



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:55 am GMT

PDB ID : 3MV9
Title : Crystal Structure of the TK3-Gln55Ala TCR in complex with HLA-B*3501/HPVG
Authors : Gras, S.; Chen, Z.; Miles, J.J.; Liu, Y.C.; Bell, M.J.; Sullivan, L.C.; Kjer-Nielsen, L.; Brennan, R.M.; Burrows, J.M.; Neller, M.A.; Khanna, R.; Purcell, A.W.; Brooks, A.G.; McCluskey, J.; Rossjohn, J.; Burrows, S.R.
Deposited on : 2010-05-03
Resolution : 2.70 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

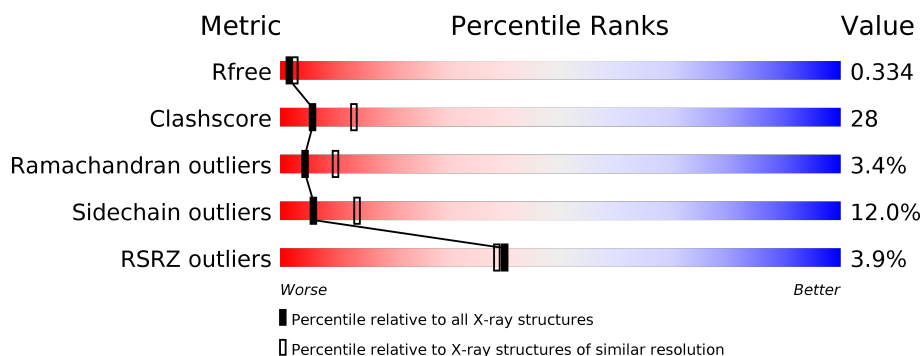
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	276	
2	B	100	
3	C	11	
4	D	200	
5	E	241	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6745 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 I histocompatibility antigen, B-35 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2254	1405	411	431	7			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	INITIATING METHIONINE	UNP P61769

- Molecule 3 is a protein called HPVG peptide from Epstein-Barr nuclear antigen 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	11	Total	C	N	O	0	0	0
			95	62	13	20			

- Molecule 4 is a protein called alpha chain of the TK3 TCR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	200	Total	C	N	O	S	0	1	0
			1568	977	261	323	7			

- Molecule 5 is a protein called beta chain of the TK3 TCR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	241	Total	C	N	O	S	0	2	0
			1924	1210	335	374	5			

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	O	S	0	0
			5	4	1		

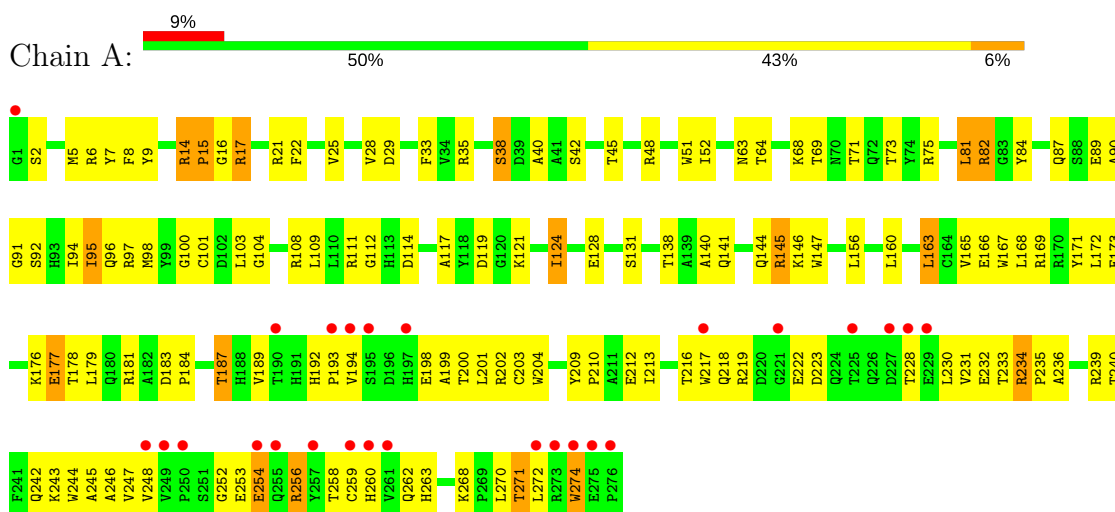
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	14	Total	O	0	0
			14	14		
7	B	4	Total	O	0	0
			4	4		
7	C	4	Total	O	0	0
			4	4		
7	D	18	Total	O	0	0
			18	18		
7	E	22	Total	O	0	0
			22	22		

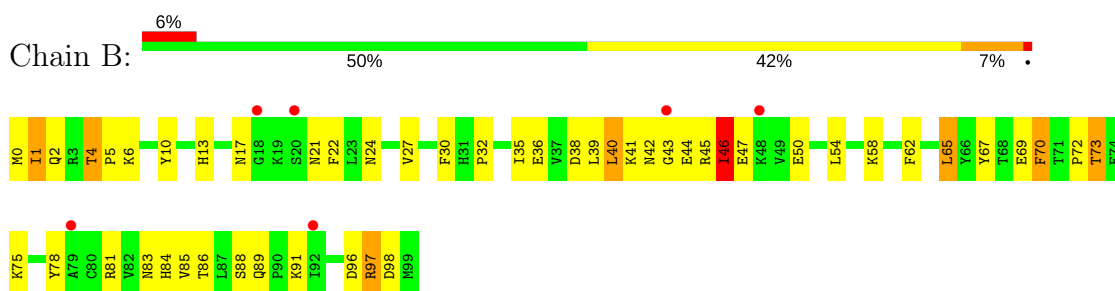
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 I histocompatibility antigen, B-35 alpha chain



- Molecule 2: Beta-2-microglobulin

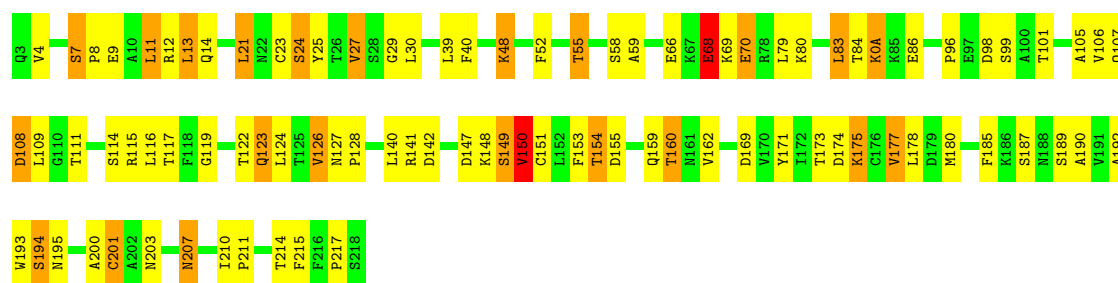


- Molecule 3: HPVG peptide from Epstein-Barr nuclear antigen 1



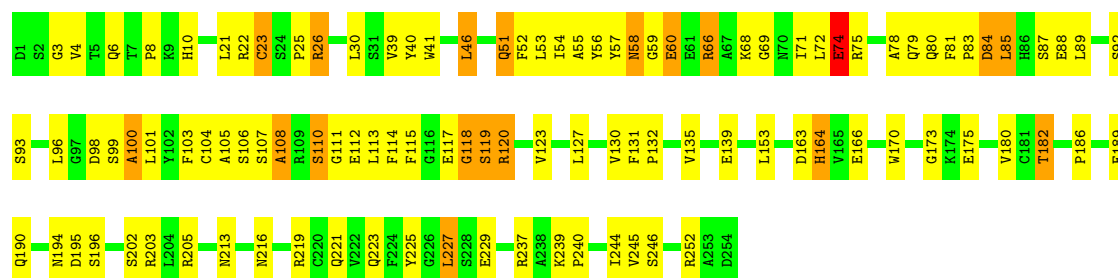
- Molecule 4: alpha chain of the TK3 TCR





• Molecule 5: beta chain of the TK3 TCR

Chain E: 56% 36% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	44.90Å 62.57Å 98.14Å 92.04° 102.29° 109.18°	Depositor
Resolution (Å)	39.25 – 2.70 39.25 – 2.70	Depositor EDS
% Data completeness (in resolution range)	83.7 (39.25-2.70) 90.8 (39.25-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.4_4)	Depositor
R, R_{free}	0.234 , 0.331 0.242 , 0.334	Depositor DCC
R_{free} test set	1283 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	45.4	Xtriage
Anisotropy	0.625	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for h,-h-k,-h-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6745	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.36	0/2317	0.53	0/3150
2	B	0.30	0/860	0.50	0/1162
3	C	0.43	0/99	0.54	0/133
4	D	0.42	0/1601	0.63	0/2167
5	E	0.40	0/1973	0.61	0/2682
All	All	0.38	0/6850	0.57	0/9294

There are no bond length outliers.

There are no bond angle outliers.

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	2254	0	2117	128	0
2	B	837	0	803	46	0
3	C	95	0	76	8	0
4	D	1568	0	1491	89	0
5	E	1924	0	1825	105	0
6	D	5	0	0	0	0
7	A	14	0	0	1	0
7	B	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	4	0	0	1	0
7	D	18	0	0	2	0
7	E	22	0	0	2	0
All	All	6745	0	6312	364	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 28.

All (364) 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:D:68:GLU:HB3	4:D:69:LYS:HA	1.25	1.17
4:D:0(A):LYS:H	4:D:0(A):LYS:HD2	1.23	0.99
5:E:59:GLY:CA	5:E:60:GLU:HB2	1.93	0.98
1:A:103:LEU:HD13	1:A:168:LEU:HD23	1.41	0.98
2:B:35:ILE:HG23	2:B:36:GLU:H	1.28	0.97
4:D:68:GLU:HB3	4:D:69:LYS:CA	1.96	0.96
5:E:135:VAL:HG22	5:E:245:VAL:HG12	1.52	0.92
5:E:59:GLY:HA3	5:E:60:GLU:HB2	1.49	0.92
4:D:142:ASP:HB3	4:D:147:ASP:HA	1.51	0.89
4:D:14:GLN:NE2	4:D:127:ASN:HD22	1.70	0.89
5:E:8:PRO:O	5:E:119:SER:HB2	1.74	0.88
1:A:145:ARG:HG3	1:A:145:ARG:HH11	1.38	0.86
5:E:3:GLY:HA3	5:E:26:ARG:HG2	1.56	0.86
5:E:110:SER:N	5:E:111:GLY:HA2	1.90	0.84
5:E:22:ARG:HG2	5:E:23:CYS:H	1.40	0.83
2:B:40:LEU:H	2:B:40:LEU:HD23	1.42	0.83
1:A:15:PRO:HG3	1:A:92:SER:HB2	1.61	0.83
4:D:0(A):LYS:CD	4:D:0(A):LYS:H	1.91	0.83
4:D:8:PRO:O	4:D:122:THR:HG23	1.79	0.82
5:E:68:LYS:HE3	5:E:71:ILE:HD11	1.59	0.82
1:A:145:ARG:CG	1:A:145:ARG:HH11	1.93	0.82
5:E:84:ASP:O	5:E:85:LEU:HG	1.79	0.81
5:E:110:SER:H	5:E:111:GLY:HA2	1.43	0.81
1:A:200:THR:HA	1:A:248:VAL:HG13	1.62	0.81
2:B:46:ILE:O	2:B:46:ILE:HG23	1.79	0.80
5:E:75:ARG:HD3	5:E:93:SER:HB2	1.63	0.80
4:D:7:SER:HB3	4:D:8:PRO:HD3	1.64	0.80
5:E:59:GLY:N	5:E:60:GLU:HB2	1.97	0.79
4:D:14:GLN:HE22	4:D:127:ASN:HD22	1.27	0.78
4:D:174:ASP:O	4:D:175:LYS:HB3	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:ARG:HH21	1:A:128:GLU:HB2	1.46	0.78
4:D:150:VAL:HG23	4:D:193:TRP:HB3	1.67	0.76
4:D:0(A):LYS:N	4:D:0(A):LYS:HD2	2.00	0.76
2:B:35:ILE:HG23	2:B:36:GLU:N	2.00	0.76
1:A:219:ARG:H	1:A:222:GLU:HB2	1.51	0.75
1:A:202:ARG:HD3	1:A:246:ALA:HB2	1.68	0.74
1:A:234:ARG:HE	1:A:242:GLN:HE21	1.33	0.74
4:D:14:GLN:HE22	4:D:127:ASN:ND2	1.85	0.74
5:E:22:ARG:HG2	5:E:23:CYS:N	2.02	0.73
4:D:21:LEU:HD12	4:D:21:LEU:N	2.03	0.73
5:E:21:LEU:HD12	5:E:89:LEU:HD23	1.72	0.72
3:C:8:TYR:CZ	5:E:108:ALA:HB2	2.25	0.72
5:E:74:GLU:HG2	5:E:75:ARG:N	2.04	0.71
1:A:234:ARG:HG3	2:B:10:TYR:CZ	2.26	0.71
4:D:40:PHE:CE1	4:D:55:THR:HB	2.25	0.70
1:A:14:ARG:NH2	1:A:21:ARG:HB2	2.06	0.70
4:D:79:LEU:N	4:D:79:LEU:HD12	2.07	0.70
1:A:259:CYS:HB3	1:A:272:LEU:HD11	1.74	0.69
4:D:96:PRO:HA	4:D:126:VAL:HB	1.74	0.69
5:E:59:GLY:H	5:E:60:GLU:HB2	1.54	0.69
5:E:110:SER:N	5:E:111:GLY:CA	2.55	0.69
1:A:189:VAL:HA	1:A:202:ARG:O	1.92	0.69
1:A:69:THR:O	1:A:73:THR:HG23	1.92	0.68
2:B:4:THR:HA	2:B:86:THR:HG21	1.75	0.68
2:B:84:HIS:ND1	2:B:86:THR:HG22	2.08	0.68
5:E:180:VAL:HA	5:E:203:ARG:O	1.93	0.67
4:D:175:LYS:HA	4:D:189:SER:O	1.95	0.67
5:E:237:ARG:HH12	5:E:240:PRO:HG3	1.59	0.67
4:D:23:CYS:O	4:D:86:GLU:HB2	1.95	0.67
2:B:24:ASN:ND2	2:B:67:TYR:HB3	2.09	0.67
1:A:51:TRP:HZ3	1:A:52:ILE:HD13	1.59	0.66
4:D:48:LYS:H	4:D:48:LYS:HD2	1.61	0.66
5:E:81:PHE:HB3	5:E:83:PRO:HD2	1.78	0.66
4:D:105:ALA:HB1	4:D:116:LEU:HD22	1.76	0.66
4:D:69:LYS:O	4:D:70:GLU:HB2	1.95	0.66
5:E:107:SER:O	5:E:108:ALA:CB	2.44	0.65
5:E:59:GLY:CA	5:E:60:GLU:CB	2.73	0.65
5:E:194:ASN:C	5:E:196:SER:H	2.00	0.65
1:A:89:GLU:O	1:A:91:GLY:HA3	1.97	0.65
1:A:203:CYS:SG	1:A:272:LEU:HD21	2.37	0.64
1:A:6:ARG:HH11	1:A:6:ARG:HG2	1.60	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:35:ILE:CG2	2:B:36:GLU:H	2.08	0.64
1:A:14:ARG:HH21	1:A:21:ARG:HB2	1.63	0.63
1:A:202:ARG:HH12	2:B:98:ASP:HB3	1.63	0.63
5:E:68:LYS:HG3	5:E:71:ILE:HD11	1.80	0.63
1:A:112:GLY:HA3	1:A:160:LEU:HD13	1.81	0.63
2:B:45:ARG:HH11	2:B:47:GLU:HB2	1.64	0.63
2:B:45:ARG:O	2:B:46:ILE:HB	1.99	0.63
3:C:8:TYR:OH	5:E:108:ALA:HB2	2.00	0.62
1:A:2:SER:HB3	1:A:104:GLY:O	2.00	0.62
4:D:174:ASP:O	4:D:175:LYS:CB	2.47	0.62
5:E:41:TRP:O	5:E:53:LEU:HB2	2.00	0.62
3:C:7:ASP:HB3	3:C:8:TYR:CD1	2.35	0.61
1:A:199:ALA:HA	7:A:277:HOH:O	2.00	0.61
4:D:207:ASN:ND2	4:D:207:ASN:H	1.97	0.61
4:D:200:ALA:O	4:D:201:CYS:HB2	2.00	0.61
1:A:6:ARG:NH1	1:A:6:ARG:HG2	2.16	0.61
1:A:94:ILE:HG22	1:A:119:ASP:HA	1.82	0.61
2:B:44:GLU:HG3	2:B:81:ARG:NH1	2.16	0.61
1:A:202:ARG:NH1	2:B:98:ASP:HB3	2.15	0.61
1:A:219:ARG:H	1:A:222:GLU:CB	2.13	0.60
1:A:95:ILE:O	1:A:95:ILE:HG13	2.01	0.60
2:B:2:GLN:HG2	2:B:32:PRO:HD3	1.84	0.60
4:D:48:LYS:N	4:D:48:LYS:HD2	2.16	0.60
5:E:72:LEU:O	5:E:75:ARG:N	2.35	0.60
1:A:173:GLU:O	1:A:176:LYS:HG2	2.02	0.60
4:D:0(A):LYS:N	4:D:0(A):LYS:CD	2.63	0.60
5:E:57:TYR:CD2	5:E:58:ASN:N	2.70	0.59
4:D:13:LEU:HD22	4:D:124:LEU:CD1	2.33	0.59
5:E:78:ALA:HB2	5:E:89:LEU:HA	1.85	0.59
2:B:70:PHE:HD1	2:B:78:TYR:CZ	2.20	0.58
5:E:135:VAL:CG2	5:E:245:VAL:HG12	2.30	0.58
1:A:14:ARG:HB3	1:A:17:ARG:HE	1.67	0.58
2:B:46:ILE:O	2:B:46:ILE:CG2	2.49	0.58
1:A:103:LEU:HD11	1:A:165:VAL:HG13	1.84	0.58
5:E:25:PRO:HB3	5:E:106:SER:HB2	1.85	0.58
5:E:68:LYS:HE3	5:E:71:ILE:CD1	2.31	0.58
1:A:209:TYR:CG	1:A:210:PRO:HA	2.39	0.57
5:E:78:ALA:HB2	5:E:89:LEU:HD12	1.87	0.57
1:A:145:ARG:NH1	1:A:145:ARG:CG	2.60	0.57
4:D:117:THR:HA	7:D:233:HOH:O	2.05	0.57
4:D:154:THR:OG1	4:D:155:ASP:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:201:CYS:C	4:D:203:ASN:H	2.08	0.57
5:E:66[A]:ARG:O	5:E:66[A]:ARG:HG3	2.05	0.57
2:B:22:PHE:CE1	2:B:69:GLU:HG2	2.39	0.56
4:D:178:LEU:H	4:D:178:LEU:HD12	1.70	0.56
4:D:27:VAL:HG22	4:D:108:ASP:CG	2.24	0.56
4:D:40:PHE:HD1	4:D:52:PHE:HE2	1.52	0.56
4:D:52:PHE:HZ	4:D:55:THR:HG22	1.69	0.56
5:E:39:VAL:HG11	5:E:87:SER:CB	2.35	0.56
1:A:201:LEU:HB2	1:A:247:VAL:HG23	1.88	0.56
5:E:59:GLY:H	5:E:60:GLU:CB	2.18	0.56
4:D:215:PHE:CD2	4:D:217:PRO:HD3	2.40	0.56
5:E:26:ARG:NH1	5:E:114:PHE:CE2	2.74	0.56
1:A:218:GLN:CG	1:A:222:GLU:H	2.19	0.56
4:D:29:GLY:O	4:D:108:ASP:HA	2.05	0.55
5:E:163:ASP:OD1	5:E:186:PRO:HG2	2.06	0.55
1:A:218:GLN:HG2	1:A:222:GLU:H	1.71	0.55
4:D:24:SER:HA	4:D:86:GLU:HB3	1.89	0.55
5:E:57:TYR:CD2	5:E:58:ASN:HB2	2.42	0.55
1:A:218:GLN:HB2	1:A:258:THR:HG23	1.88	0.55
5:E:79:GLN:HG2	5:E:80:GLN:N	2.22	0.55
4:D:21:LEU:N	4:D:21:LEU:CD1	2.68	0.55
2:B:84:HIS:CE1	2:B:85:VAL:HG12	2.41	0.55
5:E:59:GLY:N	5:E:60:GLU:CB	2.69	0.55
5:E:68:LYS:CE	5:E:71:ILE:HD11	2.32	0.55
1:A:15:PRO:HA	1:A:91:GLY:C	2.28	0.55
5:E:40:TYR:CE2	5:E:107:SER:HB3	2.43	0.54
2:B:40:LEU:CD2	2:B:40:LEU:H	2.18	0.54
7:C:61:HOH:O	5:E:66[A]:ARG:HD3	2.08	0.54
2:B:13:HIS:H	2:B:21:ASN:HD21	1.55	0.54
1:A:15:PRO:HD2	1:A:17:ARG:CZ	2.38	0.54
1:A:35:ARG:HD3	1:A:48:ARG:HH21	1.73	0.54
1:A:94:ILE:CG2	1:A:119:ASP:HA	2.37	0.54
4:D:180:MET:CE	5:E:205:ARG:HD3	2.37	0.54
1:A:9:TYR:O	1:A:96:GLN:HA	2.07	0.54
2:B:89:GLN:HG3	2:B:91:LYS:NZ	2.22	0.54
2:B:41:LYS:C	2:B:43:GLY:H	2.11	0.54
4:D:162:VAL:HG21	4:D:190:ALA:HB2	1.89	0.54
5:E:46:LEU:HG	5:E:120:ARG:NH2	2.23	0.54
4:D:79:LEU:H	4:D:79:LEU:HD12	1.73	0.53
2:B:72:PRO:O	2:B:73:THR:HG23	2.07	0.53
1:A:176:LYS:O	1:A:177:GLU:CB	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:VAL:HG13	1:A:274:TRP:HB3	1.91	0.53
1:A:198:GLU:HG2	1:A:252:GLY:HA3	1.91	0.53
2:B:5:PRO:HA	2:B:30:PHE:HB3	1.90	0.53
5:E:219:ARG:NH2	7:E:37:HOH:O	2.42	0.53
1:A:259:CYS:HB3	1:A:272:LEU:CD1	2.37	0.53
4:D:7:SER:HB3	4:D:8:PRO:CD	2.38	0.52
5:E:21:LEU:HD22	5:E:119:SER:OG	2.10	0.52
1:A:15:PRO:C	1:A:17:ARG:H	2.12	0.52
2:B:24:ASN:HD22	2:B:67:TYR:HB3	1.74	0.52
4:D:128:PRO:CG	4:D:177:VAL:HG21	2.38	0.52
4:D:178:LEU:CD2	5:E:205:ARG:HB2	2.39	0.52
2:B:54:LEU:HD11	2:B:62:PHE:CD1	2.45	0.52
5:E:139:GLU:OE2	5:E:252:ARG:HD3	2.10	0.52
1:A:259:CYS:HB3	1:A:272:LEU:CG	2.40	0.52
5:E:99:SER:O	5:E:100:ALA:HB2	2.09	0.52
1:A:169:ARG:HA	1:A:172:LEU:HD12	1.90	0.51
3:C:6:ALA:HB3	3:C:9:PHE:CE1	2.44	0.51
1:A:124:ILE:HD11	1:A:144:GLN:HB2	1.92	0.51
1:A:200:THR:HG22	1:A:202:ARG:HH21	1.76	0.51
1:A:8:PHE:HB2	1:A:25:VAL:CG2	2.41	0.51
2:B:44:GLU:HG3	2:B:81:ARG:CZ	2.40	0.51
4:D:142:ASP:HB2	4:D:148:LYS:H	1.73	0.51
4:D:140:LEU:O	4:D:149:SER:HA	2.10	0.51
5:E:74:GLU:HG2	5:E:75:ARG:H	1.73	0.51
4:D:207:ASN:H	4:D:207:ASN:HD22	1.57	0.51
1:A:176:LYS:O	1:A:177:GLU:HB3	2.09	0.51
1:A:203:CYS:HB2	1:A:217:TRP:CZ2	2.46	0.51
1:A:163:LEU:CD2	1:A:167:TRP:HE1	2.24	0.51
4:D:123:GLN:C	4:D:123:GLN:OE1	2.49	0.51
4:D:68:GLU:CB	4:D:69:LYS:CA	2.80	0.51
1:A:230:LEU:HD13	1:A:245:ALA:HB2	1.91	0.51
4:D:21:LEU:H	4:D:21:LEU:CD1	2.24	0.51
2:B:17:ASN:HD22	2:B:73:THR:HA	1.75	0.50
5:E:98:ASP:O	5:E:99:SER:C	2.50	0.50
1:A:14:ARG:HB2	1:A:17:ARG:HG3	1.94	0.50
1:A:15:PRO:HA	1:A:91:GLY:O	2.10	0.50
4:D:21:LEU:HD12	4:D:21:LEU:H	1.74	0.50
1:A:22:PHE:H	1:A:38:SER:CB	2.25	0.50
1:A:231:VAL:HG21	1:A:244:TRP:CZ2	2.47	0.50
1:A:15:PRO:HD2	1:A:17:ARG:NH2	2.26	0.50
4:D:128:PRO:HG3	4:D:177:VAL:HG21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:72:LEU:O	5:E:74:GLU:C	2.50	0.50
2:B:96:ASP:OD1	2:B:97:ARG:N	2.44	0.49
1:A:177:GLU:O	1:A:181:ARG:HB2	2.11	0.49
2:B:39:LEU:HB2	2:B:46:ILE:HG21	1.93	0.49
4:D:160:THR:HG21	4:D:211:PRO:HD3	1.94	0.49
1:A:222:GLU:HG3	1:A:223:ASP:H	1.78	0.49
1:A:260:HIS:CE1	1:A:271:THR:HG23	2.48	0.49
4:D:171:TYR:O	4:D:192:ALA:HA	2.12	0.49
5:E:84:ASP:OD1	5:E:85:LEU:N	2.45	0.49
1:A:192:HIS:HE1	2:B:98:ASP:CG	2.16	0.49
5:E:39:VAL:HG11	5:E:87:SER:HB2	1.93	0.49
5:E:54:ILE:HD13	5:E:56:TYR:OH	2.13	0.49
1:A:124:ILE:HD12	1:A:140:ALA:O	2.13	0.49
5:E:54:ILE:HG12	5:E:55:ALA:H	1.77	0.48
4:D:211:PRO:O	4:D:214:THR:OG1	2.30	0.48
5:E:112:GLU:CD	5:E:112:GLU:H	2.17	0.48
1:A:51:TRP:CZ3	1:A:52:ILE:HD13	2.46	0.48
1:A:64:THR:O	1:A:68:LYS:HB2	2.13	0.48
4:D:140:LEU:HD12	4:D:140:LEU:N	2.28	0.48
4:D:207:ASN:N	4:D:207:ASN:ND2	2.61	0.48
1:A:28:VAL:HG23	1:A:33:PHE:CE2	2.48	0.48
1:A:22:PHE:H	1:A:38:SER:HB3	1.78	0.48
1:A:256:ARG:HD2	1:A:256:ARG:O	2.14	0.48
4:D:11:LEU:HD13	4:D:124:LEU:HD13	1.94	0.48
4:D:180:MET:HE2	5:E:205:ARG:HD3	1.94	0.48
1:A:89:GLU:C	1:A:91:GLY:HA3	2.34	0.48
1:A:178:THR:HA	1:A:239:ARG:NH2	2.28	0.48
2:B:70:PHE:HD1	2:B:78:TYR:CE2	2.32	0.48
5:E:103:PHE:CE1	5:E:118:GLY:HA3	2.49	0.48
1:A:272:LEU:O	1:A:272:LEU:HD12	2.14	0.47
1:A:228:THR:HG23	1:A:246:ALA:O	2.15	0.47
5:E:100:ALA:HA	5:E:120:ARG:NH2	2.29	0.47
5:E:101:LEU:HG	5:E:120:ARG:HG2	1.97	0.47
1:A:268:LYS:HE3	1:A:268:LYS:HB2	1.69	0.47
1:A:15:PRO:O	1:A:17:ARG:HG2	2.14	0.47
5:E:107:SER:O	5:E:108:ALA:HB3	2.14	0.47
5:E:194:ASN:C	5:E:196:SER:N	2.66	0.47
4:D:98:ASP:O	4:D:124:LEU:HD23	2.15	0.47
5:E:54:ILE:HG12	5:E:55:ALA:N	2.30	0.47
5:E:10:HIS:CD2	5:E:225:TYR:CE1	3.03	0.46
1:A:28:VAL:O	1:A:29:ASP:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:4:VAL:O	4:D:119:GLY:HA2	2.15	0.46
4:D:171:TYR:HE1	5:E:189:GLU:HA	1.79	0.46
1:A:7:TYR:O	1:A:98:MET:HA	2.15	0.46
4:D:201:CYS:C	4:D:203:ASN:N	2.68	0.46
2:B:35:ILE:O	2:B:83:ASN:O	2.33	0.46
5:E:72:LEU:C	5:E:75:ARG:N	2.67	0.46
1:A:187:THR:HG21	1:A:270:LEU:HD13	1.98	0.46
1:A:218:GLN:HG2	1:A:222:GLU:O	2.15	0.46
1:A:81:LEU:HD12	1:A:84:TYR:CE2	2.51	0.46
4:D:150:VAL:O	4:D:150:VAL:CG1	2.64	0.46
4:D:69:LYS:HA	4:D:69:LYS:HD2	1.71	0.46
5:E:4:VAL:HG21	5:E:114:PHE:O	2.15	0.46
5:E:182:THR:HB	5:E:202:SER:HB2	1.97	0.46
5:E:96:LEU:HD23	5:E:123:VAL:O	2.15	0.46
1:A:177:GLU:O	1:A:181:ARG:NE	2.49	0.46
5:E:131:PHE:HA	5:E:132:PRO:HD3	1.77	0.46
1:A:209:TYR:CD1	1:A:210:PRO:HA	2.50	0.45
1:A:28:VAL:HG23	1:A:33:PHE:CD2	2.51	0.45
1:A:5:MET:O	1:A:100:GLY:HA3	2.16	0.45
1:A:203:CYS:O	1:A:244:TRP:HB2	2.16	0.45
5:E:237:ARG:NH1	5:E:240:PRO:HG3	2.29	0.45
5:E:57:TYR:HD2	5:E:58:ASN:N	2.14	0.45
5:E:244:ILE:HG13	5:E:244:ILE:O	2.15	0.45
1:A:200:THR:HG22	1:A:202:ARG:NH2	2.31	0.45
1:A:71:THR:O	1:A:75:ARG:HG3	2.17	0.45
3:C:8:TYR:CE1	5:E:108:ALA:HB2	2.51	0.45
5:E:164:HIS:HB3	5:E:225:TYR:HB2	1.99	0.45
1:A:253:GLU:H	1:A:256:ARG:HH21	1.65	0.45
4:D:83:LEU:HD22	4:D:84:THR:O	2.17	0.45
2:B:22:PHE:CZ	2:B:69:GLU:HG2	2.51	0.45
1:A:234:ARG:NE	1:A:242:GLN:HE21	2.07	0.44
4:D:13:LEU:HD22	4:D:124:LEU:HD13	2.00	0.44
4:D:149:SER:O	4:D:150:VAL:O	2.34	0.44
1:A:15:PRO:C	1:A:17:ARG:N	2.70	0.44
5:E:3:GLY:HA3	5:E:26:ARG:CG	2.37	0.44
5:E:75:ARG:HD2	5:E:92:SER:O	2.16	0.44
1:A:232:GLU:HG2	1:A:233:THR:N	2.33	0.44
2:B:5:PRO:CA	2:B:30:PHE:HB3	2.47	0.44
4:D:66:GLU:HB3	4:D:80:LYS:HE2	1.98	0.44
4:D:149:SER:O	4:D:150:VAL:HG12	2.17	0.44
5:E:170:TRP:CE3	5:E:173:GLY:O	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1:HIS:ND1	3:C:2:PRO:HD2	2.33	0.44
2:B:65:LEU:C	2:B:65:LEU:HD23	2.38	0.44
4:D:128:PRO:HG2	4:D:177:VAL:HG21	2.00	0.44
1:A:63:ASN:HD22	1:A:63:ASN:N	2.16	0.44
3:C:1:HIS:HA	3:C:2:PRO:HD3	1.76	0.44
1:A:15:PRO:O	1:A:17:ARG:N	2.51	0.44
1:A:232:GLU:HG2	1:A:233:THR:H	1.81	0.44
4:D:106:VAL:HG22	4:D:107:GLN:N	2.33	0.44
5:E:239:LYS:HA	5:E:240:PRO:HD3	1.60	0.44
5:E:83:PRO:O	5:E:84:ASP:O	2.35	0.44
2:B:50:GLU:HB2	2:B:67:TYR:CE1	2.53	0.43
4:D:25:TYR:O	4:D:25:TYR:CD1	2.72	0.43
5:E:105:ALA:HB2	5:E:115:PHE:CD2	2.54	0.43
1:A:156:LEU:O	1:A:160:LEU:HG	2.18	0.43
4:D:68:GLU:HB3	4:D:69:LYS:CB	2.45	0.43
2:B:65:LEU:CD2	2:B:67:TYR:HD2	2.30	0.43
4:D:140:LEU:O	4:D:149:SER:O	2.35	0.43
1:A:212:GLU:O	1:A:263:HIS:CD2	2.71	0.43
2:B:89:GLN:HG3	2:B:91:LYS:HZ2	1.83	0.43
1:A:202:ARG:HG2	1:A:204:TRP:CE2	2.54	0.43
5:E:46:LEU:HG	5:E:120:ARG:HH21	1.83	0.43
1:A:233:THR:OG1	1:A:243:LYS:HD2	2.19	0.43
1:A:163:LEU:HD23	1:A:167:TRP:HE1	1.83	0.43
1:A:234:ARG:HB2	1:A:235:PRO:HD2	2.01	0.43
1:A:260:HIS:HA	1:A:270:LEU:O	2.19	0.43
5:E:57:TYR:HD2	5:E:58:ASN:HB2	1.80	0.43
5:E:57:TYR:HD2	5:E:58:ASN:H	1.67	0.43
4:D:180:MET:HG3	4:D:185:PHE:HD2	1.83	0.42
1:A:97:ARG:HH21	1:A:114:ASP:CG	2.22	0.42
4:D:23:CYS:O	4:D:86:GLU:CB	2.65	0.42
5:E:68:LYS:CG	5:E:71:ILE:HD11	2.47	0.42
1:A:167:TRP:HB3	1:A:171:TYR:CE2	2.54	0.42
4:D:148:LYS:O	4:D:150:VAL:N	2.52	0.42
4:D:160:THR:HG21	4:D:211:PRO:HG3	2.00	0.42
5:E:81:PHE:HE2	5:E:88:GLU:HB2	1.83	0.42
2:B:41:LYS:HB3	2:B:41:LYS:HE2	1.86	0.42
4:D:105:ALA:CB	4:D:116:LEU:HD22	2.46	0.42
5:E:130:VAL:HG12	5:E:240:PRO:CB	2.49	0.42
5:E:30:LEU:O	5:E:57:TYR:O	2.38	0.42
1:A:2:SER:CB	1:A:104:GLY:O	2.67	0.42
1:A:179:LEU:HA	1:A:179:LEU:HD23	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:VAL:O	1:A:166:GLU:C	2.58	0.42
1:A:147:TRP:NE1	3:C:10:GLU:O	2.41	0.42
1:A:90:ALA:HA	1:A:91:GLY:HA3	1.76	0.42
4:D:178:LEU:HD12	4:D:178:LEU:N	2.34	0.42
5:E:153:LEU:HD12	5:E:153:LEU:N	2.35	0.42
5:E:51[A]:GLN:HE21	5:E:51[A]:GLN:HB2	1.46	0.42
5:E:80:GLN:HE21	5:E:85:LEU:HA	1.85	0.41
1:A:183:ASP:HA	1:A:184:PRO:HD3	1.81	0.41
2:B:30:PHE:CE1	2:B:35:ILE:HD13	2.55	0.41
4:D:27:VAL:HG11	4:D:30:LEU:HB2	2.02	0.41
4:D:39:LEU:HD23	4:D:39:LEU:C	2.40	0.41
1:A:200:THR:HG23	1:A:248:VAL:CG2	2.50	0.41
4:D:159:GLN:NE2	7:D:222:HOH:O	2.53	0.41
5:E:6:GLN:HE21	5:E:6:GLN:HB3	1.69	0.41
5:E:75:ARG:CD	5:E:93:SER:HB2	2.42	0.41
1:A:176:LYS:O	1:A:177:GLU:HG2	2.19	0.41
1:A:194:VAL:O	1:A:194:VAL:HG22	2.20	0.41
1:A:260:HIS:NE2	1:A:271:THR:CG2	2.84	0.41
4:D:141:ARG:O	4:D:141:ARG:HG3	2.19	0.41
1:A:138:THR:HA	1:A:141:GLN:CD	2.40	0.41
4:D:7:SER:O	4:D:9:GLU:N	2.53	0.41
5:E:30:LEU:HA	5:E:85:LEU:HD22	2.03	0.41
1:A:82:ARG:HA	1:A:87:GLN:OE1	2.21	0.41
2:B:22:PHE:N	2:B:22:PHE:CD2	2.89	0.41
5:E:127:LEU:HD13	5:E:227:LEU:HG	2.03	0.41
1:A:202:ARG:HG2	1:A:204:TRP:CZ2	2.55	0.41
4:D:185:PHE:CE2	4:D:187:SER:HB3	2.56	0.41
5:E:213:ASN:O	5:E:216:ASN:HB2	2.21	0.41
1:A:101:CYS:HB2	1:A:109:LEU:HD23	2.03	0.41
1:A:35:ARG:HD3	1:A:48:ARG:NH2	2.36	0.41
2:B:44:GLU:HA	2:B:81:ARG:HH12	1.86	0.41
2:B:39:LEU:CB	2:B:46:ILE:HG21	2.50	0.41
5:E:52:PHE:CD1	5:E:69:GLY:HA3	2.56	0.40
1:A:213:ILE:HG13	1:A:263:HIS:HB2	2.02	0.40
1:A:95:ILE:C	1:A:95:ILE:HD12	2.41	0.40
5:E:56:TYR:N	5:E:56:TYR:CD2	2.89	0.40
1:A:192:HIS:HA	1:A:193:PRO:HD3	1.91	0.40
2:B:65:LEU:HD21	2:B:67:TYR:HD2	1.86	0.40
5:E:175:GLU:OE2	7:E:261:HOH:O	2.22	0.40
1:A:117:ALA:HA	1:A:121:LYS:O	2.22	0.40
1:A:160:LEU:HA	1:A:160:LEU:HD23	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:ALA:HB3	1:A:240:THR:OG1	2.21	0.40
1:A:94:ILE:HG23	1:A:94:ILE:O	2.22	0.40
5:E:194:ASN:O	5:E:196:SER:N	2.55	0.40
1:A:145:ARG:NH1	1:A:145:ARG:HG3	2.19	0.40
4:D:194:SER:OG	4:D:195:ASN:N	2.53	0.40
5:E:237:ARG:HH12	5:E:240:PRO:CG	2.30	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	274/276 (99%)	229 (84%)	39 (14%)	6 (2%)	8	20
2	B	98/100 (98%)	87 (89%)	9 (9%)	2 (2%)	9	22
3	C	9/11 (82%)	8 (89%)	1 (11%)	0	100	100
4	D	199/200 (100%)	166 (83%)	23 (12%)	10 (5%)	2	4
5	E	240/241 (100%)	209 (87%)	21 (9%)	10 (4%)	3	7
All	All	820/828 (99%)	699 (85%)	93 (11%)	28 (3%)	4	10

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	PRO
2	B	46	ILE
4	D	68	GLU
4	D	175	LYS
4	D	194	SER
5	E	60	GLU
5	E	74	GLU
5	E	84	ASP

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Mol	Chain	Res	Type
5	E	108	ALA
5	E	229	GLU
1	A	16	GLY
1	A	216	THR
1	A	256	ARG
4	D	150	VAL
4	D	201	CYS
5	E	195	ASP
2	B	1	ILE
4	D	149	SER
5	E	46	LEU
5	E	85	LEU
1	A	254	GLU
4	D	70	GLU
4	D	108	ASP
1	A	40	ALA
4	D	7	SER
4	D	59	ALA
5	E	100	ALA
5	E	118	GLY

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	234/234 (100%)	213 (91%)	21 (9%)	11	25
2	B	95/95 (100%)	79 (83%)	16 (17%)	2	6
3	C	9/9 (100%)	9 (100%)	0	100	100
4	D	179/178 (101%)	149 (83%)	30 (17%)	2	6
5	E	209/208 (100%)	188 (90%)	21 (10%)	9	21
All	All	726/724 (100%)	638 (88%)	88 (12%)	6	13

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	17	ARG
1	A	38	SER
1	A	42	SER
1	A	45	THR
1	A	81	LEU
1	A	82	ARG
1	A	95	ILE
1	A	108	ARG
1	A	124	ILE
1	A	131	SER
1	A	145	ARG
1	A	146	LYS
1	A	163	LEU
1	A	177	GLU
1	A	187	THR
1	A	234	ARG
1	A	254	GLU
1	A	262	GLN
1	A	271	THR
1	A	274	TRP
2	B	0	MET
2	B	1	ILE
2	B	4	THR
2	B	6	LYS
2	B	27	VAL
2	B	38	ASP
2	B	40	LEU
2	B	42	ASN
2	B	46	ILE
2	B	58	LYS
2	B	65	LEU
2	B	70	PHE
2	B	73	THR
2	B	75	LYS
2	B	88	SER
2	B	97	ARG
4	D	11	LEU
4	D	12	ARG
4	D	13	LEU
4	D	21	LEU
4	D	24	SER
4	D	27	VAL

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Mol	Chain	Res	Type
4	D	48	LYS
4	D	55	THR
4	D	58	SER
4	D	68	GLU
4	D	83	LEU
4	D	0(A)	LYS
4	D	99	SER
4	D	101	THR
4	D	109	LEU
4	D	111	THR
4	D	114	SER
4	D	115	ARG
4	D	123	GLN
4	D	126	VAL
4	D	150	VAL
4	D	151	CYS
4	D	153	PHE
4	D	154	THR
4	D	160	THR
4	D	169	ASP
4	D	173	THR
4	D	177	VAL
4	D	207	ASN
4	D	210	ILE
5	E	23	CYS
5	E	26	ARG
5	E	51[A]	GLN
5	E	51[B]	GLN
5	E	58	ASN
5	E	66[A]	ARG
5	E	74	GLU
5	E	104	CYS
5	E	110	SER
5	E	113	LEU
5	E	117	GLU
5	E	119	SER
5	E	120	ARG
5	E	164	HIS
5	E	166	GLU
5	E	182	THR
5	E	190	GLN
5	E	221	GLN

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Mol	Chain	Res	Type
5	E	223	GLN
5	E	227	LEU
5	E	246	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	63	ASN
1	A	65	GLN
1	A	174	ASN
1	A	192	HIS
1	A	218	GLN
1	A	242	GLN
1	A	263	HIS
2	B	2	GLN
2	B	24	ASN
2	B	42	ASN
4	D	14	GLN
4	D	44	GLN
4	D	129	ASN
4	D	159	GLN
4	D	207	ASN
5	E	17	GLN
5	E	58	ASN
5	E	70	ASN
5	E	80	GLN
5	E	86	HIS
5	E	164	HIS
5	E	177	HIS
5	E	190	GLN
5	E	212	GLN
5	E	213	ASN
5	E	216	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	SO4	D	1	-	4,4,4	0.16	0	6,6,6	0.07	0

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	SO4	D	1	-	-	0/0/0/0	0/0/0/0

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	276/276 (100%)	0.38	26 (9%) 9 7	21, 48, 116, 132	0
2	B	100/100 (100%)	0.43	6 (6%) 23 21	38, 67, 91, 99	0
3	C	11/11 (100%)	-0.22	0 100 100	21, 24, 28, 30	0
4	D	200/200 (100%)	-0.26	0 100 100	19, 31, 67, 90	0
5	E	241/241 (100%)	-0.26	0 100 100	21, 34, 65, 90	0
All	All	828/828 (100%)	0.04	32 (3%) 40 39	19, 39, 101, 132	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	250	PRO	6.6
1	A	194	VAL	5.1
1	A	275	GLU	4.9
1	A	217	TRP	4.8
1	A	276	PRO	4.2
1	A	193	PRO	4.1
1	A	195	SER	4.1
1	A	227	ASP	4.1
1	A	255	GLN	3.9
1	A	190	THR	3.9
1	A	228	THR	3.6
1	A	221	GLY	3.6
1	A	257	TYR	3.2
1	A	261	VAL	2.9
2	B	79	ALA	2.8
1	A	254	GLU	2.7
1	A	260	HIS	2.7
1	A	225	THR	2.7
1	A	249	VAL	2.6
1	A	274	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	197	HIS	2.5
1	A	273	ARG	2.5
1	A	272	LEU	2.5
1	A	248	VAL	2.4
2	B	92	ILE	2.3
1	A	259	CYS	2.3
2	B	20	SER	2.2
2	B	43	GLY	2.1
1	A	1	GLY	2.1
1	A	229	GLU	2.0
2	B	48	LYS	2.0
2	B	18	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 carbohydrates 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. 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	SO4	D	1	5/5	0.91	0.33	-	72,87,99,109	0

6.5 Other polymers [i](#)

There are no such residues in this entry.