



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 29, 2026 – 01:51 AM UTC

PDB ID : 3W0W / pdb_00003w0w
Title : The complex between T36-5 TCR and HLA-A24 bound to HIV-1 Nef134-10(2F) peptide in space group P212121
Authors : Shimizu, A.; Fukai, S.; Yamagata, A.; Iwamoto, A.
Deposited on : 2012-11-05
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

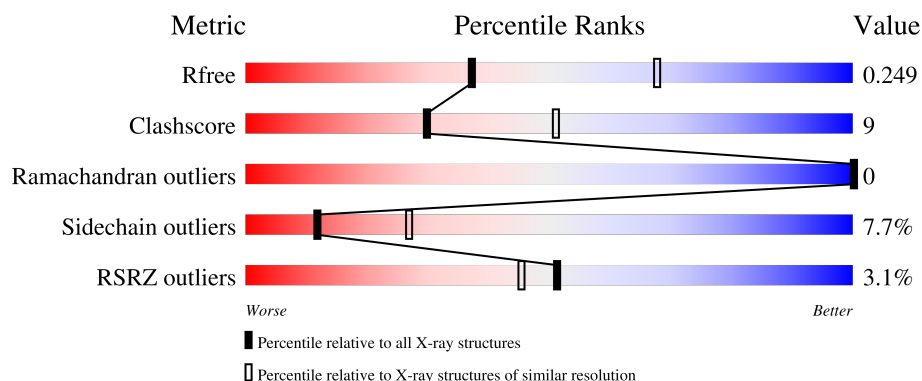
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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 ≥ 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	291	3% 75% 18% . .
2	B	100	2% 88% 11% .
3	C	10	80% 20%
4	D	205	7% 74% 23% .
5	E	242	% 85% 13% .

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7019 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, A-24 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	279	Total	C	N	O	S	0	0	0
			2247	1397	408	432	10			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP P05534
A	275	GLY	-	expression tag	UNP P05534
A	276	SER	-	expression tag	UNP P05534
A	277	LEU	-	expression tag	UNP P05534
A	278	GLY	-	expression tag	UNP P05534
A	279	GLY	-	expression tag	UNP P05534
A	280	ILE	-	expression tag	UNP P05534
A	281	PHE	-	expression tag	UNP P05534
A	282	GLU	-	expression tag	UNP P05534
A	283	ALA	-	expression tag	UNP P05534
A	284	MET	-	expression tag	UNP P05534
A	285	LYS	-	expression tag	UNP P05534
A	286	MET	-	expression tag	UNP P05534
A	287	GLU	-	expression tag	UNP P05534
A	288	LEU	-	expression tag	UNP P05534
A	289	ARG	-	expression tag	UNP P05534
A	290	ASP	-	expression tag	UNP P05534

- 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	-	expression tag	UNP P61769

- Molecule 3 is a protein called 10-mer peptide from Protein Nef.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	10	Total	C	N	O	S	0	0	0
			91	64	14	12	1			

- Molecule 4 is a protein called T36-5 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	204	Total	C	N	O	S	0	0	0
			1591	989	263	332	7			

- Molecule 5 is a protein called T36-5 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	241	Total	C	N	O	S	0	0	0
			1933	1217	336	372	8			

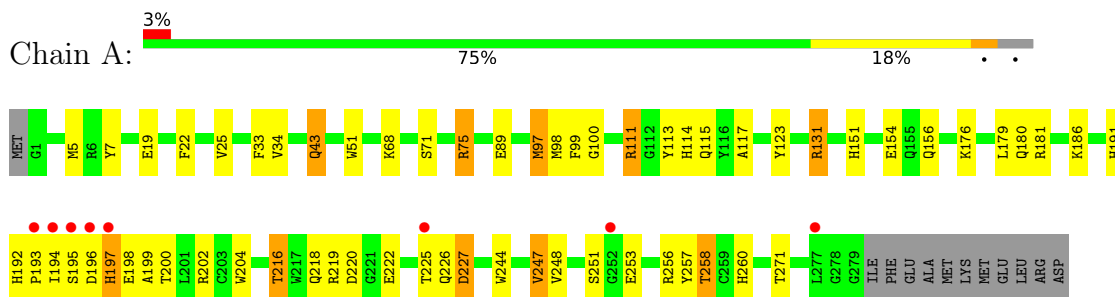
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	111	Total	O	0	0
			111	111		
6	B	53	Total	O	0	0
			53	53		
6	C	3	Total	O	0	0
			3	3		
6	D	56	Total	O	0	0
			56	56		
6	E	97	Total	O	0	0
			97	97		

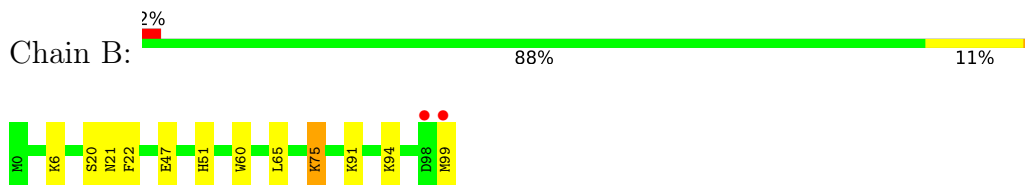
3 Residue-property plots

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.

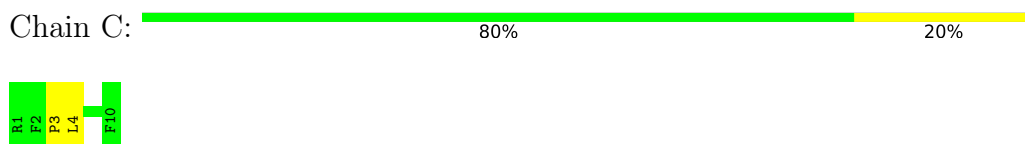
- Molecule 1: HLA class I histocompatibility antigen, A-24 alpha chain



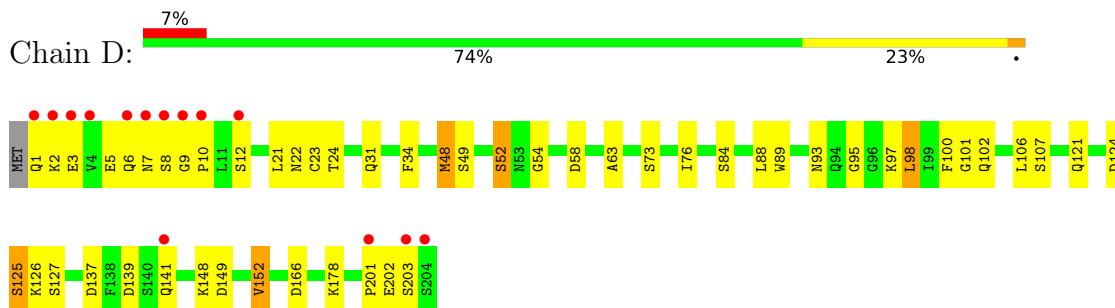
- Molecule 2: Beta-2-microglobulin



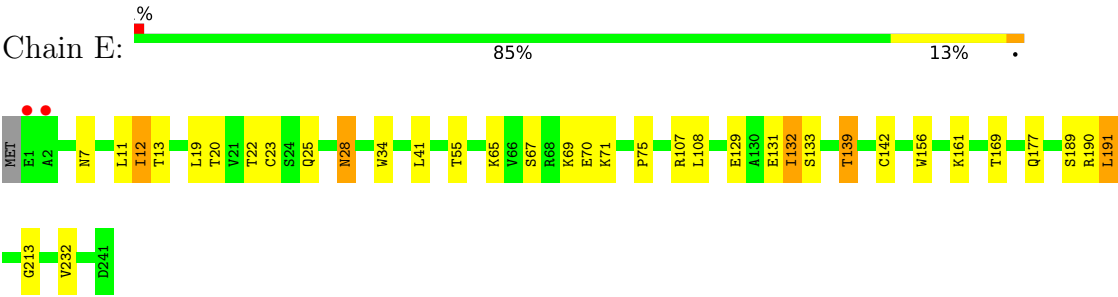
- Molecule 3: 10-mer peptide from Protein Nef



- Molecule 4: T36-5 TCR alpha chain



- Molecule 5: T36-5 TCR 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	50.92Å 86.44Å 251.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-2.60) 99.5 (50.00-2.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 2.61Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.186 , 0.250 0.186 , 0.249	Depositor DCC
R_{free} test set	1752 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 27.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7019	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.83	0/2307	0.88	1/3126 (0.0%)
2	B	0.82	0/860	0.84	0/1162
3	C	0.96	0/96	0.90	0/128
4	D	0.65	0/1626	0.90	1/2201 (0.0%)
5	E	0.81	0/1986	0.87	0/2705
All	All	0.79	0/6875	0.88	2/9322 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	54	GLY	N-CA-C	6.42	117.88	111.21
1	A	123	TYR	N-CA-C	-5.11	105.13	112.13

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	2247	0	2107	61	0
2	B	837	0	803	6	0
3	C	91	0	85	2	0
4	D	1591	0	1495	32	0
5	E	1933	0	1845	16	0
6	A	111	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	53	0	0	1	0
6	C	3	0	0	0	0
6	D	56	0	0	3	0
6	E	97	0	0	2	0
All	All	7019	0	6335	111	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 9.

All (111) 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:7:ASN:ND2	4:D:23:CYS:SG	2.37	0.96
1:A:75:ARG:HH11	1:A:75:ARG:HG3	1.36	0.90
4:D:48:MET:HG2	4:D:63:ALA:HB2	1.63	0.79
1:A:131:ARG:HH11	1:A:131:ARG:HG2	1.52	0.75
1:A:194:ILE:HG13	1:A:195:SER:N	2.03	0.74
1:A:197:HIS:H	1:A:197:HIS:CD2	2.04	0.73
1:A:75:ARG:HH11	1:A:75:ARG:CG	2.02	0.72
4:D:139:ASP:HB3	4:D:141:GLN:HG2	1.70	0.72
1:A:219:ARG:HD3	1:A:257:TYR:CZ	2.25	0.72
4:D:149:ASP:HB3	4:D:152:VAL:CG1	2.20	0.71
1:A:192:HIS:HB2	1:A:200:THR:HB	1.73	0.70
1:A:197:HIS:O	1:A:251:SER:N	2.22	0.70
1:A:194:ILE:HG13	1:A:195:SER:H	1.55	0.69
1:A:191:HIS:CE1	1:A:199:ALA:HB1	2.28	0.68
4:D:149:ASP:HB3	4:D:152:VAL:HG12	1.75	0.68
4:D:1:GLN:HG2	4:D:24:THR:O	1.94	0.67
4:D:22:ASN:HA	4:D:73:SER:HB3	1.75	0.67
1:A:114:HIS:HE1	6:A:378:HOH:O	1.78	0.66
1:A:194:ILE:CG1	1:A:198:GLU:O	2.43	0.65
1:A:219:ARG:HD2	1:A:256:ARG:NH1	2.12	0.65
4:D:7:ASN:HB2	4:D:102:GLN:HG2	1.79	0.65
4:D:203:SER:HB2	5:E:129:GLU:HB3	1.79	0.64
1:A:192:HIS:O	1:A:200:THR:N	2.28	0.64
1:A:99:PHE:CD2	1:A:99:PHE:C	2.77	0.62
1:A:99:PHE:CZ	3:C:3:PRO:CD	2.83	0.61
1:A:193:PRO:O	1:A:194:ILE:HG12	2.01	0.60
1:A:194:ILE:HG13	1:A:198:GLU:O	2.02	0.59
1:A:99:PHE:CZ	3:C:3:PRO:HD3	2.38	0.59
1:A:193:PRO:O	1:A:194:ILE:CG1	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:13:THR:HG21	5:E:19:LEU:CD2	2.33	0.58
4:D:121:GLN:OE1	4:D:201:PRO:HB3	2.04	0.57
1:A:131:ARG:HG2	1:A:131:ARG:NH1	2.15	0.56
1:A:220:ASP:OD1	1:A:256:ARG:NH2	2.38	0.56
1:A:43:GLN:HG3	6:A:393:HOH:O	2.05	0.55
1:A:154:GLU:OE2	4:D:52:SER:OG	2.25	0.55
6:D:356:HOH:O	5:E:139:THR:HG21	2.07	0.55
1:A:193:PRO:O	1:A:195:SER:N	2.39	0.55
1:A:151:HIS:HD2	6:D:337:HOH:O	1.89	0.55
4:D:1:GLN:HG3	4:D:23:CYS:HB3	1.88	0.55
1:A:75:ARG:HG3	1:A:75:ARG:NH1	2.12	0.54
4:D:93:ASN:HB3	4:D:95:GLY:H	1.71	0.54
1:A:204:TRP:CH2	2:B:99:MET:HE3	2.44	0.53
4:D:124:ASP:OD2	4:D:125:SER:N	2.42	0.53
1:A:227:ASP:O	1:A:247:VAL:HA	2.10	0.52
4:D:34:PHE:O	4:D:89:TRP:HA	2.09	0.52
5:E:12:ILE:HD11	5:E:213:GLY:HA2	1.91	0.51
4:D:1:GLN:HE21	4:D:24:THR:H	1.59	0.51
1:A:111:ARG:HD2	1:A:113:TYR:OH	2.10	0.51
5:E:131:GLU:OE1	5:E:139:THR:HG22	2.11	0.51
5:E:7:ASN:HB3	5:E:22:THR:OG1	2.11	0.51
4:D:48:MET:HE3	4:D:48:MET:HA	1.94	0.50
4:D:7:ASN:CB	4:D:102:GLN:HG2	2.42	0.50
1:A:196:ASP:OD2	1:A:197:HIS:HD2	1.94	0.50
1:A:258:THR:HG22	1:A:260:HIS:NE2	2.27	0.49
1:A:193:PRO:O	1:A:198:GLU:O	2.31	0.49
1:A:253:GLU:O	1:A:256:ARG:HG2	2.12	0.48
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.48	0.48
4:D:137:ASP:HA	6:D:345:HOH:O	2.13	0.48
1:A:97:MET:HG2	1:A:98:MET:N	2.29	0.48
4:D:84:SER:HA	4:D:106:LEU:O	2.14	0.48
4:D:48:MET:HE1	4:D:58:ASP:CB	2.44	0.47
1:A:75:ARG:CD	6:A:315:HOH:O	2.63	0.47
2:B:75:LYS:HD3	2:B:75:LYS:H	1.79	0.47
1:A:227:ASP:HB3	1:A:248:VAL:HB	1.96	0.47
1:A:219:ARG:O	1:A:222:GLU:HG2	2.15	0.47
5:E:132:ILE:HG13	5:E:133:SER:N	2.29	0.46
2:B:94:LYS:NZ	6:B:123:HOH:O	2.48	0.46
1:A:176:LYS:HD2	1:A:180:GLN:HG3	1.98	0.46
4:D:89:TRP:CZ2	4:D:101:GLY:HA3	2.51	0.46
5:E:177:GLN:HG3	6:E:392:HOH:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:ILE:HG12	1:A:198:GLU:O	2.16	0.46
1:A:191:HIS:C	1:A:191:HIS:ND1	2.74	0.45
4:D:126:LYS:HG3	4:D:127:SER:H	1.80	0.45
1:A:218:GLN:O	1:A:258:THR:N	2.47	0.45
1:A:7:TYR:HA	1:A:25:VAL:O	2.17	0.44
4:D:98:LEU:HD12	4:D:100:PHE:CE2	2.53	0.44
1:A:156:GLN:HA	1:A:156:GLN:OE1	2.17	0.44
1:A:191:HIS:CE1	1:A:199:ALA:CB	2.99	0.44
5:E:161:LYS:HE2	6:E:389:HOH:O	2.17	0.44
4:D:1:GLN:HB3	4:D:102:GLN:HB3	1.99	0.44
4:D:3:GLU:O	4:D:6:GLN:HG2	2.18	0.43
5:E:156:TRP:CE3	5:E:191:LEU:HD12	2.53	0.43
1:A:197:HIS:H	1:A:197:HIS:HD2	1.60	0.43
1:A:191:HIS:HE1	1:A:199:ALA:HB1	1.81	0.43
1:A:216:THR:HG22	1:A:260:HIS:HB2	2.01	0.43
1:A:219:ARG:O	1:A:222:GLU:CG	2.67	0.43
1:A:194:ILE:HD11	1:A:198:GLU:HB3	1.99	0.42
1:A:33:PHE:CD2	1:A:34:VAL:HG13	2.54	0.42
1:A:68:LYS:O	1:A:71:SER:OG	2.34	0.42
5:E:142:CYS:HB2	5:E:156:TRP:CZ2	2.54	0.42
5:E:67:SER:O	5:E:75:PRO:HD2	2.20	0.42
1:A:5:MET:O	1:A:100:GLY:HA3	2.19	0.42
1:A:115:GLN:HG3	6:A:323:HOH:O	2.20	0.42
1:A:51:TRP:CZ2	1:A:179:LEU:HD11	2.54	0.42
4:D:48:MET:HE1	4:D:58:ASP:HB2	2.01	0.42
5:E:11:LEU:HD23	5:E:108:LEU:HD13	2.02	0.42
5:E:23:CYS:HB2	5:E:34:TRP:CZ2	2.55	0.42
4:D:12:SER:HA	4:D:107:SER:O	2.19	0.42
1:A:251:SER:C	1:A:253:GLU:H	2.27	0.41
1:A:22:PHE:CD2	1:A:71:SER:HB3	2.56	0.41
2:B:21:ASN:OD1	2:B:22:PHE:N	2.46	0.41
5:E:28:ASN:CG	5:E:71:LYS:NZ	2.79	0.41
1:A:202:ARG:HD3	1:A:244:TRP:CD2	2.56	0.41
1:A:218:GLN:HA	1:A:222:GLU:O	2.20	0.41
4:D:1:GLN:HE21	4:D:23:CYS:HA	1.85	0.41
4:D:1:GLN:OE1	4:D:6:GLN:HA	2.21	0.41
4:D:9:GLY:HA3	4:D:10:PRO:HD3	1.84	0.41
2:B:51:HIS:HA	2:B:65:LEU:O	2.22	0.40
5:E:169:THR:HG23	5:E:189:SER:HB2	2.04	0.40
1:A:197:HIS:O	1:A:251:SER:HB2	2.21	0.40
4:D:1:GLN:OE1	4:D:7:ASN:N	2.36	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	277/291 (95%)	266 (96%)	11 (4%)	0	100	100
2	B	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
3	C	8/10 (80%)	8 (100%)	0	0	100	100
4	D	202/205 (98%)	193 (96%)	9 (4%)	0	100	100
5	E	239/242 (99%)	229 (96%)	10 (4%)	0	100	100
All	All	824/848 (97%)	792 (96%)	32 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	232/243 (96%)	215 (93%)	17 (7%)	13	29
2	B	95/95 (100%)	90 (95%)	5 (5%)	20	43
3	C	9/9 (100%)	8 (89%)	1 (11%)	6	12
4	D	182/183 (100%)	164 (90%)	18 (10%)	7	16
5	E	214/215 (100%)	199 (93%)	15 (7%)	14	31
All	All	732/745 (98%)	676 (92%)	56 (8%)	12	27

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	A	43	GLN
1	A	75	ARG
1	A	89	GLU
1	A	97	MET
1	A	111	ARG
1	A	131	ARG
1	A	181	ARG
1	A	186	LYS
1	A	197	HIS
1	A	216	THR
1	A	225	THR
1	A	226	GLN
1	A	227	ASP
1	A	247	VAL
1	A	258	THR
1	A	271	THR
2	B	6	LYS
2	B	20	SER
2	B	47	GLU
2	B	75	LYS
2	B	91	LYS
3	C	4	LEU
4	D	2	LYS
4	D	5	GLU
4	D	8	SER
4	D	21	LEU
4	D	31	GLN
4	D	48	MET
4	D	49	SER
4	D	52	SER
4	D	76	ILE
4	D	88	LEU
4	D	97	LYS
4	D	98	LEU
4	D	125	SER
4	D	148	LYS
4	D	152	VAL
4	D	166	ASP
4	D	178	LYS
4	D	202	GLU
5	E	12	ILE

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Mol	Chain	Res	Type
5	E	20	THR
5	E	25	GLN
5	E	28	ASN
5	E	41	LEU
5	E	55	THR
5	E	65	LYS
5	E	69	LYS
5	E	70	GLU
5	E	107	ARG
5	E	132	ILE
5	E	139	THR
5	E	190	ARG
5	E	191	LEU
5	E	232	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	54	GLN
1	A	114	HIS
1	A	151	HIS
1	A	188	HIS
1	A	192	HIS
1	A	197	HIS
2	B	13	HIS
4	D	7	ASN
4	D	38	GLN
4	D	111	ASN
4	D	113	GLN
4	D	143	ASN
4	D	146	GLN
4	D	177	ASN
4	D	189	ASN
5	E	37	GLN
5	E	177	GLN

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	279/291 (95%)	-0.32	8 (2%) 53 48	16, 28, 91, 123	0
2	B	100/100 (100%)	-0.43	2 (2%) 65 60	20, 31, 58, 72	0
3	C	10/10 (100%)	-0.76	0 100 100	17, 20, 24, 27	0
4	D	204/205 (99%)	0.03	14 (6%) 23 18	20, 42, 81, 117	0
5	E	241/242 (99%)	-0.58	2 (0%) 82 80	16, 29, 55, 110	0
All	All	834/848 (98%)	-0.32	26 (3%) 51 45	16, 32, 82, 123	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	4	VAL	5.7
5	E	2	ALA	4.6
4	D	203	SER	4.4
1	A	277	LEU	3.5
4	D	2	LYS	3.5
4	D	10	PRO	3.3
4	D	201	PRO	3.3
1	A	194	ILE	3.3
4	D	9	GLY	3.1
4	D	3	GLU	3.0
2	B	99	MET	2.8
4	D	7	ASN	2.8
4	D	1	GLN	2.7
1	A	252	GLY	2.6
1	A	195	SER	2.4
1	A	193	PRO	2.3
4	D	12	SER	2.3
1	A	225	THR	2.3
4	D	204	SER	2.3
4	D	141	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
5	E	1	GLU	2.2
4	D	8	SER	2.2
2	B	98	ASP	2.2
1	A	196	ASP	2.1
4	D	6	GLN	2.1
1	A	197	HIS	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.