



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 11:07 PM UTC

PDB ID : 8V4Z / pdb_00008v4z
Title : Crystal structure of a HLA-B*35:01-NP7 with D1 TCR
Authors : Littler, D.R.; Rossjohn, J.
Deposited on : 2023-11-29
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Mogul : 2022.3.0, CSD as543be (2022)
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

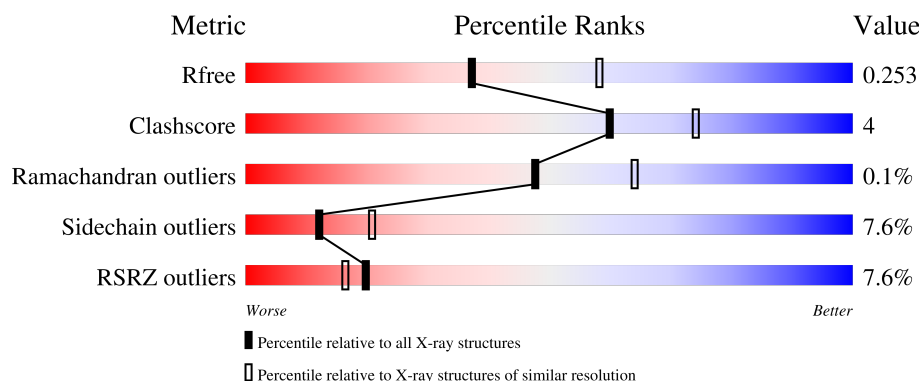
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	276	7% 83% 13% ..
1	F	276	6% 82% 13% ..
1	K	276	3% 83% 14% ..
1	P	276	8% 84% 12% ..
2	B	100	21% 59% 27% 11% ..

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	G	100	
2	L	100	
2	Q	100	
3	C	9	
3	H	9	
3	M	9	
3	R	9	
4	D	197	
4	I	197	
4	N	197	
4	S	197	
5	E	242	
5	J	242	
5	O	242	
5	T	242	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 27408 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 I antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	2	0
			2252	1403	413	429	7			
1	F	273	Total	C	N	O	S	0	3	0
			2260	1408	414	430	8			
1	K	274	Total	C	N	O	S	0	4	0
			2277	1418	416	434	9			
1	P	274	Total	C	N	O	S	0	3	0
			2269	1413	415	433	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			
2	G	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			
2	L	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			
2	Q	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
G	0	MET	-	initiating methionine	UNP P61769
L	0	MET	-	initiating methionine	UNP P61769
Q	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called LEU-PRO-PHE-GLU-LYS-SER-THR-ILE-MET.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	S	0	0	0
			74	49	10	14	1			
3	H	9	Total	C	N	O	S	0	0	0
			74	49	10	14	1			
3	M	9	Total	C	N	O	S	0	0	0
			74	49	10	14	1			
3	R	9	Total	C	N	O	S	0	0	0
			74	49	10	14	1			

- Molecule 4 is a protein called D1 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	197	Total	C	N	O	S	0	2	0
			1545	970	249	316	10			
4	I	197	Total	C	N	O	S	0	2	0
			1545	970	249	316	10			
4	N	197	Total	C	N	O	S	0	2	0
			1545	970	249	316	10			
4	S	197	Total	C	N	O	S	0	2	0
			1545	970	249	316	10			

- Molecule 5 is a protein called D1 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	242	Total	C	N	O	S	0	3	0
			1942	1221	339	375	7			
5	J	242	Total	C	N	O	S	0	3	0
			1942	1221	339	375	7			
5	O	242	Total	C	N	O	S	0	3	0
			1942	1221	339	375	7			
5	T	242	Total	C	N	O	S	0	3	0
			1942	1221	339	375	7			

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	56	Total	O	0	0
			56	56		
7	B	5	Total	O	0	0
			5	5		
7	C	4	Total	O	0	0
			4	4		
7	D	64	Total	O	0	0
			64	64		
7	E	52	Total	O	0	0
			52	52		
7	F	89	Total	O	0	0
			89	89		
7	G	11	Total	O	0	0
			11	11		
7	H	2	Total	O	0	0
			2	2		

Continued on next page...

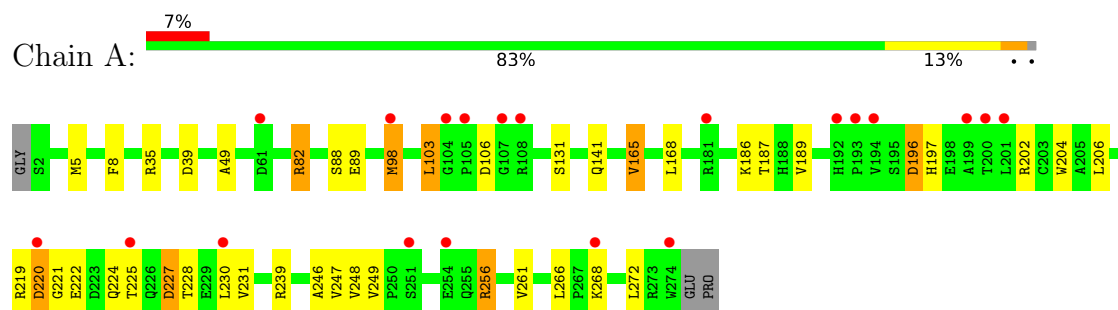
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	I	33	Total 33	O 33	0	0
7	J	63	Total 63	O 63	0	0
7	K	121	Total 121	O 121	0	0
7	L	19	Total 19	O 19	0	0
7	M	6	Total 6	O 6	0	0
7	N	62	Total 62	O 62	0	0
7	O	106	Total 106	O 106	0	0
7	P	15	Total 15	O 15	0	0
7	Q	1	Total 1	O 1	0	0
7	R	2	Total 2	O 2	0	0
7	S	40	Total 40	O 40	0	0
7	T	19	Total 19	O 19	0	0

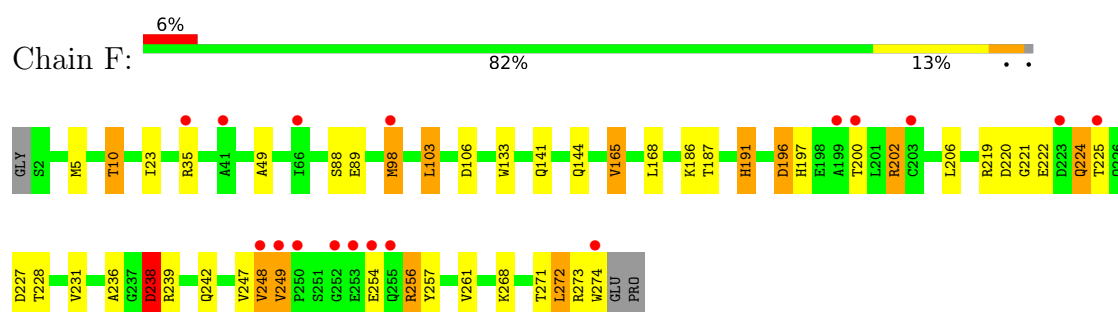
3 Residue-property plots [i](#)

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.

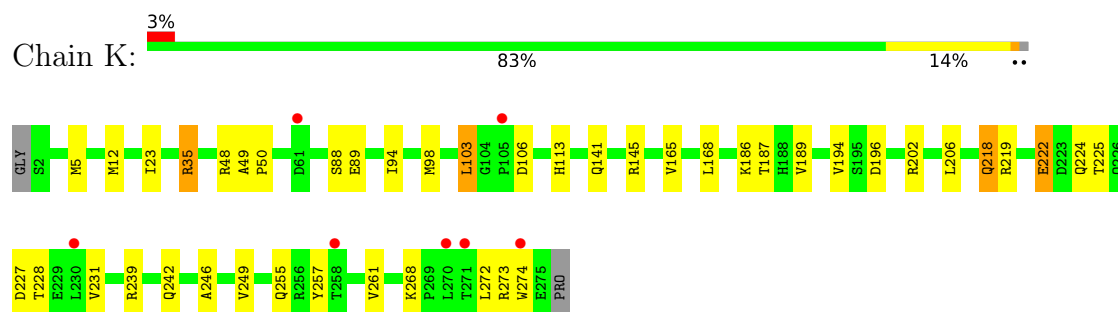
- Molecule 1: MHC class I antigen



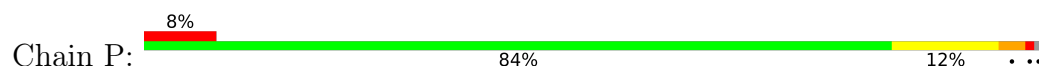
- Molecule 1: MHC class I antigen

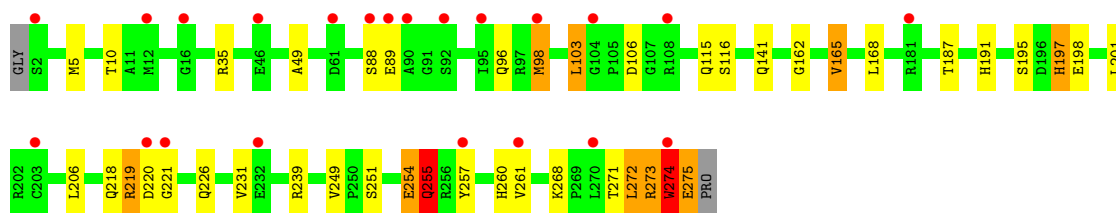


- Molecule 1: MHC class I antigen

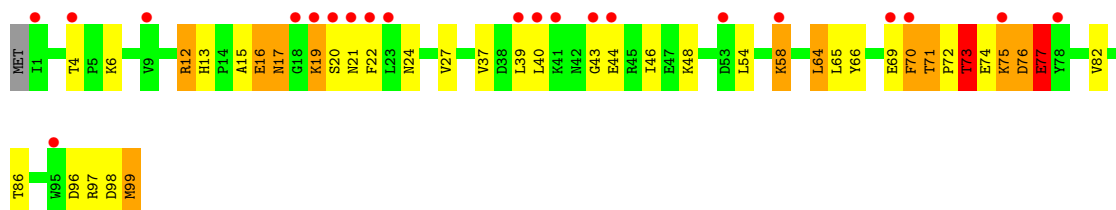


- Molecule 1: MHC class I antigen





• Molecule 2: Beta-2-microglobulin



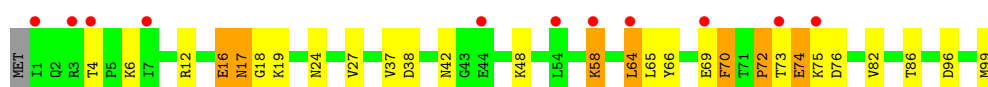
• Molecule 2: Beta-2-microglobulin



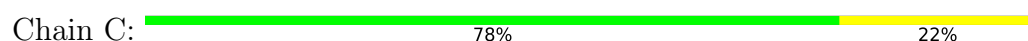
• Molecule 2: Beta-2-microglobulin



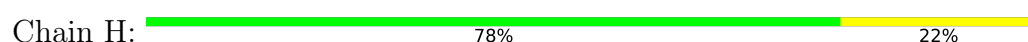
• Molecule 2: Beta-2-microglobulin



• Molecule 3: LEU-PRO-PHE-GLU-LYS-SER-THR-ILE-MET



• Molecule 3: LEU-PRO-PHE-GLU-LYS-SER-THR-ILE-MET





- Molecule 3: LEU-PRO-PHE-GLU-LYS-SER-THR-ILE-MET

Chain M: 78% 22%



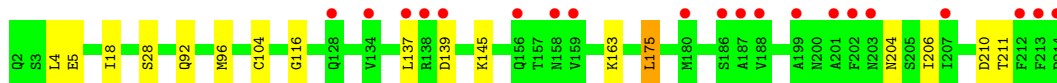
- Molecule 3: LEU-PRO-PHE-GLU-LYS-SER-THR-ILE-MET

Chain R: 78% 22%



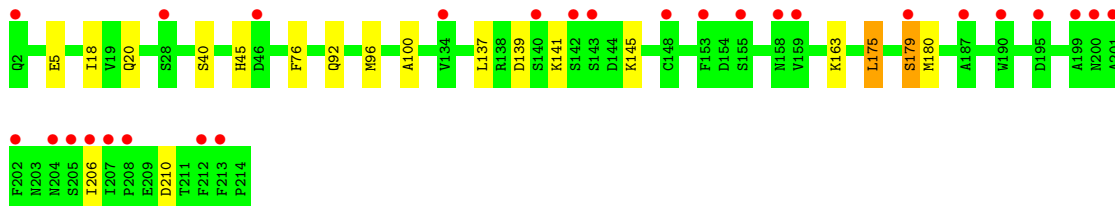
- Molecule 4: D1 TCR alpha chain

Chain D: 10% 91% 8%



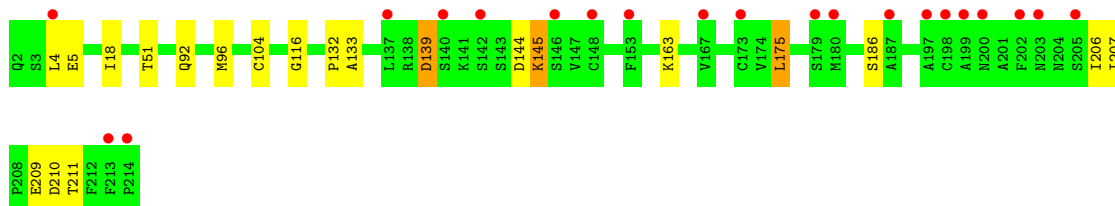
- Molecule 4: D1 TCR alpha chain

Chain I: 14% 90% 9%



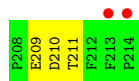
- Molecule 4: D1 TCR alpha chain

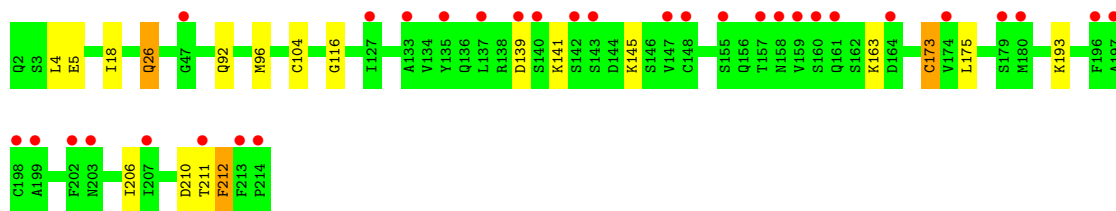
Chain N: 11% 89% 9%



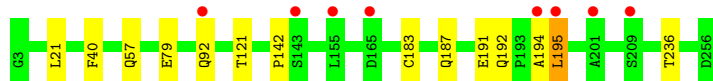
- Molecule 4: D1 TCR alpha chain

Chain S: 16% 90% 8%





● Molecule 5: D1 TCR beta chain



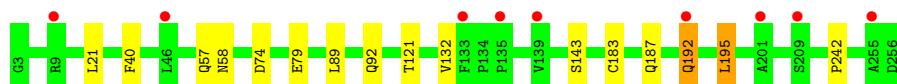
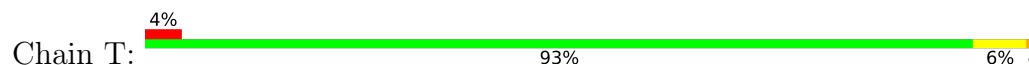
● Molecule 5: D1 TCR beta chain



● Molecule 5: D1 TCR beta chain



● Molecule 5: D1 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	78.99Å 190.21Å 250.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.06 – 2.40 49.06 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.06-2.40) 99.9 (49.06-2.40)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.39Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.218 , 0.252 0.219 , 0.253	Depositor DCC
R_{free} test set	7342 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	38.4	Xtrriage
Anisotropy	0.580	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	27408	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 26.48 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.6128e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.71	0/2314	1.21	6/3146 (0.2%)
1	F	0.69	0/2322	1.19	5/3156 (0.2%)
1	K	0.70	0/2339	1.17	0/3178
1	P	0.71	0/2331	1.26	9/3168 (0.3%)
2	B	0.81	0/852	1.34	12/1152 (1.0%)
2	G	0.71	0/852	1.24	6/1152 (0.5%)
2	L	0.73	0/852	1.60	12/1152 (1.0%)
2	Q	0.70	0/852	1.17	3/1152 (0.3%)
3	C	0.63	0/75	1.02	0/98
3	H	0.67	0/75	0.99	0/98
3	M	0.62	0/75	1.03	0/98
3	R	0.66	0/75	1.00	0/98
4	D	0.70	0/1579	1.05	1/2139 (0.0%)
4	I	0.69	0/1579	1.04	2/2139 (0.1%)
4	N	0.70	0/1579	1.05	1/2139 (0.0%)
4	S	0.69	0/1579	1.07	2/2139 (0.1%)
5	E	0.68	0/1994	1.05	3/2712 (0.1%)
5	J	0.65	0/1994	1.03	3/2712 (0.1%)
5	O	0.72	0/1994	1.07	2/2712 (0.1%)
5	T	0.67	0/1994	1.05	3/2712 (0.1%)
All	All	0.70	0/27306	1.15	70/37052 (0.2%)

There are no bond length outliers.

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	17	ASN	N-CA-C	31.32	149.23	111.33
1	P	219	ARG	CB-CA-C	14.24	145.51	113.33
1	P	219	ARG	N-CA-C	-13.04	89.46	109.79
2	B	77	GLU	N-CA-C	12.67	128.96	109.96

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	16	GLU	N-CA-C	-11.16	91.47	108.99

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	2252	0	2113	16	0
1	F	2260	0	2123	21	0
1	K	2277	0	2135	22	0
1	P	2269	0	2129	30	0
2	B	829	0	794	42	0
2	G	829	0	794	33	0
2	L	829	0	794	12	0
2	Q	829	0	794	12	0
3	C	74	0	80	0	0
3	H	74	0	80	0	0
3	M	74	0	80	0	0
3	R	74	0	80	0	0
4	D	1545	0	1437	7	0
4	I	1545	0	1437	10	0
4	N	1545	0	1437	12	0
4	S	1545	0	1438	11	0
5	E	1942	0	1837	9	0
5	J	1942	0	1837	5	0
5	O	1942	0	1837	8	0
5	T	1942	0	1839	10	0
6	D	5	0	0	0	0
6	I	5	0	0	0	0
6	N	5	0	0	0	0
6	S	5	0	0	0	0
7	A	56	0	0	0	0
7	B	5	0	0	1	0
7	C	4	0	0	0	0
7	D	64	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	52	0	0	0	0
7	F	89	0	0	0	0
7	G	11	0	0	0	0
7	H	2	0	0	0	0
7	I	33	0	0	0	0
7	J	63	0	0	0	0
7	K	121	0	0	1	0
7	L	19	0	0	0	0
7	M	6	0	0	0	0
7	N	62	0	0	0	0
7	O	106	0	0	0	0
7	P	15	0	0	0	0
7	Q	1	0	0	0	0
7	R	2	0	0	0	0
7	S	40	0	0	0	0
7	T	19	0	0	0	0
All	All	27408	0	25095	225	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 4.

The worst 5 of 225 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)
2:B:17:ASN:ND2	2:B:75:LYS:HB2	1.13	1.46
2:B:17:ASN:ND2	2:B:75:LYS:CB	2.02	1.23
2:B:17:ASN:HD21	2:B:75:LYS:CB	1.55	1.18
1:P:255:GLN:O	1:P:273:ARG:NH1	1.81	1.12
2:B:71:THR:O	2:B:73:THR:HG23	1.49	1.10

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	273/276 (99%)	264 (97%)	9 (3%)	0	100	100
1	F	274/276 (99%)	262 (96%)	12 (4%)	0	100	100
1	K	276/276 (100%)	270 (98%)	6 (2%)	0	100	100
1	P	275/276 (100%)	263 (96%)	12 (4%)	0	100	100
2	B	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
2	G	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
2	L	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
2	Q	97/100 (97%)	91 (94%)	4 (4%)	2 (2%)	5	7
3	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	H	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	M	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	R	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
4	D	197/197 (100%)	189 (96%)	8 (4%)	0	100	100
4	I	197/197 (100%)	186 (94%)	11 (6%)	0	100	100
4	N	197/197 (100%)	188 (95%)	9 (5%)	0	100	100
4	S	197/197 (100%)	187 (95%)	10 (5%)	0	100	100
5	E	243/242 (100%)	234 (96%)	9 (4%)	0	100	100
5	J	243/242 (100%)	234 (96%)	9 (4%)	0	100	100
5	O	243/242 (100%)	234 (96%)	9 (4%)	0	100	100
5	T	243/242 (100%)	232 (96%)	11 (4%)	0	100	100
All	All	3274/3296 (99%)	3136 (96%)	136 (4%)	2 (0%)	48	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Q	72	PRO
2	Q	17	ASN

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%)	205 (88%)	29 (12%)	4	6
1	F	235/234 (100%)	205 (87%)	30 (13%)	4	6
1	K	237/234 (101%)	216 (91%)	21 (9%)	9	15
1	P	236/234 (101%)	215 (91%)	21 (9%)	9	15
2	B	94/95 (99%)	79 (84%)	15 (16%)	2	3
2	G	94/95 (99%)	83 (88%)	11 (12%)	5	7
2	L	94/95 (99%)	83 (88%)	11 (12%)	5	7
2	Q	94/95 (99%)	82 (87%)	12 (13%)	4	6
3	C	9/9 (100%)	7 (78%)	2 (22%)	1	1
3	H	9/9 (100%)	7 (78%)	2 (22%)	1	1
3	M	9/9 (100%)	7 (78%)	2 (22%)	1	1
3	R	9/9 (100%)	7 (78%)	2 (22%)	1	1
4	D	173/171 (101%)	163 (94%)	10 (6%)	18	32
4	I	173/171 (101%)	162 (94%)	11 (6%)	16	28
4	N	173/171 (101%)	164 (95%)	9 (5%)	21	36
4	S	173/171 (101%)	161 (93%)	12 (7%)	14	24
5	E	211/208 (101%)	207 (98%)	4 (2%)	50	71
5	J	211/208 (101%)	207 (98%)	4 (2%)	50	71
5	O	211/208 (101%)	204 (97%)	7 (3%)	33	55
5	T	211/208 (101%)	205 (97%)	6 (3%)	38	60
All	All	2890/2868 (101%)	2669 (92%)	221 (8%)	12	21

5 of 221 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	J	92	GLN
2	L	38	ASP
5	T	192	GLN
2	Q	73	THR
1	K	88	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
5	J	225	GLN
5	T	57	GLN
2	L	42	ASN
4	S	128	GLN
5	T	225	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	PO4	N	301	-	4,4,4	2.06	2 (50%)	6,6,6	0.45	0
6	PO4	S	301	-	4,4,4	2.06	3 (75%)	6,6,6	0.43	0
6	PO4	I	301	-	4,4,4	2.55	2 (50%)	6,6,6	0.50	0
6	PO4	D	301	-	4,4,4	2.55	1 (25%)	6,6,6	0.44	0

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	I	301	PO4	P-O1	4.24	1.60	1.50
6	D	301	PO4	P-O1	4.24	1.60	1.50
6	N	301	PO4	P-O1	2.27	1.55	1.50
6	S	301	PO4	P-O1	2.24	1.55	1.50
6	I	301	PO4	P-O2	2.03	1.60	1.54

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	273/276 (98%)	0.51	20 (7%) 21 17	20, 56, 123, 169	3 (1%)
1	F	273/276 (98%)	0.48	17 (6%) 26 23	18, 55, 120, 169	3 (1%)
1	K	274/276 (99%)	0.20	7 (2%) 57 53	12, 47, 93, 126	5 (1%)
1	P	274/276 (99%)	0.80	22 (8%) 18 15	32, 74, 115, 137	3 (1%)
2	B	99/100 (99%)	1.27	21 (21%) 2 2	37, 88, 132, 168	1 (1%)
2	G	99/100 (99%)	0.71	6 (6%) 27 23	33, 68, 115, 136	1 (1%)
2	L	99/100 (99%)	0.67	6 (6%) 27 23	28, 66, 109, 130	1 (1%)
2	Q	99/100 (99%)	1.01	11 (11%) 10 7	56, 77, 111, 124	1 (1%)
3	C	9/9 (100%)	-0.23	0 100 100	27, 29, 40, 42	0
3	H	9/9 (100%)	-0.10	0 100 100	30, 33, 46, 51	0
3	M	9/9 (100%)	-0.38	0 100 100	18, 23, 36, 37	0
3	R	9/9 (100%)	0.18	0 100 100	46, 52, 62, 62	0
4	D	197/197 (100%)	0.65	20 (10%) 12 9	14, 57, 158, 206	2 (1%)
4	I	197/197 (100%)	0.71	27 (13%) 6 5	18, 67, 168, 225	3 (1%)
4	N	197/197 (100%)	0.57	21 (10%) 11 8	13, 53, 144, 209	2 (1%)
4	S	197/197 (100%)	0.76	31 (15%) 5 4	17, 65, 146, 205	2 (1%)
5	E	242/242 (100%)	0.49	8 (3%) 49 45	17, 66, 123, 166	3 (1%)
5	J	242/242 (100%)	0.39	6 (2%) 58 54	16, 63, 133, 160	3 (1%)
5	O	242/242 (100%)	0.31	16 (6%) 24 20	13, 51, 112, 158	3 (1%)
5	T	242/242 (100%)	0.74	9 (3%) 45 41	29, 73, 115, 167	3 (1%)
All	All	3282/3296 (99%)	0.58	248 (7%) 20 16	12, 65, 133, 225	39 (1%)

The worst 5 of 248 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	199	ALA	5.3
2	Q	1	ILE	5.2
1	F	254	GLU	4.4
1	F	252	GLY	4.4
2	B	22	PHE	4.2

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors($\text{\AA}^2$)	Q<0.9
6	PO4	I	301	5/5	0.86	0.10	70,71,75,77	0
6	PO4	S	301	5/5	0.87	0.09	68,74,79,86	0
6	PO4	D	301	5/5	0.89	0.10	56,60,65,75	0
6	PO4	N	301	5/5	0.92	0.08	61,62,65,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.