	Res	Type
2	P	171	ASP
2	P	207	SER
2	P	212	SER
2	P	215	ARG
2	R	1	ASP
2	R	11	LEU
2	R	53	ILE
2	R	94	MET
2	R	109	GLU
2	R	140	MET
2	R	146	ARG
2	R	203	LYS
2	R	207	SER
2	R	215	ARG
2	T	1	ASP
2	T	11	LEU
2	T	74	THR
2	T	94	MET
2	T	109	GLU
2	T	140	MET
2	T	146	ARG
2	T	147	ASP
2	T	151	LYS
2	T	203	LYS
2	T	207	SER
2	T	211	LYS
2	T	215	ARG
2	V	1	ASP
2	V	11	LEU
2	V	94	MET
2	V	109	GLU
2	V	140	MET
2	V	146	ARG
2	V	151	LYS
2	V	207	SER
2	Y	1	ASP
2	Y	8	THR
2	Y	11	LEU
2	Y	21	ILE
2	Y	25	SER
2	Y	41	LEU
2	Y	53	ILE

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Mol	Chain	Res	Type
2	Y	94	MET
2	Y	109	GLU
2	Y	126	THR
2	Y	127	GLU
2	Y	129	LEU
2	Y	157	THR
2	Y	158	GLU
2	Y	159	ARG
2	Y	160	ARG
2	Y	161	ASP
2	Y	181	SER
2	Y	191	GLU
2	Y	195	LEU
2	Y	197	THR
2	Y	203	LYS
2	Y	207	SER
3	a	422	VAL
3	e	422	VAL
3	i	423	ASN
3	m	422	VAL
3	m	423	ASN
3	x	423	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	163	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 carbohydrates 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	207/252 (82%)	-0.14	0 100 100	21, 35, 49, 66	0
1	C	205/252 (81%)	-0.10	1 (0%) 91 90	20, 32, 51, 80	0
1	E	208/252 (82%)	0.03	1 (0%) 91 90	21, 37, 57, 79	0
1	G	207/252 (82%)	-0.03	1 (0%) 91 90	22, 41, 62, 84	0
1	I	205/252 (81%)	-0.12	0 100 100	23, 36, 52, 69	0
1	K	204/252 (80%)	0.38	6 (2%) 51 49	28, 48, 71, 93	0
1	M	204/252 (80%)	0.26	2 (0%) 82 81	29, 46, 63, 78	0
1	O	205/252 (81%)	0.16	3 (1%) 73 72	23, 40, 61, 75	0
1	Q	206/252 (81%)	0.43	12 (5%) 23 21	25, 46, 73, 84	0
1	S	204/252 (80%)	-0.05	1 (0%) 91 90	18, 34, 55, 78	0
1	U	205/252 (81%)	0.42	10 (4%) 29 28	24, 49, 73, 103	0
1	X	199/252 (78%)	-0.06	1 (0%) 91 90	18, 34, 54, 87	0
2	B	215/220 (97%)	0.01	2 (0%) 84 83	18, 35, 59, 74	0
2	D	216/220 (98%)	0.01	2 (0%) 84 83	18, 31, 55, 87	0
2	F	215/220 (97%)	0.01	2 (0%) 84 83	20, 34, 62, 90	0
2	H	216/220 (98%)	-0.11	1 (0%) 91 90	18, 35, 56, 69	0
2	J	215/220 (97%)	-0.06	1 (0%) 91 90	18, 33, 56, 75	0
2	L	215/220 (97%)	0.03	1 (0%) 91 90	22, 39, 57, 68	0
2	N	215/220 (97%)	0.23	3 (1%) 75 73	30, 49, 68, 80	0
2	P	215/220 (97%)	-0.11	0 100 100	23, 37, 61, 75	0
2	R	215/220 (97%)	0.41	10 (4%) 31 29	30, 54, 78, 88	0
2	T	215/220 (97%)	0.38	12 (5%) 24 23	21, 44, 76, 90	0
2	V	212/220 (96%)	0.64	21 (9%) 7 6	27, 52, 88, 106	0
2	Y	210/220 (95%)	0.04	5 (2%) 59 57	15, 33, 72, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
3	a	12/12 (100%)	-0.03	0 100 100	23, 31, 50, 79	0
3	c	11/12 (91%)	-0.06	0 100 100	25, 28, 51, 52	0
3	e	11/12 (91%)	0.08	0 100 100	23, 30, 56, 56	0
3	g	12/12 (100%)	-0.34	0 100 100	26, 30, 46, 48	0
3	i	12/12 (100%)	-0.05	0 100 100	30, 34, 50, 65	0
3	k	11/12 (91%)	0.36	0 100 100	24, 36, 58, 59	0
3	m	12/12 (100%)	0.24	0 100 100	39, 47, 69, 78	0
3	o	11/12 (91%)	0.22	0 100 100	34, 43, 59, 61	0
3	q	10/12 (83%)	0.34	0 100 100	42, 50, 56, 68	0
3	s	11/12 (91%)	0.04	0 100 100	27, 32, 45, 48	0
3	u	10/12 (83%)	0.14	0 100 100	32, 37, 40, 54	0
3	x	12/12 (100%)	-0.09	0 100 100	23, 29, 57, 59	0
All	All	5168/5808 (88%)	0.11	98 (1%) 66 65	15, 40, 67, 106	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	75	ALA	5.6
1	Q	31	ASP	4.9
2	Y	157	THR	4.3
2	H	132	GLY	4.3
2	Y	156	GLY	4.2
1	U	157	ALA	4.1
2	V	204	THR	4.0
2	V	201	VAL	3.9
2	R	85	ALA	3.7
2	V	154	ILE	3.7
2	T	131	THR	3.6
2	V	209	VAL	3.6
2	V	210	VAL	3.5
2	R	115	ALA	3.4
2	R	173	LYS	3.4
1	U	186	THR	3.4
2	V	194	ASN	3.3
2	V	8	THR	3.2
1	Q	76	LYS	3.2
1	E	75	ALA	3.1
2	T	191	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
2	V	214	ASN	3.0
1	U	170	GLN	3.0
1	U	160	SER	3.0
1	Q	56	GLY	3.0
2	V	162	GLY	2.9
2	T	195	LEU	2.9
2	D	216	ASN	2.8
1	U	213	ASN	2.8
2	R	119	VAL	2.7
1	K	80	TYR	2.7
2	V	183	LEU	2.7
2	V	195	LEU	2.7
1	Q	26	GLY	2.7
1	Q	28	THR	2.7
2	V	173	LYS	2.6
1	Q	2	VAL	2.6
2	T	196	TYR	2.6
1	S	170	GLN	2.6
2	V	207	SER	2.5
2	R	134	ALA	2.5
2	R	206	SER	2.5
2	V	7	THR	2.5
2	V	196	TYR	2.5
1	O	76	LYS	2.5
1	Q	66	GLY	2.5
2	V	132	GLY	2.5
2	B	210	VAL	2.5
2	T	130	ALA	2.5
2	N	1	ASP	2.5
1	K	190	GLN	2.5
1	K	14	PRO	2.4
2	V	160	ARG	2.4
1	G	213	ASN	2.4
2	T	155	ASP	2.4
1	Q	75	ALA	2.3
2	Y	7	THR	2.3
1	U	155	SER	2.3
2	V	158	GLU	2.3
2	T	156	GLY	2.3
2	Y	9	PRO	2.3
1	K	20	LEU	2.3
2	T	188	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	Q	3	LYS	2.3
1	M	32	SER	2.3
2	L	195	LEU	2.3
2	T	185	LEU	2.3
2	Y	193	HIS	2.3
1	X	171	SER	2.3
2	T	204	THR	2.2
2	J	133	GLY	2.2
2	R	213	PHE	2.2
2	V	134	ALA	2.2
2	D	207	SER	2.2
1	U	210	VAL	2.2
1	Q	25	SER	2.2
1	Q	185	SER	2.2
1	O	5	GLN	2.2
2	N	27	GLN	2.2
2	V	159	ARG	2.1
2	N	161	ASP	2.1
2	F	134	ALA	2.1
2	R	7	THR	2.1
1	C	170	GLN	2.1
2	B	192	SER	2.1
1	Q	4	LEU	2.1
1	K	67	ARG	2.1
2	V	153	LYS	2.1
1	U	209	ILE	2.0
2	T	154	ILE	2.0
2	R	132	GLY	2.0
1	O	2	VAL	2.0
1	M	3	LYS	2.0
2	T	88	LEU	2.0
1	U	189	SER	2.0
2	R	205	SER	2.0
1	U	18	LEU	2.0
2	F	129	LEU	2.0

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 [i](#)

There are no carbohydrates 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.