



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 01:50 AM BST

PDB ID : 5KNM
Title : Human leukocyte antigen F (HLA-F) presents peptides and regulates immunity through interactions with NK-cell receptors
Authors : Dulberger, C.L.; Adams, E.J.
Deposited on : 2016-06-28
Resolution : 3.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

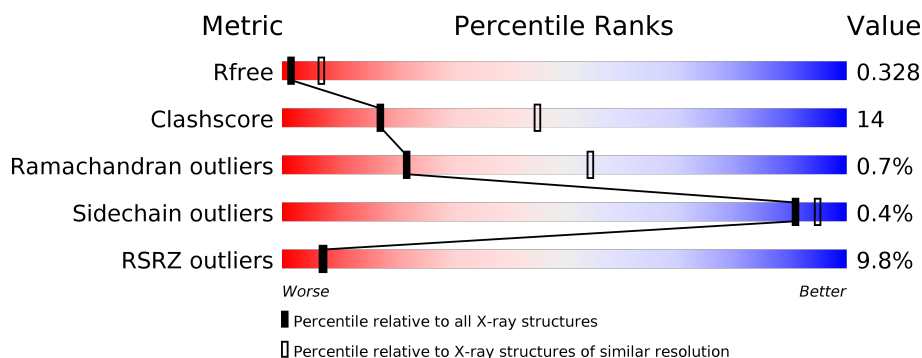
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 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	284	<div> <div>12%</div> <div>72%</div> <div>25%</div> <div>.</div> </div>
2	B	182	<div> <div>2%</div> <div>36%</div> <div>19%</div> <div>45%</div> <div>.</div> </div>
3	D	267	<div> <div>6%</div> <div>46%</div> <div>22%</div> <div>30%</div> <div>.</div> </div>
4	N	6	<div> <div>50%</div> <div>67%</div> <div>33%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4528 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 cDNA FLJ39643 fis, clone SMINT2004023, highly similar to HLA class I histocompatibility antigen, alphachain F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2211	1376	397	431	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	101	Total	C	N	O	S	0	0	0
			839	535	141	160	3			

There are 83 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-68	MET	-	initiating methionine	UNP P61769
B	-67	LEU	-	expression tag	UNP P61769
B	-66	LEU	-	expression tag	UNP P61769
B	-65	VAL	-	expression tag	UNP P61769
B	-64	ASN	-	expression tag	UNP P61769
B	-63	GLN	-	expression tag	UNP P61769
B	-62	SER	-	expression tag	UNP P61769
B	-61	HIS	-	expression tag	UNP P61769
B	-60	GLN	-	expression tag	UNP P61769
B	-59	GLY	-	expression tag	UNP P61769
B	-58	PHE	-	expression tag	UNP P61769
B	-57	ASN	-	expression tag	UNP P61769
B	-56	LYS	-	expression tag	UNP P61769
B	-55	GLU	-	expression tag	UNP P61769
B	-54	HIS	-	expression tag	UNP P61769
B	-53	THR	-	expression tag	UNP P61769
B	-52	SER	-	expression tag	UNP P61769
B	-51	LYS	-	expression tag	UNP P61769
B	-50	MET	-	expression tag	UNP P61769

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-49	VAL	-	expression tag	UNP P61769
B	-48	SER	-	expression tag	UNP P61769
B	-47	ALA	-	expression tag	UNP P61769
B	-46	ILE	-	expression tag	UNP P61769
B	-45	VAL	-	expression tag	UNP P61769
B	-44	LEU	-	expression tag	UNP P61769
B	-43	TYR	-	expression tag	UNP P61769
B	-42	VAL	-	expression tag	UNP P61769
B	-41	LEU	-	expression tag	UNP P61769
B	-40	LEU	-	expression tag	UNP P61769
B	-39	ALA	-	expression tag	UNP P61769
B	-38	ALA	-	expression tag	UNP P61769
B	-37	ALA	-	expression tag	UNP P61769
B	-36	ALA	-	expression tag	UNP P61769
B	-35	HIS	-	expression tag	UNP P61769
B	-34	SER	-	expression tag	UNP P61769
B	-33	ALA	-	expression tag	UNP P61769
B	-32	PHE	-	expression tag	UNP P61769
B	-31	ALA	-	expression tag	UNP P61769
B	-30	ALA	-	expression tag	UNP P61769
B	-29	ASP	-	expression tag	UNP P61769
B	-28	LEU	-	expression tag	UNP P61769
B	-27	HIS	-	expression tag	UNP P61769
B	-26	HIS	-	expression tag	UNP P61769
B	-25	HIS	-	expression tag	UNP P61769
B	-24	HIS	-	expression tag	UNP P61769
B	-23	HIS	-	expression tag	UNP P61769
B	-22	HIS	-	expression tag	UNP P61769
B	-21	HIS	-	expression tag	UNP P61769
B	-20	HIS	-	expression tag	UNP P61769
B	-19	GLY	-	expression tag	UNP P61769
B	-18	SER	-	expression tag	UNP P61769
B	-17	GLY	-	expression tag	UNP P61769
B	-16	GLY	-	expression tag	UNP P61769
B	-15	LEU	-	expression tag	UNP P61769
B	-14	GLU	-	expression tag	UNP P61769
B	-13	VAL	-	expression tag	UNP P61769
B	-12	LEU	-	expression tag	UNP P61769
B	-11	PHE	-	expression tag	UNP P61769
B	-10	GLN	-	expression tag	UNP P61769
B	-9	GLY	-	expression tag	UNP P61769
B	-8	PRO	-	expression tag	UNP P61769

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	GLU	-	expression tag	UNP P61769
B	-6	PHE	-	expression tag	UNP P61769
B	-5	GLY	-	expression tag	UNP P61769
B	-4	GLY	-	expression tag	UNP P61769
B	-3	SER	-	expression tag	UNP P61769
B	-2	ALA	-	expression tag	UNP P61769
B	-1	ASP	-	expression tag	UNP P61769
B	0	PRO	-	expression tag	UNP P61769
B	100	GLY	-	expression tag	UNP P61769
B	101	GLY	-	expression tag	UNP P61769
B	102	GLY	-	expression tag	UNP P61769
B	103	GLY	-	expression tag	UNP P61769
B	104	SER	-	expression tag	UNP P61769
B	105	GLY	-	expression tag	UNP P61769
B	106	GLY	-	expression tag	UNP P61769
B	107	SER	-	expression tag	UNP P61769
B	108	GLY	-	expression tag	UNP P61769
B	109	SER	-	expression tag	UNP P61769
B	110	GLY	-	expression tag	UNP P61769
B	111	GLY	-	expression tag	UNP P61769
B	112	GLY	-	expression tag	UNP P61769
B	113	SER	-	expression tag	UNP P61769

- Molecule 3 is a protein called Leukocyte immunoglobulin-like receptor subfamily B member 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	187	Total	C	N	O	S	0	0	0
			1410	892	243	269	6			

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-68	MET	-	initiating methionine	UNP Q8NHL6
D	-67	LEU	-	expression tag	UNP Q8NHL6
D	-66	LEU	-	expression tag	UNP Q8NHL6
D	-65	VAL	-	expression tag	UNP Q8NHL6
D	-64	ASN	-	expression tag	UNP Q8NHL6
D	-63	GLN	-	expression tag	UNP Q8NHL6
D	-62	SER	-	expression tag	UNP Q8NHL6
D	-61	HIS	-	expression tag	UNP Q8NHL6
D	-60	GLN	-	expression tag	UNP Q8NHL6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-59	GLY	-	expression tag	UNP Q8NHL6
D	-58	PHE	-	expression tag	UNP Q8NHL6
D	-57	ASN	-	expression tag	UNP Q8NHL6
D	-56	LYS	-	expression tag	UNP Q8NHL6
D	-55	GLU	-	expression tag	UNP Q8NHL6
D	-54	HIS	-	expression tag	UNP Q8NHL6
D	-53	THR	-	expression tag	UNP Q8NHL6
D	-52	SER	-	expression tag	UNP Q8NHL6
D	-51	LYS	-	expression tag	UNP Q8NHL6
D	-50	MET	-	expression tag	UNP Q8NHL6
D	-49	VAL	-	expression tag	UNP Q8NHL6
D	-48	SER	-	expression tag	UNP Q8NHL6
D	-47	ALA	-	expression tag	UNP Q8NHL6
D	-46	ILE	-	expression tag	UNP Q8NHL6
D	-45	VAL	-	expression tag	UNP Q8NHL6
D	-44	LEU	-	expression tag	UNP Q8NHL6
D	-43	TYR	-	expression tag	UNP Q8NHL6
D	-42	VAL	-	expression tag	UNP Q8NHL6
D	-41	LEU	-	expression tag	UNP Q8NHL6
D	-40	LEU	-	expression tag	UNP Q8NHL6
D	-39	ALA	-	expression tag	UNP Q8NHL6
D	-38	ALA	-	expression tag	UNP Q8NHL6
D	-37	ALA	-	expression tag	UNP Q8NHL6
D	-36	ALA	-	expression tag	UNP Q8NHL6
D	-35	HIS	-	expression tag	UNP Q8NHL6
D	-34	SER	-	expression tag	UNP Q8NHL6
D	-33	ALA	-	expression tag	UNP Q8NHL6
D	-32	PHE	-	expression tag	UNP Q8NHL6
D	-31	ALA	-	expression tag	UNP Q8NHL6
D	-30	ALA	-	expression tag	UNP Q8NHL6
D	-29	ASP	-	expression tag	UNP Q8NHL6
D	-28	LEU	-	expression tag	UNP Q8NHL6
D	-27	HIS	-	expression tag	UNP Q8NHL6
D	-26	HIS	-	expression tag	UNP Q8NHL6
D	-25	HIS	-	expression tag	UNP Q8NHL6
D	-24	HIS	-	expression tag	UNP Q8NHL6
D	-23	HIS	-	expression tag	UNP Q8NHL6
D	-22	HIS	-	expression tag	UNP Q8NHL6
D	-21	HIS	-	expression tag	UNP Q8NHL6
D	-20	HIS	-	expression tag	UNP Q8NHL6
D	-19	GLY	-	expression tag	UNP Q8NHL6
D	-18	SER	-	expression tag	UNP Q8NHL6

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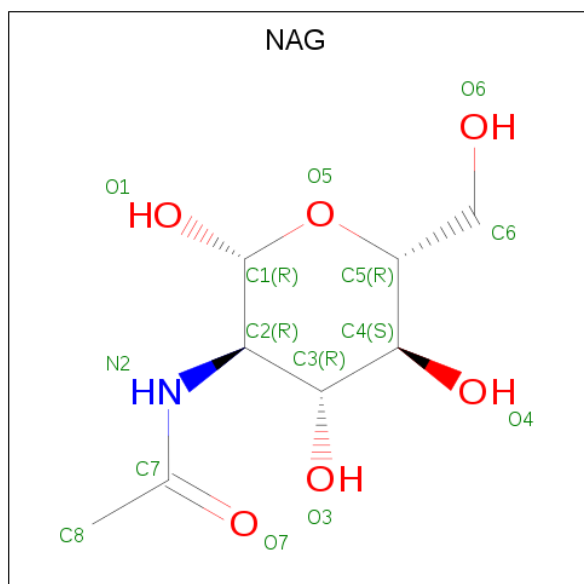
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-17	GLY	-	expression tag	UNP Q8NHL6
D	-16	GLY	-	expression tag	UNP Q8NHL6
D	-15	LEU	-	expression tag	UNP Q8NHL6
D	-14	GLU	-	expression tag	UNP Q8NHL6
D	-13	VAL	-	expression tag	UNP Q8NHL6
D	-12	LEU	-	expression tag	UNP Q8NHL6
D	-11	PHE	-	expression tag	UNP Q8NHL6
D	-10	GLN	-	expression tag	UNP Q8NHL6
D	-9	GLY	-	expression tag	UNP Q8NHL6
D	-8	PRO	-	expression tag	UNP Q8NHL6
D	-7	GLU	-	expression tag	UNP Q8NHL6
D	-6	PHE	-	expression tag	UNP Q8NHL6
D	-5	GLY	-	expression tag	UNP Q8NHL6
D	-4	GLY	-	expression tag	UNP Q8NHL6
D	-3	SER	-	expression tag	UNP Q8NHL6
D	-2	ALA	-	expression tag	UNP Q8NHL6
D	-1	ASP	-	expression tag	UNP Q8NHL6
D	0	LEU	-	expression tag	UNP Q8NHL6

- Molecule 4 is a protein called Peptide ILE-LEU-ARG-TRP-GLU-GLN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	N	6	Total	C	N	O	0	0	0
			54	33	11	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

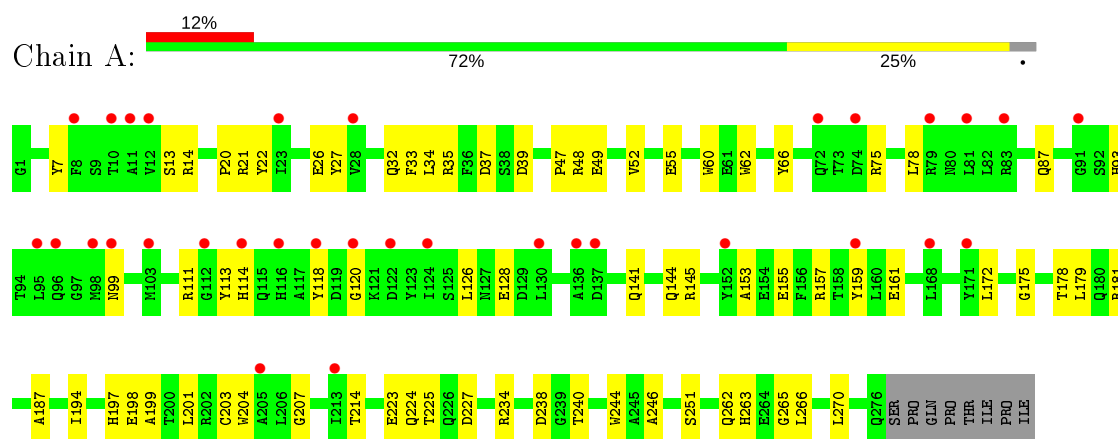


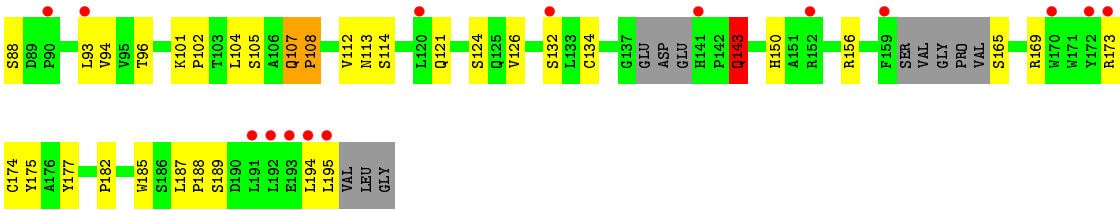
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

3 Residue-property plots

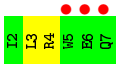
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: cDNA FLJ39643 fis, clone SMINT2004023, highly similar to HLA class I histocompatibility antigen, alphachain F





● Molecule 4: Peptide ILE-LEU-ARG-TRP-GLU-GLN



4 Data and refinement statistics

Property	Value	Source
Space group	P 6 2 2	Depositor
Cell constants a, b, c, α , β , γ	231.82Å 231.82Å 73.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.41 – 3.30 59.17 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.41-3.30) 99.7 (59.17-3.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 3.33Å)	Xtriage
Refinement program	PHENIX (1.10 _2155: ???)	Depositor
R, R_{free}	0.303 , 0.326 0.309 , 0.328	Depositor DCC
R_{free} test set	915 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	117.5	Xtriage
Anisotropy	0.541	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 122.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	4528	wwPDB-VP
Average B, all atoms (Å ²)	188.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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: 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	0.24	0/2269	0.46	0/3088
2	B	0.25	0/863	0.47	0/1170
3	D	0.26	0/1448	0.56	1/1978 (0.1%)
4	N	0.18	0/55	0.45	0/72
All	All	0.25	0/4635	0.50	1/6308 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	143	GLN	CA-CB-CG	6.34	127.34	113.40

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	2211	0	2042	52	0
2	B	839	0	799	32	0
3	D	1410	0	1322	43	0
4	N	54	0	40	3	0
5	A	14	0	13	0	0
All	All	4528	0	4216	121	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 14.

All (121) 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)
3:D:114:SER:HG	3:D:165:SER:N	1.62	0.96
3:D:105:SER:O	3:D:121:GLN:HB3	1.64	0.95
1:A:187:ALA:HA	1:A:204:TRP:O	1.77	0.83
3:D:143:GLN:HA	3:D:143:GLN:HE21	1.49	0.76
2:B:37:VAL:HG22	2:B:82:VAL:HG23	1.68	0.75
3:D:134:CYS:HB2	3:D:173:ARG:HB2	1.69	0.74
3:D:112:VAL:HG12	3:D:113:ASN:H	1.52	0.73
3:D:37:LEU:HD11	3:D:73:TYR:HB3	1.69	0.72
3:D:8:LEU:HD11	3:D:75:CYS:HB3	1.71	0.72
1:A:207:GLY:HA2	1:A:240:THR:HB	1.71	0.72
2:B:37:VAL:HB	2:B:66:TYR:CE2	2.24	0.71
2:B:45:ARG:NH1	2:B:46:ILE:O	2.23	0.71
2:B:83:ASN:HA	2:B:87:LEU:HD22	1.73	0.71
3:D:104:LEU:HD11	3:D:189:SER:HB3	1.72	0.70
1:A:203:CYS:O	1:A:244:TRP:HA	1.92	0.69
1:A:99:ASN:HA	1:A:113:TYR:O	1.93	0.67
3:D:76:TYR:HB3	3:D:87:SER:HB3	1.77	0.67
1:A:35:ARG:HD2	1:A:48:ARG:HD3	1.77	0.66
3:D:175:TYR:HE1	3:D:188:PRO:HA	1.59	0.66
1:A:201:LEU:O	1:A:246:ALA:HA	1.97	0.64
3:D:5:LYS:HE2	3:D:88:SER:HB2	1.79	0.64
1:A:197:HIS:HA	1:A:251:SER:HB3	1.79	0.63
3:D:107:GLN:HB3	3:D:108:PRO:HD2	1.80	0.63
3:D:94:VAL:HG11	3:D:185:TRP:CD2	2.35	0.62
1:A:194:ILE:HD11	3:D:40:GLU:HA	1.81	0.61
2:B:38:ASP:OD1	2:B:39:LEU:N	2.34	0.61
1:A:87:GLN:HG2	1:A:93:HIS:CE1	2.36	0.61
2:B:37:VAL:HB	2:B:66:TYR:HE2	1.63	0.60
1:A:178:THR:O	1:A:181:ARG:HG2	2.01	0.60
2:B:10:TYR:HA	2:B:95:TRP:HZ3	1.66	0.60
2:B:12:ARG:HD2	2:B:22:PHE:HB2	1.84	0.59
3:D:143:GLN:HA	3:D:143:GLN:NE2	2.17	0.59
1:A:21:ARG:NH1	1:A:22:TYR:O	2.35	0.59
1:A:34:LEU:HD23	1:A:47:PRO:HA	1.84	0.58
1:A:13:SER:HB3	1:A:78:LEU:HD21	1.86	0.57
2:B:27:VAL:HG21	2:B:37:VAL:HG21	1.86	0.57
2:B:57:SER:OG	2:B:59:ASP:OD1	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:96:THR:HG22	3:D:185:TRP:HB2	1.85	0.57
3:D:4:PRO:HG2	3:D:85:SER:HB3	1.87	0.57
1:A:120:GLY:HA3	2:B:1:ILE:CD1	2.35	0.56
3:D:28:GLY:N	3:D:35:TYR:OH	2.39	0.56
2:B:24:ASN:HB3	2:B:65:LEU:HD11	1.87	0.55
1:A:266:LEU:HD13	1:A:270:LEU:HD13	1.89	0.55
4:N:3:LEU:O	4:N:4:ARG:NH1	2.35	0.55
1:A:194:ILE:H	1:A:199:ALA:HA	1.73	0.54
3:D:24:LEU:O	3:D:60:PHE:N	2.31	0.54
2:B:86:THR:HG23	3:D:126:VAL:HG11	1.90	0.53
1:A:14:ARG:NH1	1:A:39:ASP:OD2	2.42	0.53
1:A:153:ALA:O	1:A:157:ARG:HB2	2.08	0.53
1:A:62:TRP:O	1:A:66:TYR:HB2	2.09	0.53
3:D:112:VAL:HG12	3:D:113:ASN:N	2.24	0.52
2:B:23:LEU:O	2:B:67:TYR:HA	2.09	0.52
1:A:120:GLY:HA3	2:B:1:ILE:HD11	1.91	0.52
3:D:132:SER:HB2	3:D:175:TYR:HB2	1.91	0.52
1:A:224:GLN:O	1:A:227:ASP:N	2.42	0.52
2:B:41:LYS:HG3	2:B:78:TYR:HE1	1.74	0.51
2:B:87:LEU:HD11	2:B:91:LYS:HB2	1.93	0.51
3:D:25:ARG:HG3	3:D:59:GLN:H	1.75	0.51
1:A:62:TRP:O	1:A:66:TYR:CB	2.59	0.50
3:D:132:SER:O	3:D:174:CYS:HA	2.12	0.50
3:D:150:HIS:N	3:D:156:ARG:O	2.29	0.49
2:B:21:ASN:OD1	2:B:22:PHE:N	2.46	0.49
3:D:105:SER:O	3:D:121:GLN:CB	2.50	0.49
3:D:80:ASP:O	3:D:81:THR:HG22	2.13	0.49
2:B:23:LEU:HB2	2:B:70:PHE:CE2	2.48	0.48
3:D:114:SER:OG	3:D:165:SER:N	2.38	0.48
1:A:21:ARG:NH2	1:A:37:ASP:OD1	2.47	0.48
1:A:87:GLN:HG2	1:A:93:HIS:HE1	1.79	0.48
1:A:155:GLU:OE2	4:N:4:ARG:NH2	2.47	0.48
1:A:234:ARG:HD2	2:B:10:TYR:CE2	2.48	0.48
1:A:141:GLN:HA	1:A:144:GLN:HB3	1.96	0.47
3:D:24:LEU:HD11	3:D:93:LEU:HD22	1.95	0.47
2:B:41:LYS:HG3	2:B:78:TYR:CE1	2.48	0.47
1:A:141:GLN:O	1:A:145:ARG:HG2	2.14	0.47
1:A:263:HIS:CD2	1:A:265:GLY:H	2.32	0.47
1:A:175:GLY:O	1:A:179:LEU:N	2.39	0.47
2:B:38:ASP:HB3	2:B:81:ARG:HB3	1.97	0.47
3:D:102:PRO:HG2	3:D:189:SER:OG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:THR:HB	1:A:262:GLN:HB2	1.96	0.46
1:A:55:GLU:HB2	1:A:60:TRP:NE1	2.30	0.46
1:A:14:ARG:NH1	1:A:21:ARG:HB2	2.31	0.46
2:B:14:PRO:HA	2:B:99:MET:HG3	1.98	0.46
2:B:6:LYS:N	2:B:28:SER:O	2.37	0.45
1:A:7:TYR:HD1	1:A:26:GLU:HG2	1.81	0.45
1:A:93:HIS:ND1	1:A:118:TYR:OH	2.49	0.45
1:A:172:LEU:HD23	1:A:179:LEU:HB3	1.98	0.45
1:A:159:TYR:HE2	4:N:4:ARG:HE	1.63	0.45
1:A:172:LEU:HD23	1:A:179:LEU:HD23	1.99	0.45
1:A:26:GLU:OE1	1:A:34:LEU:HD12	2.17	0.45
3:D:50:ILE:HD12	3:D:61:PRO:HD2	1.99	0.44
3:D:143:GLN:CA	3:D:143:GLN:HE21	2.20	0.44
1:A:111:ARG:NH1	1:A:128:GLU:O	2.50	0.44
1:A:114:HIS:HB3	1:A:126:LEU:HD23	1.99	0.44
2:B:95:TRP:HE1	2:B:97:ARG:NH1	2.15	0.44
2:B:35:ILE:HG13	2:B:37:VAL:HG23	2.00	0.43
1:A:157:ARG:O	1:A:161:GLU:HB2	2.18	0.43
3:D:4:PRO:HB2	3:D:77:TYR:OH	2.18	0.43
1:A:33:PHE:CD1	1:A:34:LEU:HG	2.54	0.43
1:A:20:PRO:HD2	1:A:75:ARG:HH11	1.84	0.42
1:A:20:PRO:O	1:A:75:ARG:NH1	2.40	0.42
2:B:39:LEU:O	2:B:46:ILE:HG22	2.19	0.42
1:A:14:ARG:HH12	1:A:21:ARG:HD3	1.83	0.42
3:D:177:TYR:CD1	3:D:182:PRO:HA	2.54	0.42
3:D:79:SER:O	3:D:84:ARG:HB2	2.19	0.42
1:A:194:ILE:HG22	1:A:198:GLU:C	2.39	0.42
3:D:28:GLY:HA3	3:D:29:GLY:HA3	1.69	0.42
3:D:64:SER:OG	3:D:65:ILE:N	2.50	0.42
1:A:49:GLU:O	1:A:52:VAL:HG12	2.20	0.42
2:B:70:PHE:HE1	2:B:72:PRO:HB3	1.85	0.42
3:D:169:ARG:HH11	3:D:194:LEU:HD21	1.85	0.41
2:B:12:ARG:HD2	2:B:22:PHE:CD2	2.56	0.41
1:A:223:GLU:HB3	1:A:225:THR:HG23	2.03	0.41
3:D:52:GLN:HA	3:D:55:VAL:HB	2.01	0.41
2:B:83:ASN:OD1	2:B:84:HIS:N	2.54	0.41
1:A:238:ASP:HB3	2:B:12:ARG:NH2	2.35	0.41
3:D:11:GLU:HA	3:D:12:PRO:HA	1.68	0.41
3:D:101:LYS:HB2	3:D:187:LEU:HD11	2.02	0.41
1:A:27:TYR:HA	1:A:32:GLN:HA	2.03	0.40
3:D:5:LYS:CE	3:D:88:SER:HB2	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:124:SER:OG	3:D:126:VAL:HG22	2.20	0.40
1:A:120:GLY:HA3	2:B:1:ILE:HD13	2.02	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	274/284 (96%)	263 (96%)	11 (4%)	0	100	100
2	B	99/182 (54%)	93 (94%)	5 (5%)	1 (1%)	15	46
3	D	181/267 (68%)	157 (87%)	21 (12%)	3 (2%)	9	35
4	N	4/6 (67%)	4 (100%)	0	0	100	100
All	All	558/739 (76%)	517 (93%)	37 (7%)	4 (1%)	22	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1	ILE
3	D	108	PRO
3	D	65	ILE
3	D	107	GLN

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	225/240 (94%)	225 (100%)	0	100	100
2	B	95/151 (63%)	95 (100%)	0	100	100
3	D	148/224 (66%)	146 (99%)	2 (1%)	67	82
4	N	4/6 (67%)	4 (100%)	0	100	100
All	All	472/621 (76%)	470 (100%)	2 (0%)	91	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	143	GLN
3	D	195	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	143	GLN

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
5	NAG	A	301	-	14,14,15	0.23	0	17,19,21	0.40	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
5	NAG	A	301	-	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	276/284 (97%)	0.58	33 (11%) 4 3	88, 194, 300, 320	0
2	B	101/182 (55%)	0.51	4 (3%) 38 36	116, 165, 209, 291	0
3	D	187/267 (70%)	0.64	16 (8%) 10 10	126, 195, 247, 322	0
4	N	6/6 (100%)	2.89	3 (50%) 0 0	282, 295, 308, 325	0
All	All	570/739 (77%)	0.61	56 (9%) 7 7	88, 189, 288, 325	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	N	7	GLN	7.5
1	A	137	ASP	6.3
3	D	141	HIS	4.8
3	D	14	SER	4.6
1	A	130	LEU	4.6
2	B	60	TRP	4.5
3	D	192	LEU	4.4
3	D	195	LEU	4.1
1	A	136	ALA	3.9
4	N	5	TRP	3.9
3	D	132	SER	3.9
1	A	74	ASP	3.9
1	A	81	LEU	3.8
3	D	173	ARG	3.8
1	A	83	ARG	3.7
3	D	191	LEU	3.7
1	A	10	THR	3.5
1	A	91	GLY	3.5
3	D	93	LEU	3.3
1	A	79	ARG	3.2
3	D	172	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
3	D	194	LEU	3.1
1	A	122	ASP	3.1
1	A	152	TYR	3.0
3	D	152	ARG	3.0
1	A	114	HIS	3.0
4	N	6	GLU	3.0
1	A	96	GLN	2.9
3	D	159	PHE	2.9
1	A	124	ILE	2.8
2	B	99	MET	2.8
1	A	118	TYR	2.8
1	A	171	TYR	2.8
1	A	99	ASN	2.8
1	A	28	VAL	2.8
1	A	159	TYR	2.7
1	A	116	HIS	2.7
1	A	120	GLY	2.7
3	D	120	LEU	2.7
1	A	23	ILE	2.6
1	A	95	LEU	2.6
1	A	98	MET	2.5
3	D	170	TRP	2.4
1	A	12	VAL	2.4
1	A	168	LEU	2.3
3	D	193	GLU	2.3
1	A	11	ALA	2.3
1	A	103	MET	2.1
1	A	8	PHE	2.1
2	B	37	VAL	2.1
1	A	112	GLY	2.1
1	A	205	ALA	2.1
3	D	90	PRO	2.1
1	A	72	GLN	2.0
1	A	213	ILE	2.0
2	B	33	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
5	NAG	A	301	14/15	0.83	0.21	79,96,109,109	0

6.5 Other polymers [i](#)

There are no such residues in this entry.