



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:32 AM GMT

PDB ID : 3MBE
Title : TCR 21.30 in complex with MHC class II I-Ag7HEL(11-27)
Authors : Corper, A.L.; Yoshida, K.; Teyton, L.; Wilson I.A.
Deposited on : 2010-03-25
Resolution : 2.89 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

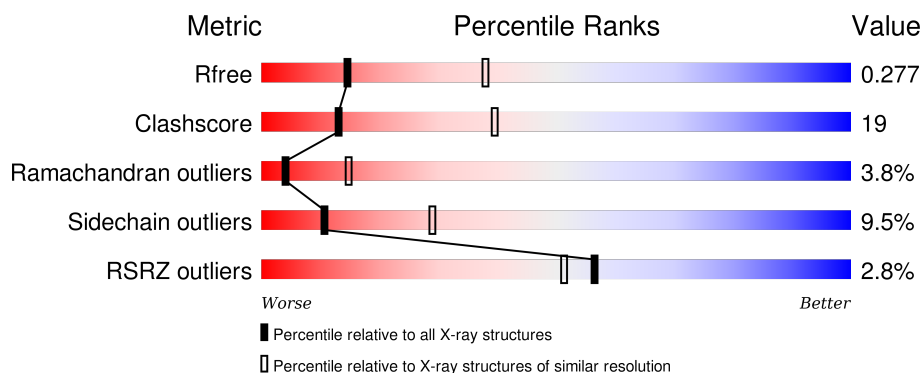
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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.





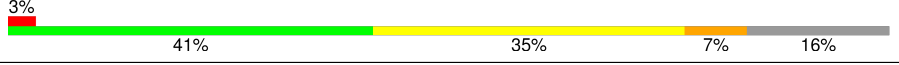
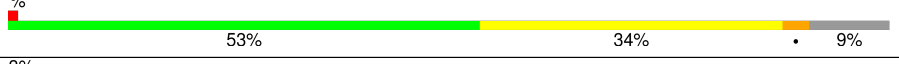
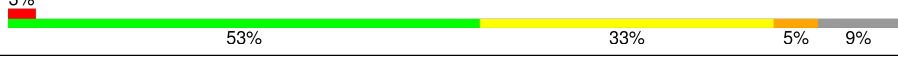
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1945 (2.90-2.86)
Clashscore	102246	2202 (2.90-2.86)
Ramachandran outliers	100387	2149 (2.90-2.86)
Sidechain outliers	100360	2152 (2.90-2.86)
RSRZ outliers	91569	1950 (2.90-2.86)

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. 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	190	<div> <div>60%</div> <div>33%</div> <div>7%</div> <div>1%</div> <div>1%</div> </div>
1	E	190	<div> <div>59%</div> <div>34%</div> <div>7%</div> <div>1%</div> <div>1%</div> </div>
2	B	201	<div> <div>52%</div> <div>29%</div> <div>7%</div> <div>11%</div> </div>
2	F	201	<div> <div>52%</div> <div>31%</div> <div>5%</div> <div>11%</div> </div>
3	P	18	<div> <div>44%</div> <div>33%</div> <div>17%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
3	Q	18	
4	C	229	
4	G	229	
5	D	259	
5	H	259	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	NAG	E	300	X	-	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13028 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 MHC CLASS II H2-IAg7 ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	184	Total	C	N	O	S	0	0	0
			1481	956	240	283	2			
1	E	184	Total	C	N	O	S	0	0	0
			1481	956	240	283	2			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	179	SER	-	EXPRESSION TAG	UNP P04228
A	180	SER	-	EXPRESSION TAG	UNP P04228
A	181	ALA	-	EXPRESSION TAG	UNP P04228
A	182	ASP	-	EXPRESSION TAG	UNP P04228
A	183	LEU	-	EXPRESSION TAG	UNP P04228
A	184	VAL	-	EXPRESSION TAG	UNP P04228
A	185	PRO	-	EXPRESSION TAG	UNP P04228
A	186	ARG	-	EXPRESSION TAG	UNP P04228
E	179	SER	-	EXPRESSION TAG	UNP P04228
E	180	SER	-	EXPRESSION TAG	UNP P04228
E	181	ALA	-	EXPRESSION TAG	UNP P04228
E	182	ASP	-	EXPRESSION TAG	UNP P04228
E	183	LEU	-	EXPRESSION TAG	UNP P04228
E	184	VAL	-	EXPRESSION TAG	UNP P04228
E	185	PRO	-	EXPRESSION TAG	UNP P04228
E	186	ARG	-	EXPRESSION TAG	UNP P04228

- Molecule 2 is a protein called MHC CLASS II H2-IAg7 BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	178	Total	C	N	O	S	0	0	0
			1487	934	269	278	6			
2	F	178	Total	C	N	O	S	0	0	0
			1487	934	269	278	6			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	GLY	-	EXPRESSION TAG	UNP Q31135
B	-4	SER	-	EXPRESSION TAG	UNP Q31135
B	-3	GLY	-	EXPRESSION TAG	UNP Q31135
B	-2	SER	-	EXPRESSION TAG	UNP Q31135
B	-1	GLY	-	EXPRESSION TAG	UNP Q31135
B	0	SER	-	EXPRESSION TAG	UNP Q31135
B	189	SER	-	EXPRESSION TAG	UNP Q31135
B	190	SER	-	EXPRESSION TAG	UNP Q31135
B	191	ALA	-	EXPRESSION TAG	UNP Q31135
B	192	ASP	-	EXPRESSION TAG	UNP Q31135
B	193	LEU	-	EXPRESSION TAG	UNP Q31135
B	194	VAL	-	EXPRESSION TAG	UNP Q31135
B	195	PRO	-	EXPRESSION TAG	UNP Q31135
B	196	ARG	-	EXPRESSION TAG	UNP Q31135
F	-5	GLY	-	EXPRESSION TAG	UNP Q31135
F	-4	SER	-	EXPRESSION TAG	UNP Q31135
F	-3	GLY	-	EXPRESSION TAG	UNP Q31135
F	-2	SER	-	EXPRESSION TAG	UNP Q31135
F	-1	GLY	-	EXPRESSION TAG	UNP Q31135
F	0	SER	-	EXPRESSION TAG	UNP Q31135
F	189	SER	-	EXPRESSION TAG	UNP Q31135
F	190	SER	-	EXPRESSION TAG	UNP Q31135
F	191	ALA	-	EXPRESSION TAG	UNP Q31135
F	192	ASP	-	EXPRESSION TAG	UNP Q31135
F	193	LEU	-	EXPRESSION TAG	UNP Q31135
F	194	VAL	-	EXPRESSION TAG	UNP Q31135
F	195	PRO	-	EXPRESSION TAG	UNP Q31135
F	196	ARG	-	EXPRESSION TAG	UNP Q31135

- Molecule 3 is a protein called PEPTIDE HEL 11-27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	17	Total	C	N	O	S	0	0	0
			132	81	27	23	1			
3	Q	17	Total	C	N	O	S	0	0	0
			132	81	27	23	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	10	GLY	ALA	CONFLICT	UNP P00698

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	10	GLY	ALA	CONFLICT	UNP P00698

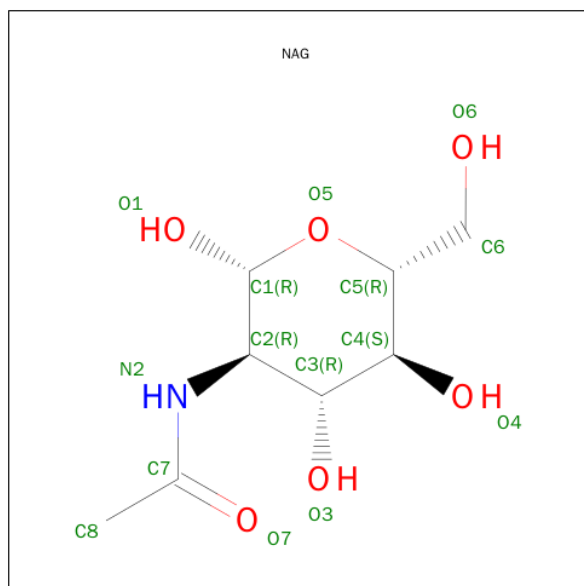
- Molecule 4 is a protein called TCR 21.3 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	192	Total	C	N	O	S	0	0	0
			1494	932	253	299	10			
4	G	192	Total	C	N	O	S	0	0	0
			1494	932	253	299	10			

- Molecule 5 is a protein called TCR 21.3 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	236	Total	C	N	O	S	0	0	0
			1878	1184	333	355	6			
5	H	236	Total	C	N	O	S	0	0	0
			1878	1184	333	355	6			

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	E	1	Total	C	N	O	0	0
			14	8	1	5		

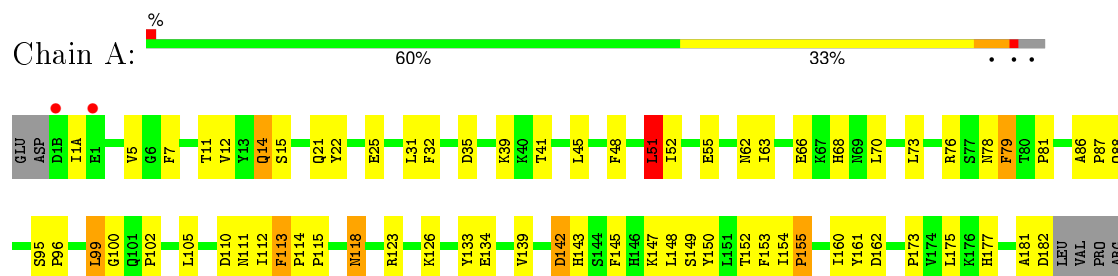
- Molecule 7 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	D	2	Total	C	N	O	0	0
			28	16	2	10		
7	H	2	Total	C	N	O	0	0
			28	16	2	10		

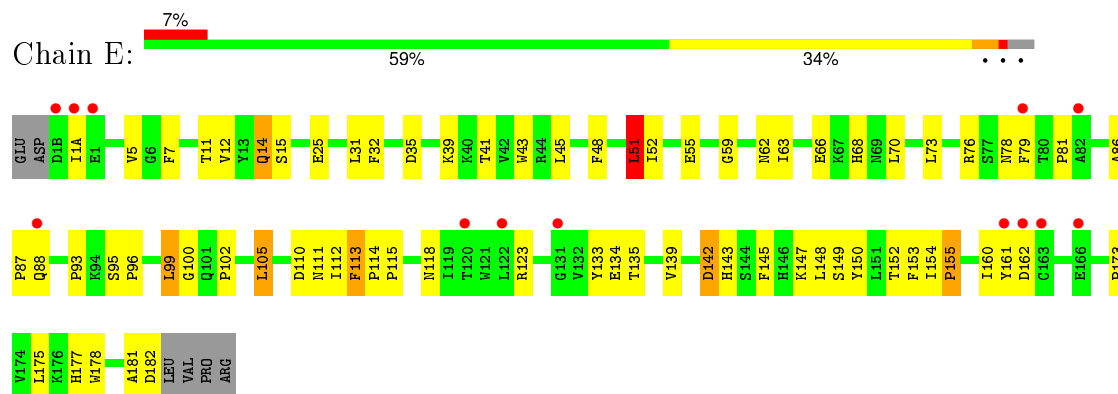
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

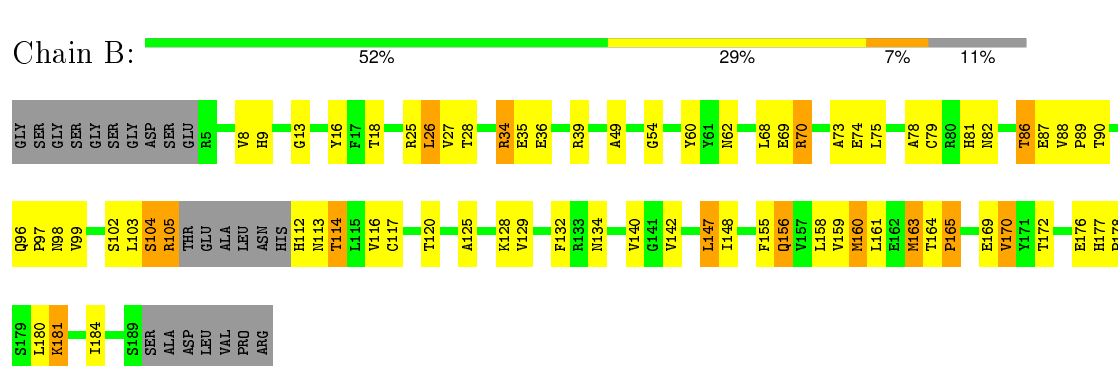
• Molecule 1: MHC CLASS II H2-IAg7 ALPHA CHAIN



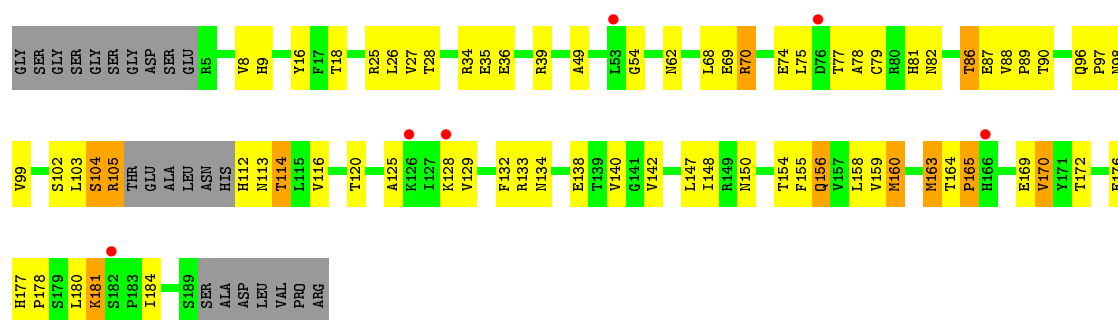
• Molecule 1: MHC CLASS II H2-IAg7 ALPHA CHAIN



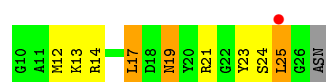
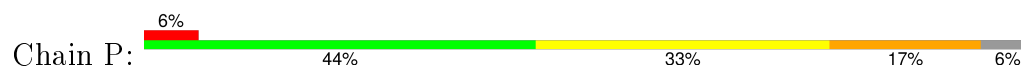
• Molecule 2: MHC CLASS II H2-IAg7 BETA CHAIN



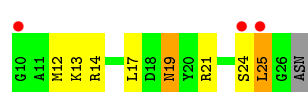
• Molecule 2: MHC CLASS II H2-IAg7 BETA CHAIN



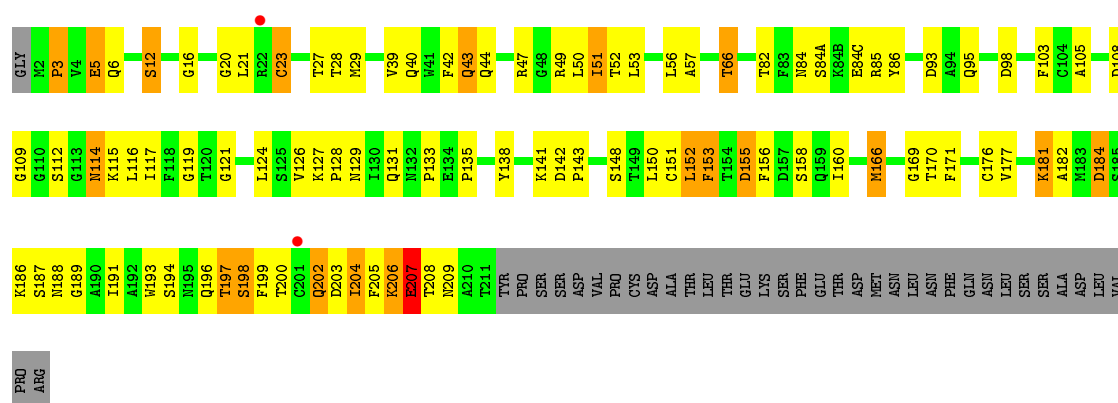
- Molecule 3: PEPTIDE HEL 11-27



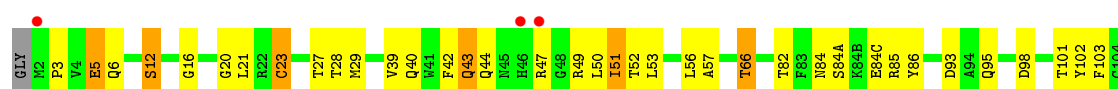
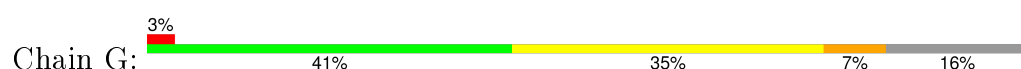
- Molecule 3: PEPTIDE HEL 11-27

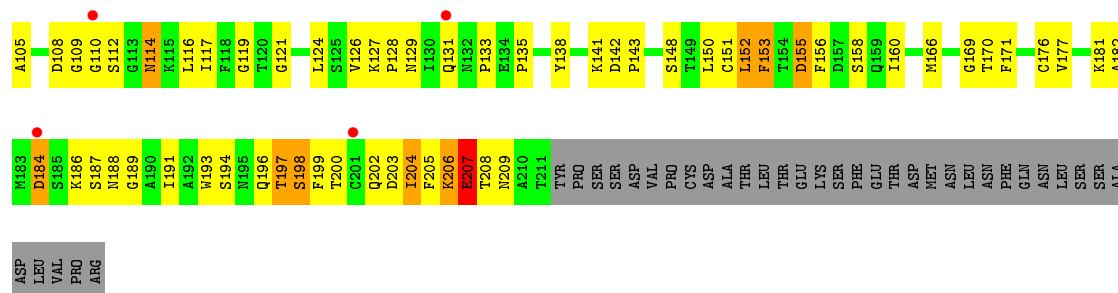


- Molecule 4: TCR 21.3 alpha chain

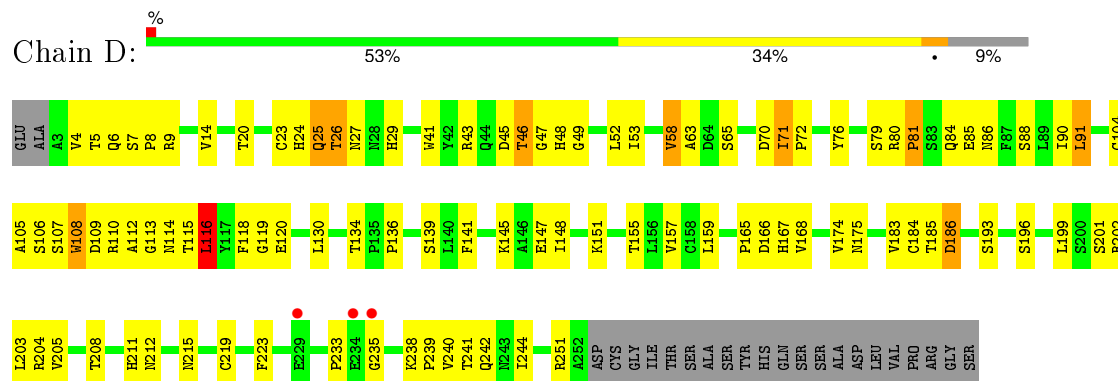


- Molecule 4: TCR 21.3 alpha chain

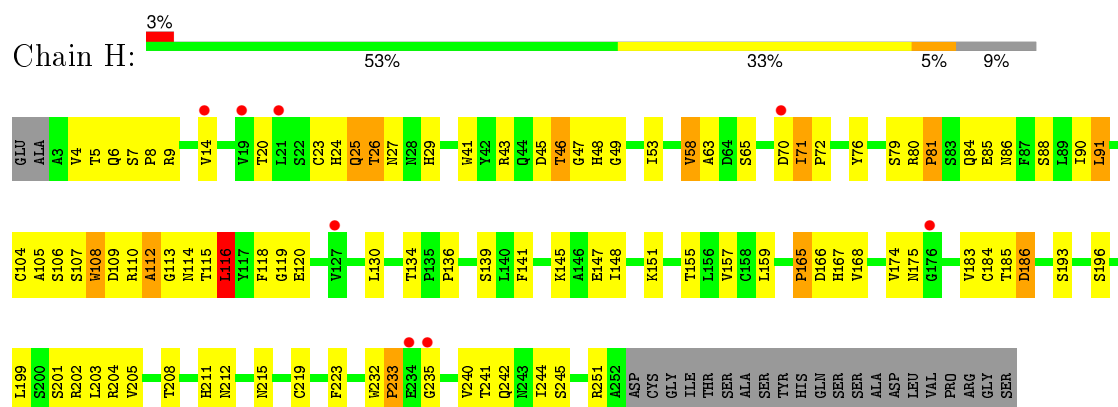




• Molecule 5: TCR 21.3 beta chain



• Molecule 5: TCR 21.3 beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.47Å 99.39Å 404.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.26 – 2.89 48.26 – 2.89	Depositor EDS
% Data completeness (in resolution range)	54.7 (48.26-2.89) 54.7 (48.26-2.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.253 , 0.281 0.250 , 0.277	Depositor DCC
R_{free} test set	725 reflections (2.12%)	DCC
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 38.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 34214 reflections	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	13028	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.41	0/1526	0.53	0/2083
1	E	0.33	0/1526	0.51	0/2083
2	B	0.39	0/1523	0.52	0/2064
2	F	0.34	0/1523	0.51	0/2064
3	P	0.32	0/134	0.54	0/176
3	Q	0.29	0/134	0.51	0/176
4	C	0.34	0/1523	0.54	0/2058
4	G	0.32	0/1523	0.53	0/2058
5	D	0.42	0/1932	0.56	1/2627 (0.0%)
5	H	0.34	0/1932	0.54	1/2627 (0.0%)
All	All	0.36	0/13276	0.53	2/18016 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	116	LEU	CA-CB-CG	5.96	129.02	115.30
5	H	116	LEU	CA-CB-CG	5.86	128.79	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of 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	1481	0	1412	57	0
1	E	1481	0	1412	60	0
2	B	1487	0	1422	61	0
2	F	1487	0	1422	54	0
3	P	132	0	126	9	0
3	Q	132	0	126	7	0
4	C	1494	0	1443	79	0
4	G	1494	0	1443	79	0
5	D	1878	0	1785	64	0
5	H	1878	0	1785	66	0
6	A	14	0	13	1	0
6	E	14	0	13	0	0
7	D	28	0	25	1	0
7	H	28	0	25	0	0
All	All	13028	0	12452	483	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 19.

All (483) 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)
5:H:193:SER:HB2	5:H:196:SER:HB3	1.48	0.95
5:H:136:PRO:HD2	5:H:244:ILE:HD12	1.49	0.95
5:D:136:PRO:HD2	5:D:244:ILE:HD12	1.50	0.94
5:D:193:SER:HB2	5:D:196:SER:HB3	1.50	0.93
1:A:115:PRO:HG3	1:A:145:PHE:CE1	2.04	0.93
2:F:181:LYS:H	2:F:181:LYS:HD2	1.33	0.92
2:B:181:LYS:H	2:B:181:LYS:HD2	1.30	0.91
1:E:115:PRO:HG3	1:E:145:PHE:CE1	2.06	0.91
1:E:55:GLU:HG3	4:G:112:SER:HA	1.50	0.90
2:F:99:VAL:HG21	2:F:184:ILE:HG21	1.52	0.90
2:B:99:VAL:HG21	2:B:184:ILE:HG21	1.55	0.89
4:C:85:ARG:HG3	4:C:85:ARG:HH11	1.43	0.83
4:C:105:ALA:HB1	4:C:116:LEU:HD22	1.61	0.83
4:G:105:ALA:HB1	4:G:116:LEU:HD22	1.61	0.83
1:A:55:GLU:HG3	4:C:112:SER:HA	1.59	0.82
1:E:52:ILE:HD11	3:Q:14:ARG:HH21	1.44	0.82
4:G:85:ARG:HH11	4:G:85:ARG:HG3	1.44	0.81
2:F:129:VAL:HG11	2:F:159:VAL:HG21	1.63	0.80
5:D:58:VAL:HG13	5:D:65:SER:HB3	1.62	0.80
1:A:112:ILE:O	1:A:113:PHE:HB2	1.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:58:VAL:HG13	5:H:65:SER:HB3	1.62	0.80
2:B:129:VAL:HG11	2:B:159:VAL:HG21	1.65	0.79
4:G:152:LEU:HD13	5:H:155:THR:HG21	1.66	0.78
1:A:115:PRO:HG3	1:A:145:PHE:HE1	1.48	0.77
1:E:115:PRO:HG3	1:E:145:PHE:HE1	1.49	0.77
4:C:152:LEU:HD13	5:D:155:THR:HG21	1.68	0.75
4:C:95:GLN:O	4:C:126:VAL:HG11	1.87	0.74
1:E:112:ILE:O	1:E:113:PHE:HB2	1.85	0.74
2:B:132:PHE:HB2	2:B:172:THR:HB	1.69	0.74
2:F:132:PHE:HB2	2:F:172:THR:HB	1.70	0.74
4:G:95:GLN:O	4:G:126:VAL:HG11	1.88	0.74
4:G:43:GLN:HG3	4:G:43:GLN:O	1.87	0.73
4:C:156:PHE:HB2	4:C:160:ILE:HD11	1.69	0.73
3:Q:21:ARG:HD2	5:H:109:ASP:OD1	1.89	0.72
4:G:156:PHE:HB2	4:G:160:ILE:HD11	1.69	0.72
5:H:108:TRP:C	5:H:108:TRP:CD1	2.63	0.72
4:C:43:GLN:O	4:C:43:GLN:HG3	1.91	0.70
5:D:108:TRP:CD1	5:D:108:TRP:C	2.66	0.68
4:C:128:PRO:HG2	4:C:188:ASN:HD21	1.59	0.67
5:H:9:ARG:NH1	5:H:9:ARG:HB3	2.10	0.67
5:D:20:THR:HG23	5:D:90:ILE:HG13	1.75	0.67
4:G:128:PRO:HG2	4:G:188:ASN:HD21	1.59	0.66
1:A:52:ILE:HD11	3:P:14:ARG:HH21	1.61	0.65
2:B:87:GLU:OE1	2:B:87:GLU:HA	1.96	0.65
4:G:84:ASN:ND2	4:G:84(C):GLU:HB2	2.12	0.64
5:H:20:THR:HG23	5:H:90:ILE:HG13	1.78	0.64
4:C:205:PHE:O	4:C:207:GLU:N	2.31	0.64
4:G:152:LEU:CD1	5:H:155:THR:HG21	2.27	0.64
4:G:197:THR:HB	4:G:199:PHE:CE1	2.33	0.64
4:G:205:PHE:O	4:G:207:GLU:N	2.31	0.63
5:H:25:GLN:HG2	5:H:27:ASN:H	1.63	0.63
4:C:108:ASP:OD2	4:C:112:SER:HB3	1.96	0.63
4:C:84:ASN:ND2	4:C:84(C):GLU:HB2	2.14	0.63
5:H:14:VAL:HG22	5:H:130:LEU:HG	1.80	0.63
4:G:153:PHE:O	4:G:189:GLY:HA2	1.97	0.63
1:A:78:ASN:O	1:A:79:PHE:HB2	1.99	0.63
4:C:66:THR:HB	4:C:82:THR:HG22	1.80	0.63
4:G:108:ASP:OD2	4:G:112:SER:HB3	1.99	0.63
5:H:106:SER:O	5:H:116:LEU:HA	1.99	0.63
5:H:91:LEU:HD23	5:H:91:LEU:N	2.13	0.63
4:G:66:THR:HB	4:G:82:THR:HG22	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:91:LEU:HD23	5:D:91:LEU:N	2.14	0.62
2:F:69:GLU:HG2	4:G:57:ALA:HB3	1.80	0.62
2:F:180:LEU:HD13	2:F:184:ILE:HG13	1.80	0.62
5:D:9:ARG:NH1	5:D:9:ARG:HB3	2.14	0.62
4:C:153:PHE:O	4:C:189:GLY:HA2	1.99	0.62
5:H:104:CYS:O	5:H:119:GLY:N	2.33	0.62
5:D:14:VAL:HG22	5:D:130:LEU:HG	1.80	0.62
5:D:9:ARG:NE	5:D:120:GLU:HG3	2.14	0.62
1:E:14:GLN:HB2	2:F:8:VAL:HG22	1.82	0.62
5:H:58:VAL:HG13	5:H:65:SER:CB	2.29	0.62
5:H:9:ARG:HH11	5:H:9:ARG:HB3	1.65	0.62
1:E:62:ASN:HA	5:H:110:ARG:HH22	1.64	0.62
4:C:142:ASP:HB2	5:D:141:PHE:CE2	2.34	0.62
5:D:106:SER:O	5:D:116:LEU:HA	1.99	0.62
1:A:1(A):ILE:H	1:A:1(A):ILE:HD12	1.65	0.62
2:F:87:GLU:OE1	2:F:87:GLU:HA	1.99	0.62
4:C:197:THR:HB	4:C:199:PHE:CE1	2.35	0.62
5:H:136:PRO:HD2	5:H:244:ILE:CD1	2.27	0.61
1:E:78:ASN:O	1:E:79:PHE:HB2	2.00	0.61
2:F:75:LEU:O	2:F:79:CYS:HB2	2.00	0.61
2:B:180:LEU:HD13	2:B:184:ILE:HG13	1.82	0.61
2:F:70:ARG:HA	4:G:57:ALA:HB1	1.82	0.61
5:H:9:ARG:NE	5:H:120:GLU:HG3	2.16	0.60
5:D:25:GLN:HG2	5:D:27:ASN:H	1.66	0.60
5:D:58:VAL:HG13	5:D:65:SER:CB	2.30	0.60
4:C:128:PRO:O	4:C:129:ASN:HB3	2.01	0.60
4:G:42:PHE:HE2	4:G:52:THR:HG22	1.65	0.60
3:P:21:ARG:HD2	5:D:109:ASP:OD1	2.01	0.60
5:D:165:PRO:O	5:D:167:HIS:N	2.24	0.60
2:B:125:ALA:HB2	2:B:155:PHE:CE2	2.35	0.60
4:G:12:SER:OG	4:G:127:LYS:HE3	2.01	0.60
1:A:160:ILE:HD12	1:A:177:HIS:HE1	1.67	0.60
5:H:165:PRO:O	5:H:167:HIS:N	2.25	0.60
4:C:152:LEU:CD1	5:D:155:THR:HG21	2.30	0.60
2:F:102:SER:OG	2:F:103:LEU:N	2.35	0.60
2:F:125:ALA:HB2	2:F:155:PHE:CE2	2.36	0.60
4:C:6:GLN:HG3	4:C:119:GLY:HA3	1.84	0.60
1:A:68:HIS:CD2	3:P:21:ARG:HG2	2.37	0.59
3:P:24:SER:O	3:P:25:LEU:HB3	2.02	0.59
4:G:142:ASP:HB2	5:H:141:PHE:CE2	2.36	0.59
5:D:104:CYS:O	5:D:119:GLY:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:44:GLN:HE21	4:G:50:LEU:CD1	2.15	0.59
4:G:6:GLN:HG3	4:G:119:GLY:HA3	1.84	0.59
1:E:1(A):ILE:HD12	1:E:1(A):ILE:H	1.67	0.59
1:E:68:HIS:CD2	3:Q:21:ARG:HG2	2.37	0.59
2:F:36:GLU:OE2	2:F:39:ARG:HB2	2.03	0.59
1:E:160:ILE:HD12	1:E:177:HIS:HE1	1.67	0.59
5:H:45:ASP:O	5:H:46:THR:C	2.41	0.59
4:G:42:PHE:CE2	4:G:52:THR:HG22	2.38	0.58
4:C:42:PHE:HE2	4:C:52:THR:HG22	1.68	0.58
4:G:109:GLY:H	4:G:114:ASN:HA	1.69	0.58
1:A:5:VAL:HG22	2:B:16:TYR:CD1	2.39	0.58
5:H:70:ASP:C	5:H:72:PRO:HD3	2.24	0.58
4:G:197:THR:HB	4:G:199:PHE:HE1	1.69	0.58
4:C:12:SER:OG	4:C:127:LYS:HE3	2.03	0.58
2:B:102:SER:OG	2:B:103:LEU:N	2.35	0.58
5:D:9:ARG:HB3	5:D:9:ARG:HH11	1.69	0.58
4:C:98:ASP:O	4:C:124:LEU:HD23	2.04	0.58
3:Q:24:SER:O	3:Q:25:LEU:HB3	2.03	0.58
5:D:136:PRO:HD2	5:D:244:ILE:CD1	2.28	0.57
2:B:27:VAL:HG12	2:B:28:THR:N	2.18	0.57
5:H:185:THR:HG22	5:H:201:SER:OG	2.05	0.57
5:D:185:THR:HG22	5:D:201:SER:OG	2.04	0.57
1:E:95:SER:HB2	1:E:96:PRO:HD2	1.86	0.57
5:D:168:VAL:HG12	5:D:223:PHE:HA	1.86	0.57
2:B:75:LEU:O	2:B:79:CYS:HB2	2.05	0.57
5:H:80:ARG:HD2	5:H:86:ASN:O	2.05	0.57
5:H:108:TRP:HD1	5:H:108:TRP:C	2.04	0.57
5:D:53:ILE:HG12	5:D:71:ILE:HD12	1.87	0.57
5:D:45:ASP:O	5:D:46:THR:C	2.43	0.57
2:F:129:VAL:CG1	2:F:159:VAL:HG21	2.33	0.56
4:G:44:GLN:HE21	4:G:50:LEU:HD13	1.69	0.56
4:G:128:PRO:O	4:G:129:ASN:HB3	2.04	0.56
1:E:87:PRO:HA	1:E:110:ASP:O	2.05	0.56
4:C:85:ARG:HG3	4:C:85:ARG:NH1	2.18	0.56
5:H:29:HIS:HB3	5:H:107:SER:O	2.05	0.56
4:C:43:GLN:HG2	4:C:53:LEU:HD21	1.87	0.56
5:D:70:ASP:C	5:D:72:PRO:HD3	2.25	0.56
5:H:168:VAL:HG12	5:H:223:PHE:HA	1.86	0.56
2:B:128:LYS:HB2	2:B:176:GLU:HB2	1.87	0.56
2:F:160:MET:SD	2:F:160:MET:N	2.78	0.56
4:C:42:PHE:CE2	4:C:52:THR:HG22	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1(A):ILE:HD12	1:A:1(A):ILE:N	2.21	0.56
4:C:197:THR:HB	4:C:199:PHE:HE1	1.71	0.56
2:B:160:MET:SD	2:B:160:MET:N	2.78	0.56
4:C:109:GLY:H	4:C:114:ASN:HA	1.71	0.56
2:B:81:HIS:HE1	3:P:12:MET:HE3	1.71	0.56
4:C:44:GLN:HE21	4:C:50:LEU:HD13	1.71	0.56
2:F:27:VAL:HG12	2:F:28:THR:N	2.21	0.56
5:D:29:HIS:HB3	5:D:107:SER:O	2.06	0.55
4:C:44:GLN:HE21	4:C:50:LEU:CD1	2.18	0.55
2:B:36:GLU:OE2	2:B:39:ARG:HB2	2.05	0.55
4:G:3:PRO:HB2	4:G:117:ILE:HG21	1.89	0.55
5:D:108:TRP:HD1	5:D:108:TRP:C	2.09	0.55
1:A:95:SER:HB2	1:A:96:PRO:HD2	1.87	0.55
4:G:44:GLN:NE2	4:G:50:LEU:HD13	2.21	0.55
4:C:206:LYS:O	4:C:208:THR:N	2.39	0.55
4:G:98:ASP:O	4:G:124:LEU:HD23	2.06	0.55
5:H:53:ILE:HG12	5:H:71:ILE:HD12	1.89	0.55
1:E:139:VAL:HG12	1:E:145:PHE:HE2	1.71	0.54
4:C:169:GLY:O	4:C:194:SER:HA	2.07	0.54
4:C:44:GLN:NE2	4:C:50:LEU:HD13	2.21	0.54
4:C:105:ALA:CB	4:C:116:LEU:HD22	2.36	0.54
1:A:87:PRO:HA	1:A:110:ASP:O	2.07	0.54
1:E:110:ASP:OD1	1:E:111:ASN:N	2.35	0.54
2:B:177:HIS:CG	2:B:178:PRO:HD2	2.43	0.54
4:G:43:GLN:HG2	4:G:53:LEU:HD21	1.90	0.54
5:H:45:ASP:HB2	5:H:48:HIS:HE1	1.73	0.54
1:E:102:PRO:HA	1:E:154:ILE:HD13	1.90	0.54
1:E:5:VAL:HG22	2:F:16:TYR:CD1	2.42	0.54
5:D:45:ASP:HB2	5:D:48:HIS:CE1	2.43	0.54
2:F:88:VAL:HB	2:F:89:PRO:HD3	1.90	0.54
2:B:129:VAL:CG1	2:B:159:VAL:HG21	2.34	0.54
5:D:29:HIS:CD2	5:D:108:TRP:HB3	2.43	0.54
1:E:1(A):ILE:HD12	1:E:1(A):ILE:N	2.23	0.54
1:A:99:LEU:HA	1:A:155:PRO:HB2	1.90	0.54
2:F:128:LYS:HB2	2:F:176:GLU:HB2	1.88	0.54
2:B:120:THR:HG22	2:B:156:GLN:HB2	1.91	0.53
4:C:150:LEU:HD21	5:D:157:VAL:HG11	1.90	0.53
2:F:134:ASN:HD21	2:F:169:GLU:HG3	1.73	0.53
4:G:169:GLY:O	4:G:194:SER:HA	2.08	0.53
5:H:45:ASP:HB2	5:H:48:HIS:CE1	2.42	0.53
2:B:88:VAL:HB	2:B:89:PRO:HD3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:ASP:OD1	1:A:111:ASN:N	2.34	0.53
2:B:134:ASN:HD21	2:B:169:GLU:HG3	1.73	0.53
5:H:24:HIS:HA	5:H:85:GLU:O	2.09	0.53
2:F:177:HIS:CG	2:F:178:PRO:HD2	2.43	0.53
1:E:52:ILE:HD11	3:Q:14:ARG:NH2	2.20	0.53
1:A:52:ILE:C	1:A:52:ILE:HD12	2.27	0.53
2:F:120:THR:HG22	2:F:156:GLN:HB2	1.90	0.53
4:G:85:ARG:HH11	4:G:85:ARG:CG	2.19	0.53
5:D:45:ASP:HB2	5:D:48:HIS:HE1	1.74	0.53
4:G:206:LYS:O	4:G:208:THR:N	2.41	0.53
2:B:181:LYS:CD	2:B:181:LYS:H	2.08	0.53
4:C:3:PRO:HB2	4:C:117:ILE:HG21	1.91	0.53
1:A:139:VAL:HG12	1:A:145:PHE:HE2	1.73	0.52
2:F:105:ARG:HG2	2:F:105:ARG:O	2.08	0.52
1:A:66:GLU:HG2	3:P:19:ASN:OD1	2.09	0.52
5:H:7:SER:HA	5:H:8:PRO:C	2.30	0.52
4:G:105:ALA:CB	4:G:116:LEU:HD22	2.38	0.52
5:D:80:ARG:HD2	5:D:86:ASN:O	2.10	0.52
4:C:184:ASP:HA	4:C:186:LYS:NZ	2.24	0.52
5:D:113:GLY:C	5:D:115:THR:H	2.13	0.52
1:A:102:PRO:HA	1:A:154:ILE:HD13	1.90	0.52
2:B:105:ARG:O	2:B:105:ARG:HG2	2.08	0.52
4:C:85:ARG:CG	4:C:85:ARG:HH11	2.18	0.52
4:G:150:LEU:HD21	5:H:157:VAL:HG11	1.91	0.52
5:H:113:GLY:C	5:H:115:THR:H	2.13	0.52
5:D:76:TYR:CD1	5:D:91:LEU:HD22	2.44	0.52
2:B:69:GLU:HG2	4:C:57:ALA:HB3	1.91	0.51
1:A:115:PRO:HG3	1:A:145:PHE:CD1	2.44	0.51
5:H:76:TYR:CD1	5:H:91:LEU:HD22	2.46	0.51
1:E:1(A):ILE:HG12	2:F:25:ARG:NH1	2.25	0.51
5:D:7:SER:HA	5:D:8:PRO:C	2.31	0.51
1:A:5:VAL:HG22	2:B:16:TYR:HD1	1.76	0.51
5:D:211:HIS:HA	5:D:251:ARG:O	2.11	0.51
2:F:82:ASN:HA	2:F:86:THR:HG23	1.92	0.51
1:A:76:ARG:O	1:A:76:ARG:HG2	2.10	0.51
1:E:99:LEU:HA	1:E:155:PRO:HB2	1.91	0.51
2:F:62:ASN:HA	2:F:68:LEU:HB2	1.92	0.51
4:C:170:THR:HG21	4:C:204:ILE:HG21	1.93	0.51
5:D:24:HIS:HA	5:D:85:GLU:O	2.11	0.51
2:B:177:HIS:ND1	2:B:178:PRO:HD2	2.26	0.50
2:B:62:ASN:HA	2:B:68:LEU:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:116:LEU:HD12	5:H:116:LEU:O	2.11	0.50
1:A:1(A):ILE:HG12	2:B:25:ARG:NH1	2.25	0.50
1:A:14:GLN:HB2	2:B:8:VAL:HG22	1.93	0.50
2:F:77:THR:HA	4:G:28:THR:HG21	1.94	0.50
1:E:52:ILE:C	1:E:52:ILE:HD12	2.31	0.50
1:E:115:PRO:HG3	1:E:145:PHE:CD1	2.46	0.50
5:D:43:ARG:HB3	5:D:53:ILE:HD11	1.94	0.50
5:H:174:VAL:O	5:H:175:ASN:HB2	2.11	0.50
5:H:43:ARG:HB3	5:H:53:ILE:HD11	1.92	0.50
2:F:177:HIS:ND1	2:F:178:PRO:HD2	2.26	0.50
4:G:191:ILE:HD11	5:H:202:ARG:HD3	1.92	0.50
4:G:170:THR:HG21	4:G:204:ILE:HG21	1.94	0.50
5:D:116:LEU:HD12	5:D:116:LEU:O	2.11	0.50
2:B:13:GLY:HA3	3:P:17:LEU:HD12	1.93	0.50
5:H:211:HIS:HA	5:H:251:ARG:O	2.12	0.50
1:A:115:PRO:CG	1:A:145:PHE:CE1	2.89	0.49
5:H:155:THR:OG1	5:H:204:ARG:HD2	2.12	0.49
5:D:145:LYS:HA	5:D:148:ILE:HD12	1.93	0.49
1:E:76:ARG:O	1:E:76:ARG:HG2	2.12	0.49
5:D:203:LEU:HD12	5:D:204:ARG:H	1.77	0.49
5:H:29:HIS:CD2	5:H:108:TRP:HB3	2.46	0.49
1:A:62:ASN:HA	5:D:110:ARG:HH22	1.78	0.49
5:D:84:GLN:HG2	5:D:84:GLN:O	2.12	0.49
4:G:49:ARG:HH21	4:G:51:ILE:HG12	1.77	0.49
4:G:20:GLY:C	4:G:21:LEU:HD12	2.33	0.49
2:B:82:ASN:HA	2:B:86:THR:HG23	1.93	0.49
5:H:145:LYS:HA	5:H:148:ILE:HD12	1.94	0.49
4:G:171:PHE:HD1	4:G:193:TRP:NE1	2.10	0.49
4:G:184:ASP:HA	4:G:186:LYS:NZ	2.27	0.49
4:G:103:PHE:CE2	5:H:49:GLY:HA2	2.48	0.49
5:H:105:ALA:HB2	5:H:118:PHE:CD2	2.47	0.49
4:C:20:GLY:C	4:C:21:LEU:HD12	2.33	0.49
4:C:103:PHE:CE2	5:D:49:GLY:HA2	2.47	0.49
5:D:105:ALA:HB2	5:D:118:PHE:CD2	2.48	0.48
1:E:100:GLY:HA2	1:E:154:ILE:CG2	2.43	0.48
1:A:142:ASP:O	1:A:143:HIS:HB2	2.12	0.48
5:H:203:LEU:HD12	5:H:204:ARG:H	1.77	0.48
4:C:152:LEU:HD23	4:C:152:LEU:O	2.13	0.48
4:G:152:LEU:HD23	4:G:152:LEU:O	2.13	0.48
2:F:104:SER:HB3	2:F:114:THR:HB	1.96	0.48
1:E:133:TYR:CG	1:E:134:GLU:N	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ILE:O	1:A:52:ILE:HD12	2.14	0.48
2:B:35:GLU:O	2:B:35:GLU:HG2	2.13	0.48
4:G:155:ASP:HB2	5:H:151:LYS:HZ3	1.79	0.48
5:D:155:THR:OG1	5:D:204:ARG:HD2	2.14	0.48
1:A:100:GLY:HA2	1:A:154:ILE:CG2	2.44	0.47
4:C:191:ILE:HD11	5:D:202:ARG:HD3	1.95	0.47
1:E:66:GLU:HG2	3:Q:19:ASN:OD1	2.14	0.47
4:C:171:PHE:HD1	4:C:193:TRP:NE1	2.12	0.47
4:C:49:ARG:HH21	4:C:51:ILE:HG12	1.79	0.47
1:E:139:VAL:HG12	1:E:145:PHE:CE2	2.48	0.47
4:G:39:VAL:HG12	4:G:56:LEU:HB2	1.97	0.47
5:H:186:ASP:O	5:H:199:LEU:HD11	2.14	0.47
1:A:133:TYR:CG	1:A:134:GLU:N	2.81	0.47
2:F:113:ASN:HB2	2:F:163:MET:HE3	1.95	0.47
4:G:27:THR:HG23	4:G:29:MET:HE3	1.96	0.47
1:A:113:PHE:HA	1:A:114:PRO:C	2.35	0.47
2:B:181:LYS:N	2:B:181:LYS:HD2	2.14	0.47
2:B:113:ASN:HB2	2:B:163:MET:HE3	1.97	0.47
5:D:186:ASP:O	5:D:199:LEU:HD11	2.15	0.46
2:F:99:VAL:CG2	2:F:184:ILE:HG21	2.34	0.46
1:E:113:PHE:HA	1:E:114:PRO:C	2.35	0.46
1:E:162:ASP:HB3	1:E:175:LEU:HB3	1.97	0.46
4:G:47:ARG:CZ	4:G:47:ARG:HB3	2.45	0.46
2:F:99:VAL:HG21	2:F:184:ILE:CG2	2.36	0.46
1:E:5:VAL:HG22	2:F:16:TYR:HD1	1.78	0.46
4:C:39:VAL:HG12	4:C:56:LEU:HB2	1.97	0.46
5:H:71:ILE:HG13	5:H:71:ILE:H	1.63	0.46
1:E:35:ASP:O	1:E:39:LYS:N	2.47	0.46
1:E:160:ILE:HG23	1:E:177:HIS:CE1	2.50	0.46
5:D:174:VAL:O	5:D:175:ASN:HB2	2.16	0.46
2:F:164:THR:HA	2:F:165:PRO:HD3	1.68	0.46
1:A:139:VAL:HG12	1:A:145:PHE:CE2	2.50	0.46
2:F:177:HIS:CE1	2:F:178:PRO:HD2	2.51	0.46
5:H:84:GLN:O	5:H:84:GLN:HG2	2.15	0.46
1:A:160:ILE:HG23	1:A:177:HIS:CE1	2.51	0.46
5:H:223:PHE:O	5:H:241:THR:HG23	2.16	0.46
2:B:177:HIS:CE1	2:B:178:PRO:HD2	2.50	0.46
1:E:142:ASP:O	1:E:143:HIS:HB2	2.16	0.46
4:G:85:ARG:HG3	4:G:85:ARG:NH1	2.20	0.46
1:A:162:ASP:HB3	1:A:175:LEU:HB3	1.98	0.46
2:B:164:THR:HA	2:B:165:PRO:HD3	1.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:148:ILE:HB	2:B:156:GLN:HG2	1.98	0.45
4:G:186:LYS:H	4:G:186:LYS:HG2	1.44	0.45
2:F:35:GLU:HG2	2:F:35:GLU:O	2.16	0.45
1:A:41:THR:O	1:A:41:THR:HG22	2.15	0.45
1:A:51:LEU:HD12	2:B:90:THR:HG22	1.98	0.45
4:C:114:ASN:N	4:C:114:ASN:OD1	2.49	0.45
2:F:81:HIS:HE1	3:Q:12:MET:HE3	1.79	0.45
4:G:27:THR:OG1	4:G:28:THR:N	2.48	0.45
1:A:45:LEU:HD12	1:A:48:PHE:HE1	1.81	0.45
4:C:47:ARG:HB3	4:C:47:ARG:CZ	2.46	0.45
4:C:27:THR:OG1	4:C:28:THR:N	2.49	0.45
2:F:148:ILE:HB	2:F:156:GLN:HG2	1.98	0.45
2:B:104:SER:HB3	2:B:114:THR:HB	1.97	0.45
1:A:147:LYS:C	1:A:148:LEU:HD12	2.37	0.45
5:H:25:GLN:HG2	5:H:26:THR:N	2.28	0.45
2:B:27:VAL:HG12	2:B:28:THR:H	1.82	0.45
2:B:49:ALA:HB2	2:B:54:GLY:O	2.17	0.45
1:E:123:ARG:HD3	1:E:161:TYR:CE1	2.52	0.45
4:C:128:PRO:HD2	4:C:158:SER:OG	2.16	0.45
4:C:5:GLU:O	4:C:23:CYS:HA	2.17	0.45
1:A:11:THR:HG22	1:A:12:VAL:N	2.31	0.45
4:C:27:THR:HG23	4:C:29:MET:HE3	1.99	0.44
1:A:148:LEU:N	1:A:148:LEU:HD12	2.32	0.44
1:E:45:LEU:HD12	1:E:48:PHE:HE1	1.82	0.44
1:A:7:PHE:HB2	1:A:25:GLU:HB2	1.99	0.44
4:G:131:GLN:C	4:G:133:PRO:HD3	2.38	0.44
4:G:128:PRO:HD2	4:G:158:SER:OG	2.17	0.44
2:F:134:ASN:HA	2:F:170:VAL:HG12	2.00	0.44
1:E:14:GLN:HG3	1:E:15:SER:N	2.33	0.44
1:A:86:ALA:HA	1:A:87:PRO:HD3	1.56	0.44
1:A:35:ASP:O	1:A:39:LYS:N	2.49	0.44
2:B:99:VAL:CG2	2:B:184:ILE:HG21	2.36	0.44
2:B:27:VAL:CG1	2:B:28:THR:N	2.79	0.44
4:C:186:LYS:H	4:C:186:LYS:HG2	1.47	0.44
1:A:175:LEU:H	1:A:175:LEU:HD12	1.83	0.44
5:D:223:PHE:O	5:D:241:THR:HG23	2.18	0.44
2:B:70:ARG:HA	4:C:57:ALA:HB1	1.99	0.44
2:B:125:ALA:HB1	2:B:147:LEU:HD11	2.00	0.44
2:B:81:HIS:HE1	3:P:12:MET:CE	2.30	0.44
4:C:44:GLN:NE2	4:C:50:LEU:CD1	2.80	0.44
4:G:208:THR:HB	4:G:209:ASN:H	1.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:16:GLY:O	4:G:93:ASP:HA	2.18	0.44
1:E:150:TYR:CD1	1:E:150:TYR:N	2.85	0.44
2:F:27:VAL:CG1	2:F:28:THR:N	2.81	0.43
5:D:25:GLN:HG2	5:D:26:THR:N	2.28	0.43
4:C:131:GLN:C	4:C:133:PRO:HD3	2.38	0.43
4:C:155:ASP:HB2	5:D:151:LYS:HZ3	1.83	0.43
1:E:147:LYS:C	1:E:148:LEU:HD12	2.37	0.43
4:C:115:LYS:HD2	5:D:52:LEU:HD23	2.00	0.43
2:F:26:LEU:HB3	2:F:75:LEU:HD12	2.00	0.43
1:E:86:ALA:HA	1:E:87:PRO:HD3	1.56	0.43
1:E:135:THR:O	1:E:147:LYS:HG3	2.18	0.43
4:C:16:GLY:O	4:C:93:ASP:HA	2.17	0.43
2:F:181:LYS:HD2	2:F:181:LYS:N	2.16	0.43
4:G:42:PHE:HB2	4:G:103:PHE:HB2	2.01	0.43
4:C:42:PHE:HB2	4:C:103:PHE:HB2	2.01	0.43
2:B:96:GLN:HA	2:B:97:PRO:HD3	1.70	0.43
5:H:212:ASN:HB3	5:H:215:ASN:ND2	2.33	0.43
4:C:66:THR:CG2	4:C:82:THR:HG22	2.48	0.43
5:D:70:ASP:O	5:D:72:PRO:HD3	2.18	0.43
1:A:175:LEU:N	1:A:175:LEU:HD12	2.33	0.43
2:F:49:ALA:HB2	2:F:54:GLY:O	2.19	0.43
2:B:26:LEU:HB3	2:B:75:LEU:HD12	2.01	0.43
2:B:134:ASN:HA	2:B:170:VAL:HG12	2.01	0.43
1:A:14:GLN:HG3	1:A:15:SER:N	2.33	0.43
4:C:39:VAL:HG22	4:C:40:GLN:H	1.84	0.43
4:G:128:PRO:HG3	4:G:177:VAL:HG11	2.00	0.43
4:G:197:THR:CB	4:G:199:PHE:HE1	2.32	0.43
5:H:4:VAL:HG22	5:H:25:GLN:HB2	2.00	0.43
1:E:142:ASP:N	1:E:142:ASP:OD1	2.52	0.43
5:D:238:LYS:HA	5:D:239:PRO:HD3	1.84	0.43
5:H:23:CYS:HB2	5:H:41:TRP:CZ2	2.54	0.43
4:C:29:MET:HE2	4:C:108:ASP:HA	2.00	0.43
4:G:44:GLN:NE2	4:G:50:LEU:CD1	2.79	0.43
1:A:70:LEU:HD13	2:B:9:HIS:HB2	2.01	0.43
4:G:138:TYR:CE2	5:H:147:GLU:HB2	2.54	0.43
2:F:8:VAL:CG1	2:F:9:HIS:N	2.82	0.42
4:C:150:LEU:HG	4:C:151:CYS:N	2.33	0.42
5:D:183:VAL:HG12	5:D:184:CYS:N	2.34	0.42
5:H:58:VAL:O	5:H:65:SER:HB3	2.19	0.42
4:G:196:GLN:O	4:G:197:THR:C	2.56	0.42
1:E:70:LEU:HD13	2:F:9:HIS:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:7:PHE:HB2	1:E:25:GLU:HB2	2.00	0.42
1:E:32:PHE:CD1	1:E:32:PHE:C	2.92	0.42
1:A:79:PHE:O	1:A:81:PRO:HD3	2.18	0.42
1:A:123:ARG:HD3	1:A:161:TYR:CE1	2.54	0.42
4:C:141:LYS:O	4:C:143:PRO:HD3	2.19	0.42
1:A:126:LYS:HB2	1:A:126:LYS:HE3	1.68	0.42
2:F:98:ASN:HB2	2:F:120:THR:OG1	2.18	0.42
4:G:5:GLU:O	4:G:23:CYS:HA	2.19	0.42
5:D:212:ASN:HB3	5:D:215:ASN:ND2	2.35	0.42
1:A:150:TYR:CD1	1:A:150:TYR:N	2.87	0.42
4:C:181:LYS:HG3	4:C:181:LYS:H	1.72	0.42
4:C:142:ASP:HB3	4:C:148:SER:HB2	2.02	0.42
1:E:93:PRO:HG3	1:E:178:TRP:CZ2	2.55	0.42
1:E:41:THR:HG22	1:E:41:THR:O	2.19	0.42
2:B:99:VAL:HG21	2:B:184:ILE:CG2	2.38	0.42
5:D:58:VAL:O	5:D:63:ALA:C	2.57	0.42
4:G:153:PHE:CD1	4:G:153:PHE:C	2.92	0.42
4:G:114:ASN:N	4:G:114:ASN:OD1	2.53	0.42
1:A:143:HIS:HB2	2:B:34:ARG:HG3	2.01	0.42
4:G:39:VAL:HG22	4:G:40:GLN:H	1.85	0.42
1:E:175:LEU:HD12	1:E:175:LEU:H	1.85	0.42
5:H:183:VAL:HG12	5:H:184:CYS:N	2.34	0.42
2:F:74:GLU:O	2:F:78:ALA:HB3	2.19	0.42
4:G:66:THR:CG2	4:G:82:THR:HG22	2.50	0.42
4:C:208:THR:HB	4:C:209:ASN:H	1.61	0.42
2:B:98:ASN:HB2	2:B:120:THR:OG1	2.19	0.42
1:E:51:LEU:HD12	2:F:90:THR:HG22	2.01	0.42
1:E:115:PRO:CG	1:E:145:PHE:CE1	2.91	0.42
4:C:66:THR:CB	4:C:82:THR:HG22	2.47	0.42
4:G:142:ASP:HB3	4:G:148:SER:HB2	2.01	0.42
1:E:52:ILE:HD12	1:E:52:ILE:O	2.20	0.42
4:C:153:PHE:C	4:C:153:PHE:CD1	2.91	0.42
4:C:196:GLN:O	4:C:197:THR:C	2.58	0.42
1:E:175:LEU:HD12	1:E:175:LEU:N	2.34	0.42
2:B:140:VAL:C	2:B:142:VAL:H	2.23	0.42
4:C:166:MET:N	4:C:166:MET:SD	2.93	0.42
1:E:11:THR:HG23	1:E:63:ILE:HD13	2.02	0.42
2:B:60:TYR:CE1	3:P:23:TYR:HB2	2.55	0.41
1:E:79:PHE:O	1:E:81:PRO:HD3	2.20	0.41
2:B:73:ALA:C	2:B:75:LEU:N	2.73	0.41
4:G:23:CYS:O	4:G:86:TYR:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:51:LEU:HG	1:E:51:LEU:H	1.52	0.41
1:E:11:THR:HG22	1:E:12:VAL:N	2.35	0.41
5:H:58:VAL:O	5:H:63:ALA:C	2.58	0.41
1:A:51:LEU:HB2	1:A:52:ILE:H	1.73	0.41
4:G:66:THR:CB	4:G:82:THR:HG22	2.48	0.41
1:A:11:THR:HG23	1:A:63:ILE:HD13	2.02	0.41
1:A:118:ASN:HB2	6:A:300:NAG:HN2	1.86	0.41
2:F:96:GLN:HA	2:F:97:PRO:HD3	1.70	0.41
4:G:194:SER:OG	4:G:196:GLN:HB3	2.21	0.41
4:G:197:THR:HB	4:G:199:PHE:CD1	2.56	0.41
5:H:79:SER:O	5:H:81:PRO:HD2	2.19	0.41
5:D:23:CYS:HB2	5:D:41:TRP:CZ2	2.56	0.41
5:H:71:ILE:N	5:H:72:PRO:HD3	2.34	0.41
5:D:241:THR:HG22	7:D:300:NAG:C8	2.51	0.41
1:E:105:LEU:HD23	1:E:105:LEU:HA	1.74	0.41
4:C:85:ARG:CG	4:C:85:ARG:NH1	2.78	0.41
4:G:85:ARG:NH1	4:G:85:ARG:CG	2.79	0.41
2:B:177:HIS:CG	2:B:178:PRO:CD	3.03	0.41
2:B:8:VAL:CG1	2:B:9:HIS:N	2.84	0.41
4:C:23:CYS:O	4:C:86:TYR:HA	2.20	0.41
5:D:79:SER:O	5:D:81:PRO:HD2	2.20	0.41
2:F:133:ARG:HD3	2:F:138:GLU:OE2	2.20	0.41
2:B:117:CYS:SG	2:B:117:CYS:O	2.78	0.41
5:H:112:ALA:HA	5:H:113:GLY:HA2	1.80	0.41
4:G:141:LYS:O	4:G:143:PRO:HD3	2.20	0.41
4:G:29:MET:HE2	4:G:108:ASP:HA	2.02	0.41
4:C:128:PRO:HG3	4:C:177:VAL:HG11	2.01	0.41
5:H:70:ASP:O	5:H:72:PRO:HD3	2.21	0.41
2:F:160:MET:CE	2:F:160:MET:H	2.34	0.41
2:F:177:HIS:CG	2:F:178:PRO:CD	3.04	0.41
4:G:150:LEU:HG	4:G:151:CYS:N	2.35	0.41
1:E:148:LEU:HD12	1:E:148:LEU:N	2.36	0.41
4:C:138:TYR:CE2	5:D:147:GLU:HB2	2.56	0.41
5:H:232:TRP:HA	5:H:233:PRO:HD3	1.84	0.41
1:E:32:PHE:CB	1:E:43:TRP:HA	2.51	0.41
5:H:232:TRP:CD2	5:H:233:PRO:HD2	2.56	0.41
4:G:108:ASP:C	4:G:110:GLY:H	2.23	0.40
1:E:59:GLY:O	1:E:63:ILE:HG12	2.21	0.40
4:C:202:GLN:HB2	4:C:202:GLN:HE21	1.64	0.40
1:A:32:PHE:C	1:A:32:PHE:CD1	2.93	0.40
2:B:74:GLU:O	2:B:78:ALA:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:43:GLN:HG3	4:G:51:ILE:HG22	2.03	0.40
4:C:197:THR:CB	4:C:199:PHE:HE1	2.34	0.40
2:F:150:ASN:HB2	2:F:154:THR:O	2.21	0.40
4:C:197:THR:HB	4:C:199:PHE:CD1	2.56	0.40
1:A:21:GLN:HG2	1:A:22:TYR:N	2.36	0.40
2:F:140:VAL:C	2:F:142:VAL:H	2.23	0.40
5:D:107:SER:HB3	5:D:116:LEU:HB3	2.03	0.40
5:D:4:VAL:HG22	5:D:25:GLN:HB2	2.02	0.40
4:C:194:SER:OG	4:C:196:GLN:HB3	2.22	0.40
2:B:27:VAL:CG1	2:B:28:THR:H	2.33	0.40
2:B:142:VAL:HG22	2:B:161:LEU:HD13	2.03	0.40
4:G:101:THR:HG22	4:G:102:TYR:N	2.37	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	182/190 (96%)	154 (85%)	22 (12%)	6 (3%)	5	18
1	E	182/190 (96%)	155 (85%)	22 (12%)	5 (3%)	6	23
2	B	174/201 (87%)	144 (83%)	26 (15%)	4 (2%)	8	28
2	F	174/201 (87%)	144 (83%)	26 (15%)	4 (2%)	8	28
3	P	15/18 (83%)	10 (67%)	3 (20%)	2 (13%)	0	0
3	Q	15/18 (83%)	10 (67%)	3 (20%)	2 (13%)	0	0
4	C	190/229 (83%)	156 (82%)	23 (12%)	11 (6%)	2	6
4	G	190/229 (83%)	157 (83%)	23 (12%)	10 (5%)	2	7
5	D	234/259 (90%)	208 (89%)	18 (8%)	8 (3%)	5	17
5	H	234/259 (90%)	207 (88%)	19 (8%)	8 (3%)	5	17
All	All	1590/1794 (89%)	1345 (85%)	185 (12%)	60 (4%)	4	15

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	51	LEU
1	A	113	PHE
2	B	104	SER
3	P	17	LEU
4	C	182	ALA
4	C	197	THR
4	C	200	THR
4	C	206	LYS
5	D	46	THR
5	D	166	ASP
1	E	113	PHE
2	F	104	SER
3	Q	17	LEU
4	G	155	ASP
4	G	182	ALA
4	G	197	THR
4	G	200	THR
4	G	206	LYS
5	H	46	THR
5	H	166	ASP
4	C	121	GLY
4	C	155	ASP
4	C	207	GLU
5	D	47	GLY
5	D	112	ALA
1	E	51	LEU
4	G	207	GLU
5	H	47	GLY
4	C	184	ASP
4	C	198	SER
5	D	81	PRO
5	D	233	PRO
4	G	121	GLY
4	G	184	ASP
4	G	198	SER
5	H	81	PRO
5	H	112	ALA
5	H	233	PRO
1	A	181	ALA
2	B	160	MET
4	C	135	PRO
5	D	240	VAL

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Mol	Chain	Res	Type
4	G	135	PRO
5	H	240	VAL
1	A	79	PHE
1	A	173	PRO
3	P	25	LEU
1	E	173	PRO
1	E	181	ALA
2	F	116	VAL
2	F	160	MET
3	Q	25	LEU
2	B	116	VAL
2	B	165	PRO
5	D	235	GLY
2	F	165	PRO
5	H	235	GLY
1	E	155	PRO
1	A	155	PRO
4	C	3	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	165/171 (96%)	152 (92%)	13 (8%)	15	39
1	E	165/171 (96%)	152 (92%)	13 (8%)	15	39
2	B	164/181 (91%)	150 (92%)	14 (8%)	13	35
2	F	164/181 (91%)	151 (92%)	13 (8%)	15	39
3	P	12/13 (92%)	10 (83%)	2 (17%)	3	7
3	Q	12/13 (92%)	10 (83%)	2 (17%)	3	7
4	C	168/202 (83%)	149 (89%)	19 (11%)	7	20
4	G	168/202 (83%)	149 (89%)	19 (11%)	7	20
5	D	204/222 (92%)	185 (91%)	19 (9%)	11	30
5	H	204/222 (92%)	183 (90%)	21 (10%)	9	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1426/1578 (90%)	1291 (90%)	135 (10%)	11	29

All (135) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	31	LEU
1	A	51	LEU
1	A	73	LEU
1	A	88	GLN
1	A	99	LEU
1	A	105	LEU
1	A	118	ASN
1	A	142	ASP
1	A	149	SER
1	A	152	THR
1	A	153	PHE
1	A	182	ASP
2	B	18	THR
2	B	26	LEU
2	B	34	ARG
2	B	70	ARG
2	B	86	THR
2	B	105	ARG
2	B	112	HIS
2	B	114	THR
2	B	147	LEU
2	B	156	GLN
2	B	158	LEU
2	B	163	MET
2	B	170	VAL
2	B	181	LYS
3	P	13	LYS
3	P	19	ASN
4	C	5	GLU
4	C	12	SER
4	C	23	CYS
4	C	43	GLN
4	C	51	ILE
4	C	66	THR
4	C	84(A)	SER
4	C	114	ASN

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Mol	Chain	Res	Type
4	C	152	LEU
4	C	153	PHE
4	C	166	MET
4	C	176	CYS
4	C	181	LYS
4	C	187	SER
4	C	198	SER
4	C	202	GLN
4	C	203	ASP
4	C	204	ILE
4	C	207	GLU
5	D	5	THR
5	D	6	GLN
5	D	25	GLN
5	D	26	THR
5	D	58	VAL
5	D	71	ILE
5	D	88	SER
5	D	91	LEU
5	D	108	TRP
5	D	114	ASN
5	D	116	LEU
5	D	134	THR
5	D	139	SER
5	D	159	LEU
5	D	186	ASP
5	D	205	VAL
5	D	208	THR
5	D	219	CYS
5	D	242	GLN
1	E	14	GLN
1	E	31	LEU
1	E	51	LEU
1	E	73	LEU
1	E	88	GLN
1	E	99	LEU
1	E	105	LEU
1	E	118	ASN
1	E	142	ASP
1	E	149	SER
1	E	152	THR
1	E	153	PHE

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Mol	Chain	Res	Type
1	E	182	ASP
2	F	18	THR
2	F	34	ARG
2	F	70	ARG
2	F	86	THR
2	F	105	ARG
2	F	112	HIS
2	F	114	THR
2	F	147	LEU
2	F	156	GLN
2	F	158	LEU
2	F	163	MET
2	F	170	VAL
2	F	181	LYS
3	Q	13	LYS
3	Q	19	ASN
4	G	5	GLU
4	G	12	SER
4	G	23	CYS
4	G	43	GLN
4	G	51	ILE
4	G	66	THR
4	G	84(A)	SER
4	G	114	ASN
4	G	152	LEU
4	G	153	PHE
4	G	166	MET
4	G	176	CYS
4	G	181	LYS
4	G	187	SER
4	G	198	SER
4	G	202	GLN
4	G	203	ASP
4	G	204	ILE
4	G	207	GLU
5	H	5	THR
5	H	6	GLN
5	H	25	GLN
5	H	26	THR
5	H	58	VAL
5	H	71	ILE
5	H	88	SER

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Mol	Chain	Res	Type
5	H	91	LEU
5	H	108	TRP
5	H	114	ASN
5	H	116	LEU
5	H	134	THR
5	H	139	SER
5	H	159	LEU
5	H	165	PRO
5	H	186	ASP
5	H	205	VAL
5	H	208	THR
5	H	219	CYS
5	H	242	GLN
5	H	245	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	61	GLN
1	A	78	ASN
1	A	177	HIS
2	B	64	GLN
2	B	81	HIS
4	C	84	ASN
4	C	188	ASN
4	C	202	GLN
5	D	28	ASN
5	D	48	HIS
5	D	167	HIS
1	E	14	GLN
1	E	61	GLN
1	E	78	ASN
1	E	177	HIS
2	F	64	GLN
2	F	81	HIS
4	G	188	ASN
4	G	202	GLN
5	H	28	ASN
5	H	48	HIS
5	H	167	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

4 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
7	NAG	D	300	5,7	14,14,15	0.75	1 (7%)	15,19,21	1.52	2 (13%)
7	NAG	D	301	7	14,14,15	0.55	0	15,19,21	1.35	1 (6%)
7	NAG	H	300	5,7	14,14,15	0.74	1 (7%)	15,19,21	1.51	2 (13%)
7	NAG	H	301	7	14,14,15	0.59	0	15,19,21	1.34	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	D	300	5,7	-	0/6/23/26	0/1/1/1
7	NAG	D	301	7	-	0/6/23/26	0/1/1/1
7	NAG	H	300	5,7	-	0/6/23/26	0/1/1/1
7	NAG	H	301	7	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	300	NAG	O5-C1	-2.26	1.39	1.43
7	H	300	NAG	O5-C1	-2.07	1.40	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	300	NAG	C4-C3-C2	3.05	115.97	111.23
7	H	300	NAG	C4-C3-C2	3.39	116.50	111.23
7	H	301	NAG	C1-O5-C5	3.42	116.58	112.25
7	D	301	NAG	C1-O5-C5	3.60	116.82	112.25
7	H	300	NAG	C1-O5-C5	3.62	116.85	112.25
7	D	300	NAG	C1-O5-C5	4.15	117.51	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	300	NAG	1	0

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	NAG	A	300	1	14,14,15	0.45	0	15,19,21	0.89	0
6	NAG	E	300	1	14,14,15	0.50	0	15,19,21	0.95	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	A	300	1	-	0/6/23/26	0/1/1/1
6	NAG	E	300	1	1/1/5/7	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
6	E	300	NAG	C1-O5-C5	2.10	114.91	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	E	300	NAG	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	300	NAG	1	0

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, 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	184/190 (96%)	-0.18	2 (1%) 82 80	15, 39, 92, 151	0
1	E	184/190 (96%)	0.44	13 (7%) 19 13	48, 93, 146, 164	0
2	B	178/201 (88%)	-0.28	0 100 100	16, 51, 104, 149	0
2	F	178/201 (88%)	0.28	6 (3%) 49 42	43, 91, 153, 192	0
3	P	17/18 (94%)	-0.01	1 (5%) 26 20	14, 30, 89, 90	0
3	Q	17/18 (94%)	0.94	3 (17%) 2 1	51, 83, 139, 144	0
4	C	192/229 (83%)	-0.04	2 (1%) 84 82	13, 60, 125, 156	0
4	G	192/229 (83%)	0.23	7 (3%) 46 40	45, 84, 136, 169	0
5	D	236/259 (91%)	-0.29	3 (1%) 79 78	9, 37, 86, 139	0
5	H	236/259 (91%)	0.35	8 (3%) 49 42	50, 84, 135, 166	0
All	All	1614/1794 (89%)	0.07	45 (2%) 56 51	9, 69, 133, 192	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1(B)	ASP	4.8
1	E	1(A)	ILE	4.6
3	Q	25	LEU	4.3
1	E	1	GLU	4.0
5	H	234	GLU	3.7
4	G	2	MET	3.6
4	G	46	HIS	3.6
5	D	234	GLU	3.3
5	H	235	GLY	3.2
4	G	131	GLN	3.1
4	C	22	ARG	2.9
1	A	1(B)	ASP	2.7
2	F	53	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	120	THR	2.6
4	G	110	GLY	2.6
5	H	70	ASP	2.6
4	G	47	ARG	2.6
4	C	201	CYS	2.5
2	F	76	ASP	2.5
2	F	182	SER	2.4
5	D	229	GLU	2.3
1	E	122	LEU	2.3
1	E	162	ASP	2.3
1	E	131	GLY	2.3
1	E	161	TYR	2.3
3	P	25	LEU	2.3
5	H	14	VAL	2.2
5	D	235	GLY	2.2
1	E	88	GLN	2.2
2	F	128	LYS	2.2
1	E	82	ALA	2.2
3	Q	24	SER	2.2
4	G	184	ASP	2.2
5	H	127	VAL	2.2
5	H	176	GLY	2.1
5	H	19	VAL	2.1
1	A	1	GLU	2.1
1	E	79	PHE	2.1
5	H	21	LEU	2.1
1	E	163	CYS	2.1
1	E	166	GLU	2.0
4	G	201	CYS	2.0
2	F	126	LYS	2.0
2	F	166	HIS	2.0
3	Q	10	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](#)

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. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(Å ²)	Q<0.9
7	NAG	D	300	14/15	0.91	0.17	0.56	39,41,42,43	0
7	NAG	H	300	14/15	0.94	0.16	-0.82	71,73,74,75	0
7	NAG	D	301	14/15	0.81	0.27	-	122,123,125,126	0
7	NAG	H	301	14/15	0.63	0.30	-	128,130,132,132	0

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(Å ²)	Q<0.9
6	NAG	A	300	14/15	0.76	0.35	-	119,121,122,123	0
6	NAG	E	300	14/15	0.81	0.33	-	169,171,172,173	0

6.5 Other polymers

There are no such residues in this entry.