



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:38 PM UTC

PDB ID : 4E41 / pdb\_00004e41  
Title : Structural basis for the recognition of mutant self by a tumor-specific, MHC class II-restricted T cell receptor G4  
Authors : Deng, L.; Langley, R.J.; Wang, Q.; Topalian, S.L.; Mariuzza, R.A.  
Deposited on : 2012-03-11  
Resolution : 2.60 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](mailto: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>.

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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

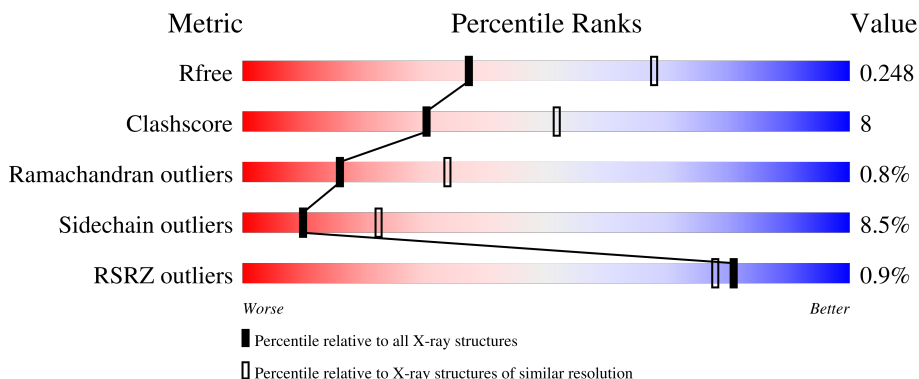
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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.





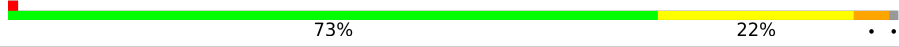
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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  $\geq 3$ , 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	182	<div style="display: flex; align-items: center;"> <div style="width: 81%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">81%</div> <div style="width: 16%; height: 10px; background: linear-gradient(to right, yellow, green);"></div> <div style="margin-left: 10px;">16%</div> <div style="width: 3%; height: 10px; background-color: grey;"></div> <div style="margin-left: 10px;">..</div> </div>
1	F	182	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red;"></div> <div style="margin-left: 5px;">%</div> <div style="width: 74%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">74%</div> <div style="width: 19%; height: 10px; background: linear-gradient(to right, yellow, green);"></div> <div style="margin-left: 10px;">19%</div> <div style="width: 5%; height: 10px; background: linear-gradient(to right, orange, yellow, green);"></div> <div style="margin-left: 10px;">5%</div> <div style="width: 1%; height: 10px; background-color: grey;"></div> <div style="margin-left: 10px;">.</div> </div>
2	B	190	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red;"></div> <div style="margin-left: 5px;">%</div> <div style="width: 72%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">72%</div> <div style="width: 20%; height: 10px; background: linear-gradient(to right, yellow, green);"></div> <div style="margin-left: 10px;">20%</div> <div style="width: 6%; height: 10px; background: linear-gradient(to right, orange, yellow, green);"></div> <div style="margin-left: 10px;">.. 6%</div> </div>
2	G	190	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red;"></div> <div style="margin-left: 5px;">2%</div> <div style="width: 67%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">67%</div> <div style="width: 23%; height: 10px; background: linear-gradient(to right, yellow, green);"></div> <div style="margin-left: 10px;">23%</div> <div style="width: 7%; height: 10px; background: linear-gradient(to right, orange, yellow, green);"></div> <div style="margin-left: 10px;">.. 7%</div> </div>
3	C	15	<div style="display: flex; align-items: center;"> <div style="width: 7%; height: 10px; background-color: red;"></div> <div style="margin-left: 5px;">7%</div> <div style="width: 67%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">67%</div> <div style="width: 27%; height: 10px; background: linear-gradient(to right, yellow, green);"></div> <div style="margin-left: 10px;">27%</div> <div style="width: 7%; height: 10px; background: linear-gradient(to right, orange, yellow, green);"></div> <div style="margin-left: 10px;">7%</div> </div>

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Mol	Chain	Length	Quality of chain
3	H	15	 60% 33% 7%
4	D	203	 % 67% 17% 11%
4	I	203	 73% 17% 6%
5	E	239	 % 73% 22% 6%
5	J	239	 75% 21% 6%

## 2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 12983 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 HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	179	1473	954	239	275	5	0	0	0
1	F	179	1473	954	239	275	5	0	0	0

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	179	1468	926	261	275	6	0	0	0
2	G	177	1450	915	256	273	6	0	0	0

- Molecule 3 is a protein called Triosephosphate isomerase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	15	104	66	17	21	0	0	0
3	H	15	104	66	17	21	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	28	ILE	THR	conflict	UNP P60174
H	28	ILE	THR	conflict	UNP P60174

- Molecule 4 is a protein called T cell receptor G4 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	181	1432	903	240	282	7	0	1	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	I	190	Total	C	N	O	S	0	0	0
			1497	940	252	298	7			

- Molecule 5 is a protein called T cell receptor G4 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	236	Total	C	N	O	S	0	0	0
			1898	1200	334	359	5			
5	J	238	Total	C	N	O	S	0	0	0
			1910	1208	336	361	5			

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Na	0	0
			1	1		
6	B	1	Total	Na	0	0
			1	1		


- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	26	Total	O	0	0
			26	26		
7	B	20	Total	O	0	0
			20	20		
7	C	1	Total	O	0	0
			1	1		
7	D	22	Total	O	0	0
			22	22		
7	E	13	Total	O	0	0
			13	13		
7	F	21	Total	O	0	0
			21	21		
7	G	21	Total	O	0	0
			21	21		
7	H	4	Total	O	0	0
			4	4		
7	I	26	Total	O	0	0
			26	26		
7	J	18	Total	O	0	0
			18	18		

### 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 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.

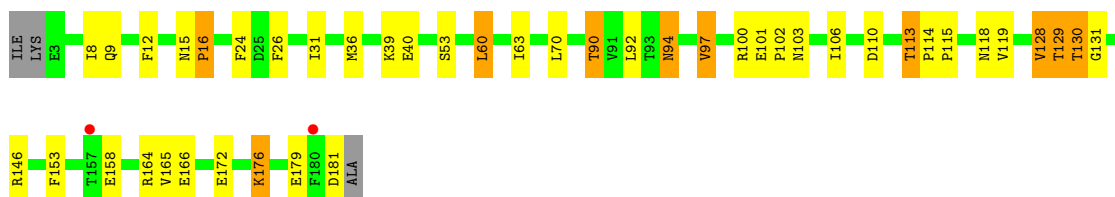
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

Chain A: 



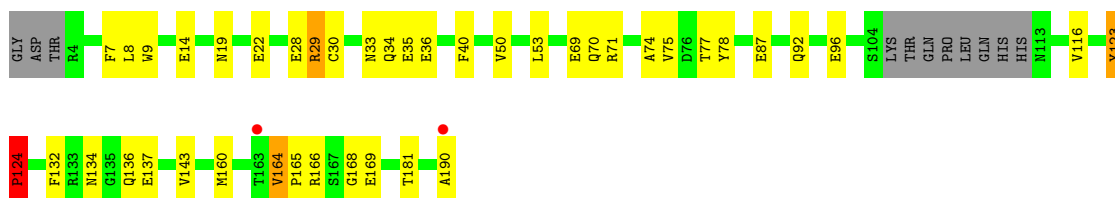
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

Chain F: 



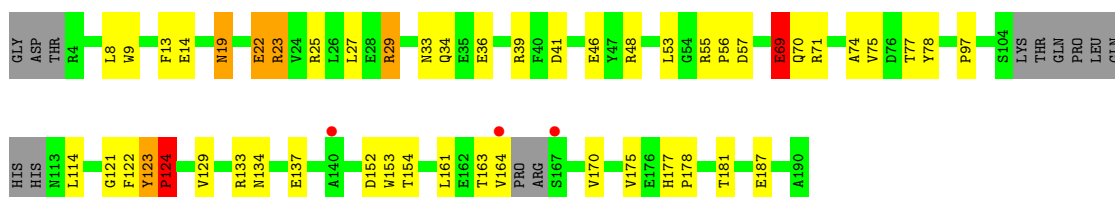
- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain

Chain B: 

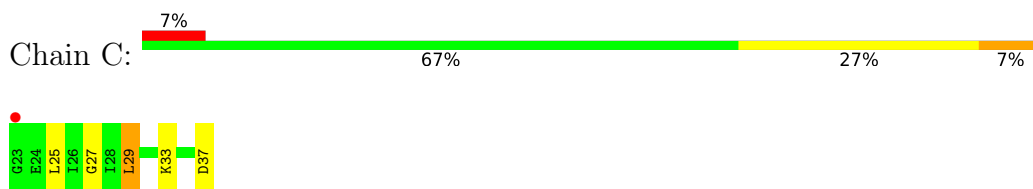


- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain

Chain G: 



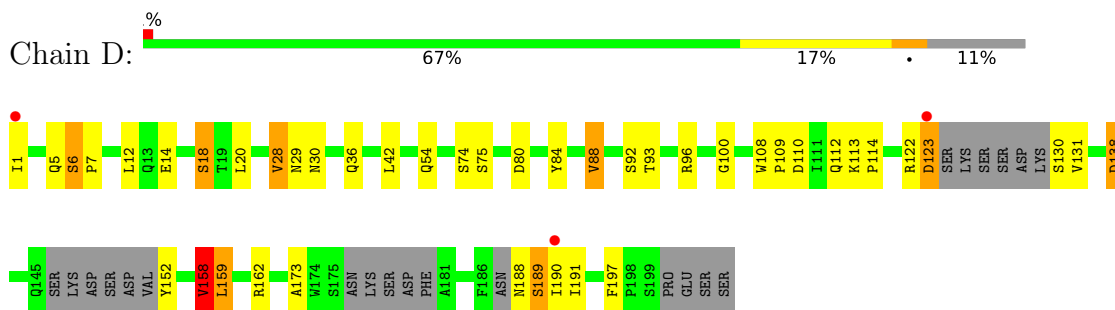
- Molecule 3: Triosephosphate isomerase



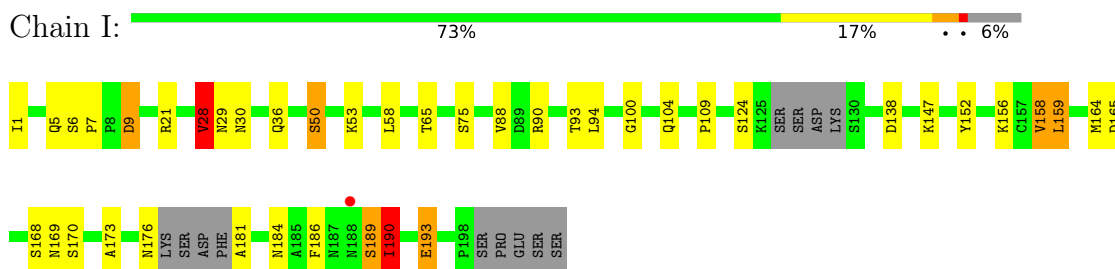
- Molecule 3: Triosephosphate isomerase



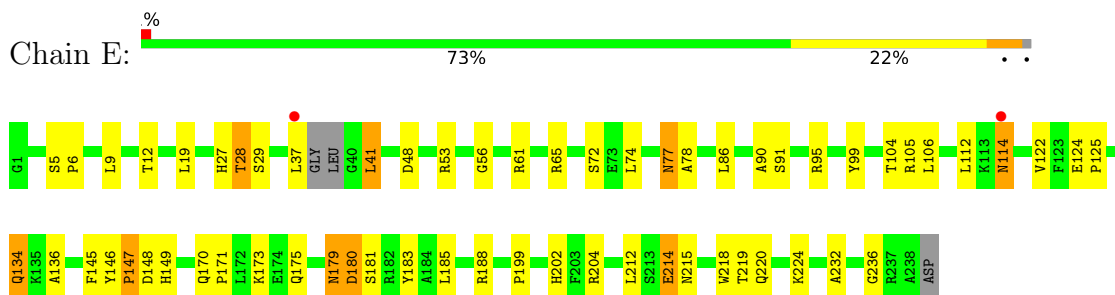
- Molecule 4: T cell receptor G4 alpha chain



- Molecule 4: T cell receptor G4 alpha chain

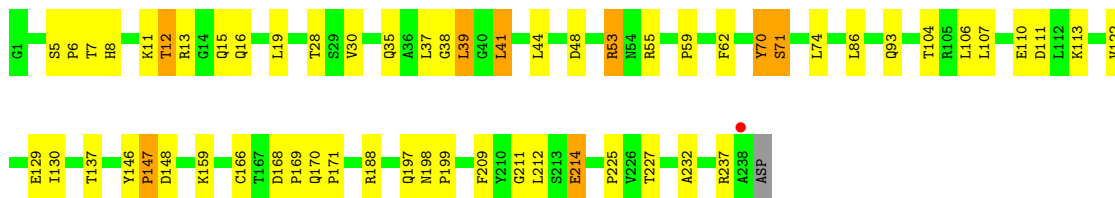


- Molecule 5: T cell receptor G4 beta chain



- Molecule 5: T cell receptor G4 beta chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.13Å 175.61Å 88.65Å 90.00° 110.75° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 30.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.2 (30.00-2.60) 97.2 (30.00-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 2.42Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.197 , 0.264 (Not available) , 0.248	Depositor DCC
$R_{free}$ test set	3102 reflections (4.46%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.2	Xtrriage
Anisotropy	0.266	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 32.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12983	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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

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	0.72	2/1518 (0.1%)	1.16	5/2070 (0.2%)
1	F	0.75	1/1518 (0.1%)	0.99	5/2070 (0.2%)
2	B	0.69	1/1504 (0.1%)	0.92	2/2041 (0.1%)
2	G	0.67	0/1484	0.92	4/2012 (0.2%)
3	C	0.79	0/104	0.98	0/139
3	H	0.79	0/104	0.95	0/139
4	D	0.76	2/1468 (0.1%)	0.95	2/1995 (0.1%)
4	I	0.70	0/1530	0.91	3/2081 (0.1%)
5	E	0.74	2/1951 (0.1%)	0.98	5/2658 (0.2%)
5	J	0.76	3/1964 (0.2%)	0.96	4/2677 (0.1%)
All	All	0.73	11/13145 (0.1%)	0.98	30/17882 (0.2%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	15	ASN	C-O	-6.41	1.17	1.24
5	J	5	SER	C-O	-6.21	1.18	1.24
1	A	16	PRO	N-CD	5.66	1.55	1.47
4	D	6	SER	C-O	-5.63	1.18	1.24
4	D	7	PRO	N-CD	5.50	1.55	1.47
1	F	16	PRO	N-CD	5.42	1.55	1.47
5	E	147	PRO	N-CD	5.25	1.55	1.47
5	E	6	PRO	N-CD	5.24	1.55	1.47
2	B	124	PRO	N-CD	5.04	1.54	1.47
5	J	6	PRO	N-CD	5.04	1.54	1.47
5	J	147	PRO	N-CD	5.03	1.54	1.47

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	THR	CA-C-N	18.48	171.35	127.00
1	A	113	THR	C-N-CA	18.48	171.35	127.00
1	A	113	THR	C-N-CD	-18.40	80.12	120.60
1	F	128	VAL	N-CA-C	11.87	121.58	110.42
5	J	5	SER	C-N-CD	8.55	139.42	120.60
5	J	146	TYR	C-N-CD	8.50	139.29	120.60
5	E	146	TYR	C-N-CD	8.34	138.95	120.60
5	E	5	SER	C-N-CD	8.29	138.85	120.60
4	I	6	SER	C-N-CD	8.14	138.51	120.60
1	F	113	THR	C-N-CD	8.13	138.49	120.60
2	G	123	TYR	C-N-CD	8.04	138.28	120.60
1	F	15	ASN	C-N-CD	7.92	138.03	120.60
1	A	15	ASN	C-N-CD	7.90	137.99	120.60
2	B	123	TYR	C-N-CD	7.82	137.81	120.60
4	D	6	SER	C-N-CD	7.69	137.53	120.60
5	E	77	ASN	N-CA-C	6.89	121.54	112.72
5	E	175	GLN	CA-C-N	6.35	126.56	119.32
5	E	175	GLN	C-N-CA	6.35	126.56	119.32
4	I	190	ILE	CB-CA-C	5.42	117.08	111.23
4	D	158	VAL	CB-CA-C	-5.30	104.31	111.63
1	F	97	VAL	N-CA-C	5.29	115.87	108.89
2	G	69	GLU	CA-C-N	5.27	127.29	120.44
2	G	69	GLU	C-N-CA	5.27	127.29	120.44
1	F	40	GLU	N-CA-C	5.25	117.06	109.07
2	G	124	PRO	CA-N-CD	-5.25	104.15	111.50
4	I	28	VAL	CB-CA-C	5.21	117.45	110.42
1	A	159	ASP	N-CA-C	5.17	117.71	109.96
5	J	59	PRO	CA-C-N	5.14	126.27	119.84
5	J	59	PRO	C-N-CA	5.14	126.27	119.84
2	B	50	VAL	N-CA-C	-5.07	106.73	111.45

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	1473	0	1407	13	0
1	F	1473	0	1407	28	0
2	B	1468	0	1402	22	0
2	G	1450	0	1381	39	0
3	C	104	0	109	3	0
3	H	104	0	109	6	0
4	D	1432	0	1357	29	0
4	I	1497	0	1420	32	0
5	E	1898	0	1805	30	0
5	J	1910	0	1820	31	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	26	0	0	1	0
7	B	20	0	0	0	0
7	C	1	0	0	0	0
7	D	22	0	0	1	0
7	E	13	0	0	2	0
7	F	21	0	0	0	0
7	G	21	0	0	0	0
7	H	4	0	0	0	0
7	I	26	0	0	4	0
7	J	18	0	0	1	0
All	All	12983	0	12217	210	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 8.

All (210) 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)
4:I:36:GLN:HE22	5:J:35:GLN:HE22	1.15	0.89
2:G:8:LEU:H	2:G:33:ASN:ND2	1.74	0.85
5:J:237:ARG:HH11	5:J:237:ARG:HB2	1.42	0.84
4:I:109:PRO:HD3	4:I:158:VAL:HG11	1.61	0.83
4:I:158:VAL:HG13	4:I:169:ASN:ND2	1.99	0.78
5:J:53:ARG:HG3	5:J:53:ARG:HH11	1.52	0.74
2:G:133:ARG:NH2	2:G:163:THR:HG21	2.04	0.73
5:J:70:TYR:O	5:J:71:SER:HB3	1.89	0.73
1:A:8:ILE:HG12	2:B:14:GLU:HG2	1.70	0.73
5:J:237:ARG:HB2	5:J:237:ARG:NH1	2.03	0.72
2:G:23:ARG:HG3	2:G:23:ARG:HH11	1.54	0.72
2:G:70:GLN:HE22	2:G:71:ARG:HH11	1.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:128:VAL:O	1:F:129:THR:HB	1.89	0.71
5:J:122:VAL:HG23	5:J:232:ALA:HB3	1.71	0.71
2:G:46:GLU:OE2	2:G:48:ARG:NH1	2.23	0.71
2:G:8:LEU:H	2:G:33:ASN:HD21	1.37	0.70
5:J:148:ASP:OD1	5:J:171:PRO:HG3	1.92	0.69
5:E:122:VAL:HG23	5:E:232:ALA:HB3	1.72	0.69
5:J:168:ASP:CG	5:J:188:ARG:HH22	2.00	0.69
4:D:1:ILE:N	7:D:309:HOH:O	2.26	0.68
2:G:23:ARG:HH11	2:G:23:ARG:CG	2.06	0.67
5:E:19:LEU:HD22	5:E:104:THR:HG21	1.77	0.67
5:J:28:THR:HG23	5:J:48:ASP:OD1	1.95	0.66
5:E:61:ARG:HD2	5:E:78:ALA:H	1.61	0.66
4:I:158:VAL:HG13	4:I:169:ASN:HD22	1.60	0.66
5:E:179:ASN:O	5:E:180:ASP:HB3	1.95	0.66
5:E:105:ARG:HD3	7:E:305:HOH:O	1.97	0.65
4:D:93:THR:HG21	4:D:96:ARG:HD2	1.78	0.64
2:G:22:GLU:HG3	2:G:23:ARG:N	2.12	0.64
1:F:8:ILE:HG12	2:G:14:GLU:HG2	1.78	0.64
4:I:109:PRO:CD	4:I:158:VAL:HG11	2.25	0.64
4:I:158:VAL:CG1	4:I:169:ASN:ND2	2.60	0.64
2:B:70:GLN:HG3	4:D:29:ASN:HD21	1.62	0.63
1:A:114:PRO:HD2	1:A:167:HIS:HE2	1.63	0.63
5:E:28:THR:HG23	5:E:48:ASP:OD1	1.98	0.63
1:F:118:ASN:HB2	1:F:166:GLU:HB2	1.80	0.62
4:I:28:VAL:HG21	4:I:88:VAL:HB	1.82	0.62
2:G:70:GLN:HE22	2:G:71:ARG:NH1	1.97	0.61
5:J:53:ARG:HG3	5:J:53:ARG:NH1	2.12	0.61
2:G:69:GLU:OE1	4:I:53:LYS:CE	2.50	0.60
2:G:133:ARG:HH22	2:G:163:THR:CG2	2.15	0.60
2:G:70:GLN:HG3	4:I:29:ASN:HD21	1.65	0.59
2:B:70:GLN:HE22	2:B:71:ARG:HH11	1.49	0.59
5:J:111:ASP:OD1	5:J:113:LYS:HG2	2.01	0.59
2:G:25:ARG:NH2	2:G:41:ASP:OD2	2.34	0.59
4:I:1:ILE:N	7:I:322:HOH:O	2.36	0.59
4:I:109:PRO:HG3	4:I:158:VAL:CG1	2.32	0.59
1:F:26:PHE:HB2	1:F:31:ILE:HD11	1.84	0.58
2:G:133:ARG:NH2	2:G:163:THR:CG2	2.66	0.58
1:F:114:PRO:HB2	1:F:115:PRO:HD2	1.84	0.58
1:A:95:SER:HB2	1:A:96:PRO:CD	2.34	0.58
2:G:129:VAL:HG22	2:G:175:VAL:HG22	1.86	0.58
4:I:109:PRO:HG3	4:I:158:VAL:HG11	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:29:ASN:HD22	4:D:30:ASN:HD22	1.52	0.58
5:E:112:LEU:HD13	5:E:212:LEU:HD22	1.85	0.57
4:D:36:GLN:HB2	4:D:42:LEU:HD23	1.86	0.57
4:I:156:LYS:HA	4:I:170:SER:O	2.04	0.57
2:B:70:GLN:HE22	2:B:71:ARG:NH1	2.04	0.56
4:D:28:VAL:HG22	4:D:88:VAL:HG13	1.87	0.55
1:F:100:ARG:O	1:F:100:ARG:HG2	2.07	0.55
4:D:188:ASN:CG	4:D:189:SER:H	2.12	0.55
4:I:170:SER:OG	5:J:188:ARG:HD2	2.07	0.55
2:B:70:GLN:NE2	2:B:71:ARG:HH11	2.05	0.55
5:E:173:LYS:HE2	5:E:181:SER:HB3	1.89	0.55
4:D:188:ASN:ND2	4:D:189:SER:H	2.04	0.55
5:J:212:LEU:HD12	5:J:225:PRO:HD2	1.88	0.55
4:I:28:VAL:CG2	4:I:88:VAL:HB	2.37	0.55
2:B:8:LEU:H	2:B:33:ASN:ND2	2.05	0.54
1:F:130:THR:HG23	1:F:131:GLY:N	2.23	0.54
5:J:11:LYS:HE3	5:J:16:GLN:O	2.07	0.54
5:E:65:ARG:O	5:E:72:SER:HB2	2.08	0.54
1:F:36:MET:CE	1:F:63:ILE:HG13	2.37	0.54
1:F:94:ASN:HB3	1:F:106:ILE:HD11	1.89	0.53
2:G:133:ARG:HG2	2:G:134:ASN:HD22	1.71	0.53
1:F:53:SER:HB2	3:H:25:LEU:HD13	1.89	0.53
1:A:12:PHE:CD1	1:A:12:PHE:C	2.87	0.53
2:B:134:ASN:HD21	2:B:169:GLU:HG2	1.74	0.53
2:B:29:ARG:HD2	2:B:36:GLU:OE2	2.09	0.52
5:E:112:LEU:HD13	5:E:212:LEU:CD2	2.39	0.52
1:F:90:THR:HA	1:F:176:LYS:HD2	1.91	0.52
2:G:57:ASP:OD1	3:H:35:PRO:HD2	2.08	0.52
5:J:41:LEU:N	5:J:41:LEU:HD23	2.25	0.52
4:I:109:PRO:CG	4:I:158:VAL:HG11	2.40	0.52
4:I:158:VAL:CG1	4:I:169:ASN:HD22	2.22	0.52
2:B:70:GLN:HG3	4:D:29:ASN:ND2	2.25	0.52
4:D:12:LEU:HD11	4:D:18:SER:OG	2.10	0.52
2:G:23:ARG:CG	2:G:23:ARG:NH1	2.69	0.51
2:G:69:GLU:OE1	4:I:53:LYS:NZ	2.41	0.51
1:F:128:VAL:HG13	1:F:129:THR:N	2.25	0.51
1:F:158:GLU:OE1	1:F:158:GLU:N	2.44	0.50
2:G:133:ARG:HH22	2:G:163:THR:HG22	1.75	0.50
5:J:19:LEU:HD22	5:J:104:THR:HG21	1.93	0.50
5:J:129:GLU:OE2	5:J:137:THR:OG1	2.26	0.50
1:A:114:PRO:HD2	1:A:167:HIS:NE2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:CYS:HB2	1:A:121:TRP:CH2	2.47	0.50
5:J:12:THR:O	5:J:15:GLN:HB2	2.12	0.50
4:D:29:ASN:ND2	4:D:30:ASN:HD22	2.09	0.49
2:G:13:PHE:CD1	3:H:29:LEU:HD23	2.46	0.49
2:G:27:LEU:HD11	2:G:39:ARG:HD3	1.94	0.49
2:G:121:GLY:HA2	2:G:154:THR:HB	1.94	0.49
4:D:109:PRO:HG3	4:D:158:VAL:HG13	1.94	0.49
4:I:186:PHE:O	4:I:189:SER:HB2	2.12	0.49
2:B:116:VAL:HG22	2:B:160:MET:HG2	1.95	0.49
2:G:187:GLU:N	2:G:187:GLU:CD	2.71	0.49
4:I:181:ALA:HB3	4:I:184:ASN:HD21	1.77	0.49
4:D:189:SER:O	4:D:191:ILE:N	2.46	0.49
1:A:9:GLN:HB2	1:A:24:PHE:CZ	2.48	0.49
5:J:214:GLU:HA	7:J:314:HOH:O	2.13	0.48
5:E:125:PRO:HG3	5:E:136:ALA:HB1	1.96	0.48
2:G:74:ALA:HA	2:G:77:THR:OG1	2.14	0.48
5:J:198:ASN:C	5:J:198:ASN:ND2	2.72	0.48
4:D:29:ASN:HD22	4:D:30:ASN:ND2	2.10	0.47
5:E:61:ARG:HD2	5:E:78:ALA:N	2.26	0.47
5:E:134:GLN:HE21	5:E:134:GLN:HA	1.79	0.47
5:E:145:PHE:CE1	5:E:183:TYR:HB2	2.48	0.47
2:B:19:ASN:HB3	2:B:22:GLU:HG2	1.97	0.47
5:E:148:ASP:OD1	5:E:171:PRO:HG3	2.14	0.47
5:J:7:THR:HB	5:J:8:HIS:HD2	1.80	0.47
4:D:28:VAL:CG2	4:D:88:VAL:HG13	2.44	0.47
1:F:110:ASP:OD1	1:F:146:ARG:HG2	2.15	0.47
1:A:158:GLU:HG3	7:A:323:HOH:O	2.14	0.46
5:E:41:LEU:N	5:E:41:LEU:HD23	2.29	0.46
4:D:108:TRP:HB3	4:D:109:PRO:HD2	1.97	0.46
2:G:22:GLU:HG3	2:G:23:ARG:H	1.76	0.46
5:J:7:THR:HB	5:J:8:HIS:CD2	2.50	0.46
2:B:87:GLU:OE2	2:B:92:GLN:NE2	2.49	0.46
2:B:132:PHE:CE2	2:B:137:GLU:HG2	2.51	0.46
3:C:33:LYS:NZ	5:E:48:ASP:OD2	2.49	0.46
1:A:122:LEU:HB2	1:A:162:ASP:HB2	1.97	0.46
5:J:55:ARG:NH2	5:J:62:PHE:O	2.42	0.46
1:F:9:GLN:HB2	1:F:24:PHE:CZ	2.50	0.46
1:A:45:LEU:HD12	1:A:48:PHE:CZ	2.50	0.46
4:D:5:GLN:HE21	4:D:100:GLY:HA3	1.81	0.46
4:I:152:TYR:O	4:I:173:ALA:HA	2.16	0.45
2:B:123:TYR:CG	2:B:124:PRO:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:159:LEU:HB3	5:J:166:CYS:HB2	1.96	0.45
3:H:30:ASN:HB3	4:I:94:LEU:HD21	1.99	0.45
5:E:27:HIS:HD2	5:E:91:SER:OG	2.00	0.45
1:F:103:ASN:HB3	1:F:153:PHE:CE1	2.52	0.45
4:I:190:ILE:HD12	4:I:190:ILE:HA	1.88	0.45
5:E:105:ARG:CD	7:E:305:HOH:O	2.62	0.44
4:D:159:LEU:HD23	4:D:159:LEU:O	2.17	0.44
1:F:114:PRO:HB2	1:F:115:PRO:CD	2.47	0.44
1:F:101:GLU:HG2	1:F:102:PRO:HD2	2.00	0.44
4:I:159:LEU:HD12	7:I:302:HOH:O	2.18	0.44
5:E:199:PRO:HA	5:E:236:GLY:O	2.17	0.44
1:F:130:THR:CG2	1:F:131:GLY:N	2.81	0.44
2:G:114:LEU:HD12	2:G:161:LEU:O	2.17	0.44
2:G:19:ASN:O	2:G:22:GLU:HG2	2.18	0.43
5:J:198:ASN:HD22	5:J:199:PRO:CD	2.31	0.43
5:J:209:PHE:O	5:J:227:THR:HA	2.18	0.43
1:F:12:PHE:CD1	1:F:12:PHE:C	2.97	0.43
2:G:70:GLN:HG3	4:I:29:ASN:ND2	2.33	0.43
1:A:11:GLU:HA	1:A:21:GLU:O	2.18	0.43
4:D:112:GLN:O	4:D:114:PRO:HD3	2.17	0.43
1:F:39:LYS:HG2	1:F:60:LEU:HD21	1.99	0.43
1:F:179:GLU:HG3	1:F:181:ASP:HB3	1.99	0.43
2:G:78:TYR:CD2	3:H:29:LEU:HD22	2.53	0.43
1:A:92:LEU:HD12	1:A:93:THR:H	1.84	0.43
2:B:164:VAL:HA	2:B:165:PRO:HD3	1.90	0.43
2:B:168:GLY:H	2:B:190:ALA:HA	1.82	0.43
3:C:27:GLY:HA2	4:D:92:SER:HA	2.01	0.43
1:F:36:MET:HE3	1:F:63:ILE:HG13	2.00	0.43
2:G:29:ARG:HD2	2:G:36:GLU:OE2	2.19	0.43
4:D:80:ASP:O	4:D:84:TYR:OH	2.33	0.43
5:E:218:TRP:HB2	5:E:224:LYS:HE3	2.01	0.43
1:F:70:LEU:HD13	2:G:9:TRP:HB2	2.00	0.43
5:J:197:GLN:HG2	5:J:237:ARG:O	2.19	0.43
5:J:198:ASN:C	5:J:198:ASN:HD22	2.27	0.43
4:D:96:ARG:HH21	5:E:56:GLY:HA2	1.83	0.43
1:F:119:VAL:HG22	1:F:165:VAL:HG22	2.01	0.43
4:D:138:ASP:OD1	4:D:138:ASP:C	2.62	0.42
4:I:9:ASP:HB2	4:I:104:GLN:HB2	2.01	0.42
4:I:21:ARG:NH2	7:I:325:HOH:O	2.51	0.42
1:A:93:THR:HG22	1:A:105:LEU:HD23	2.00	0.42
1:F:119:VAL:HA	1:F:164:ARG:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:168:ASP:HA	5:J:169:PRO:HD3	1.87	0.42
4:D:74:SER:O	4:D:75:SER:C	2.62	0.42
4:D:159:LEU:HD23	4:D:159:LEU:C	2.45	0.42
5:E:147:PRO:C	5:E:149:HIS:H	2.28	0.42
4:I:5:GLN:HE21	4:I:100:GLY:HA3	1.85	0.42
2:G:97:PRO:HB3	2:G:122:PHE:HB3	2.00	0.42
2:B:9:TRP:CH2	2:B:30:CYS:HB3	2.55	0.42
5:E:37:LEU:HD12	5:E:37:LEU:H	1.84	0.41
5:E:114:ASN:OD1	5:E:114:ASN:N	2.53	0.41
1:F:36:MET:HE1	1:F:63:ILE:HG13	2.01	0.41
5:E:90:ALA:HA	5:E:99:TYR:O	2.20	0.41
2:G:152:ASP:O	2:G:153:TRP:HB2	2.19	0.41
4:I:159:LEU:HD13	4:I:168:SER:O	2.20	0.41
2:G:123:TYR:CG	2:G:124:PRO:HA	2.54	0.41
4:D:123:ASP:OD1	4:D:123:ASP:N	2.52	0.41
3:H:36:ALA:O	3:H:37:ASP:HB2	2.19	0.41
5:E:202:HIS:HE1	5:E:204:ARG:NH2	2.18	0.41
5:J:38:GLY:O	5:J:39:LEU:O	2.38	0.41
4:D:110:ASP:OD1	4:D:112:GLN:HG2	2.21	0.41
2:G:177:HIS:CD2	2:G:178:PRO:HD2	2.56	0.41
4:D:29:ASN:ND2	5:E:95:ARG:HD2	2.35	0.41
4:D:152:TYR:O	4:D:173:ALA:HA	2.20	0.41
2:B:28:GLU:HB3	2:B:40:PHE:HB3	2.03	0.41
2:B:74:ALA:HA	2:B:77:THR:OG1	2.21	0.41
2:B:143:VAL:O	2:B:160:MET:HE3	2.21	0.41
2:B:78:TYR:CD2	3:C:29:LEU:HD22	2.57	0.41
5:J:209:PHE:CE2	5:J:211:GLY:HA3	2.56	0.40
1:F:113:THR:OG1	1:F:114:PRO:HA	2.22	0.40
2:B:7:PHE:HA	2:B:33:ASN:HD21	1.87	0.40
5:E:214:GLU:HG3	5:E:215:ASN:ND2	2.37	0.40
2:G:55:ARG:HB3	2:G:56:PRO:HD3	2.03	0.40
4:I:50:SER:HB2	7:I:310:HOH:O	2.20	0.40
5:E:171:PRO:HB3	5:E:185:LEU:HD13	2.01	0.40
2:G:69:GLU:OE1	4:I:53:LYS:HE2	2.21	0.40

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	177/182 (97%)	169 (96%)	8 (4%)	0	100	100
1	F	177/182 (97%)	169 (96%)	8 (4%)	0	100	100
2	B	175/190 (92%)	166 (95%)	8 (5%)	1 (1%)	21	42
2	G	171/190 (90%)	158 (92%)	11 (6%)	2 (1%)	10	23
3	C	13/15 (87%)	13 (100%)	0	0	100	100
3	H	13/15 (87%)	12 (92%)	1 (8%)	0	100	100
4	D	172/203 (85%)	159 (92%)	11 (6%)	2 (1%)	10	23
4	I	184/203 (91%)	179 (97%)	4 (2%)	1 (0%)	24	46
5	E	232/239 (97%)	215 (93%)	14 (6%)	3 (1%)	9	21
5	J	236/239 (99%)	221 (94%)	12 (5%)	3 (1%)	9	21
All	All	1550/1658 (94%)	1461 (94%)	77 (5%)	12 (1%)	16	34

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	190	ILE
5	E	180	ASP
5	J	39	LEU
5	J	71	SER
5	E	214	GLU
5	J	70	TYR
4	I	193	GLU
2	G	124	PRO
4	D	131	VAL
5	E	179	ASN
2	G	19	ASN
2	B	124	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	164/166 (99%)	154 (94%)	10 (6%)	17	37
1	F	164/166 (99%)	154 (94%)	10 (6%)	17	37
2	B	161/171 (94%)	149 (92%)	12 (8%)	12	28
2	G	159/171 (93%)	148 (93%)	11 (7%)	14	32
3	C	10/10 (100%)	7 (70%)	3 (30%)	0	0
3	H	10/10 (100%)	9 (90%)	1 (10%)	7	16
4	D	163/184 (89%)	145 (89%)	18 (11%)	6	13
4	I	171/184 (93%)	150 (88%)	21 (12%)	4	9
5	E	206/208 (99%)	189 (92%)	17 (8%)	10	23
5	J	207/208 (100%)	189 (91%)	18 (9%)	9	21
All	All	1415/1478 (96%)	1294 (91%)	121 (9%)	10	22

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	PRO
1	A	53	SER
1	A	97	VAL
1	A	105	LEU
1	A	120	THR
1	A	141	GLU
1	A	154	LEU
1	A	160	VAL
1	A	175	LEU
1	A	177	HIS
2	B	29	ARG
2	B	34	GLN
2	B	35	GLU
2	B	53	LEU
2	B	69	GLU
2	B	75	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	96	GLU
2	B	124	PRO
2	B	136	GLN
2	B	164	VAL
2	B	166	ARG
2	B	181	THR
3	C	25	LEU
3	C	29	LEU
3	C	37	ASP
4	D	6	SER
4	D	14	GLU
4	D	18	SER
4	D	20	LEU
4	D	28	VAL
4	D	54[A]	GLN
4	D	54[B]	GLN
4	D	88	VAL
4	D	113	LYS
4	D	122	ARG
4	D	123	ASP
4	D	130	SER
4	D	138	ASP
4	D	158	VAL
4	D	159	LEU
4	D	162	ARG
4	D	189	SER
4	D	197	PHE
5	E	9	LEU
5	E	12	THR
5	E	28	THR
5	E	29	SER
5	E	41	LEU
5	E	53	ARG
5	E	74	LEU
5	E	77	ASN
5	E	86	LEU
5	E	106	LEU
5	E	114	ASN
5	E	124	GLU
5	E	134	GLN
5	E	170	GLN
5	E	188	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
5	E	219	THR
5	E	220	GLN
1	F	16	PRO
1	F	60	LEU
1	F	90	THR
1	F	92	LEU
1	F	94	ASN
1	F	97	VAL
1	F	129	THR
1	F	130	THR
1	F	172	GLU
1	F	176	LYS
2	G	22	GLU
2	G	23	ARG
2	G	29	ARG
2	G	34	GLN
2	G	53	LEU
2	G	69	GLU
2	G	75	VAL
2	G	137	GLU
2	G	164	VAL
2	G	170	VAL
2	G	181	THR
3	H	29	LEU
4	I	7	PRO
4	I	9	ASP
4	I	28	VAL
4	I	30	ASN
4	I	50	SER
4	I	58	LEU
4	I	65	THR
4	I	75	SER
4	I	90	ARG
4	I	93	THR
4	I	124	SER
4	I	138	ASP
4	I	147	LYS
4	I	158	VAL
4	I	159	LEU
4	I	164	MET
4	I	165	ASP
4	I	176	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	I	189	SER
4	I	190	ILE
4	I	193	GLU
5	J	12	THR
5	J	13	ARG
5	J	30	VAL
5	J	37	LEU
5	J	41	LEU
5	J	44	LEU
5	J	53	ARG
5	J	74	LEU
5	J	86	LEU
5	J	93	GLN
5	J	106	LEU
5	J	107	LEU
5	J	110	GLU
5	J	130	ILE
5	J	147	PRO
5	J	159	LYS
5	J	170	GLN
5	J	214	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	18	GLN
1	A	84	ASN
1	A	149	HIS
1	A	177	HIS
2	B	33	ASN
2	B	70	GLN
2	B	134	ASN
2	B	136	GLN
2	B	150	ASN
2	B	156	GLN
4	D	5	GLN
4	D	29	ASN
4	D	36	GLN
4	D	104	GLN
4	D	169	ASN
4	D	184	ASN
4	D	188	ASN

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Mol	Chain	Res	Type
5	E	16	GLN
5	E	27	HIS
5	E	35	GLN
5	E	75	ASN
5	E	93	GLN
5	E	134	GLN
5	E	149	HIS
5	E	170	GLN
5	E	215	ASN
5	E	220	GLN
1	F	18	GLN
1	F	62	ASN
1	F	177	HIS
2	G	10	GLN
2	G	33	ASN
2	G	70	GLN
2	G	92	GLN
2	G	134	ASN
2	G	150	ASN
2	G	156	GLN
4	I	5	GLN
4	I	29	ASN
4	I	30	ASN
4	I	35	HIS
4	I	44	ASN
4	I	169	ASN
4	I	176	ASN
4	I	184	ASN
5	J	4	GLN
5	J	8	HIS
5	J	27	HIS
5	J	35	GLN
5	J	42	GLN
5	J	114	ASN
5	J	149	HIS
5	J	198	ASN

### 5.3.3 RNA

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 2 ligands modelled in this entry, 2 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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	179/182 (98%)	-0.32	0 <b>100</b> <b>100</b>	30, 43, 63, 72	0
1	F	179/182 (98%)	-0.18	2 (1%) 78 74	33, 44, 63, 77	0
2	B	179/190 (94%)	-0.25	2 (1%) 78 74	27, 45, 72, 75	0
2	G	177/190 (93%)	-0.04	3 (1%) 69 64	31, 48, 80, 91	0
3	C	15/15 (100%)	-0.12	1 (6%) 24 19	32, 38, 56, 58	0
3	H	15/15 (100%)	-0.12	0 <b>100</b> <b>100</b>	33, 38, 55, 61	0
4	D	181/203 (89%)	-0.11	3 (1%) 69 64	26, 42, 78, 81	1 (0%)
4	I	190/203 (93%)	-0.21	1 (0%) 87 85	27, 40, 74, 77	0
5	E	236/239 (98%)	0.07	2 (0%) 82 80	31, 55, 72, 85	0
5	J	238/239 (99%)	-0.15	1 (0%) 88 86	28, 49, 66, 76	0
All	All	1589/1658 (95%)	-0.14	15 (0%) 81 78	26, 47, 73, 91	1 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	140	ALA	3.0
2	B	190	ALA	2.9
5	J	238	ALA	2.8
2	G	167	SER	2.7
2	G	164	VAL	2.3
4	D	190	ILE	2.3
4	I	188	ASN	2.3
4	D	123	ASP	2.2
1	F	180	PHE	2.2
2	B	163	THR	2.1
4	D	1	ILE	2.1
5	E	37	LEU	2.1
5	E	114	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	157	THR	2.0
3	C	23	GLY	2.0

## 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 [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q < 0.9
6	NA	B	201	1/1	0.75	0.22	53,53,53,53	0
6	NA	A	201	1/1	0.78	0.19	72,72,72,72	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.