



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2020 – 01:50 AM BST

PDB ID : 4QRP
Title : Crystal Structure of HLA B*0801 in complex with HSKKKCDEL and DD31 TCR
Authors : Gras, S.; Berry, R.; Lucet, I.S.; Rossjohn, J.
Deposited on : 2014-07-02
Resolution : 2.90 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
Xtriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

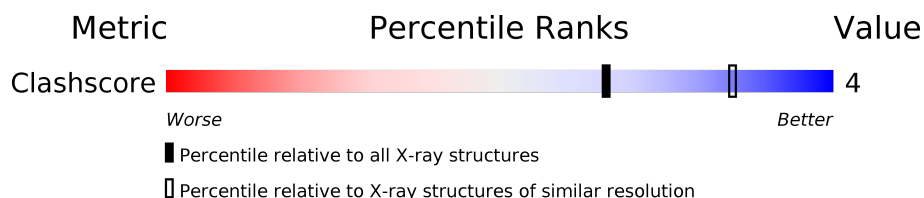
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.




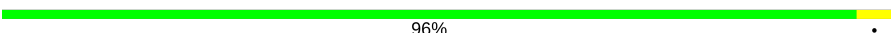






Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2172 (2.90-2.90)

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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	276	 88% 12%
1	F	276	 92% 8%
2	B	100	 87% 11% ..
2	G	100	 96% .
3	C	9	 100%
3	H	9	 89% 11%
4	D	206	 90% 9% .
4	J	206	 92% 7% .
4	K	206	 88% 10% .
5	E	245	 94% 5% .

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Mol	Chain	Length	Quality of chain
5	I	245	<div><div></div><div>89%</div><div>10%</div><div></div></div>
5	L	245	<div><div></div><div>88%</div><div>11%</div><div></div></div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 16924 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-8 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2251	1395	411	438	7			
1	F	276	Total	C	N	O	S	0	0	0
			2251	1395	411	438	7			

- 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	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	expression tag	UNP P61769
G	0	MET	-	expression tag	UNP P61769

- Molecule 3 is a protein called NS3-4A protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	S	0	0	0
			75	45	14	15	1			
3	H	9	Total	C	N	O	S	0	0	0
			75	45	14	15	1			

- Molecule 4 is a protein called DD31 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	203	Total	C	N	O	S	0	0	0
			1573	987	254	322	10			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	203	Total	C	N	O	S	0	0	0
			1573	987	254	322	10			
4	K	202	Total	C	N	O	S	0	2	0
			1578	990	257	322	9			

- Molecule 5 is a protein called DD31 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	243	Total	C	N	O	S	0	0	0
			1937	1223	344	365	5			
5	I	243	Total	C	N	O	S	0	0	0
			1937	1223	344	365	5			
5	L	243	Total	C	N	O	S	0	0	0
			1937	1223	344	365	5			

- Molecule 6 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	1	Total	I	0	0
			1	1		
6	J	1	Total	I	0	0
			1	1		
6	D	1	Total	I	0	0
			1	1		
6	K	2	Total	I	0	0
			2	2		
6	E	2	Total	I	0	0
			2	2		
6	I	2	Total	I	0	0
			2	2		
6	L	3	Total	I	0	0
			3	3		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	G	1	Total	Na	0	0
			1	1		
7	L	1	Total	Na	0	0
			1	1		
7	E	1	Total	Na	0	0
			1	1		

- Molecule 8 is water.

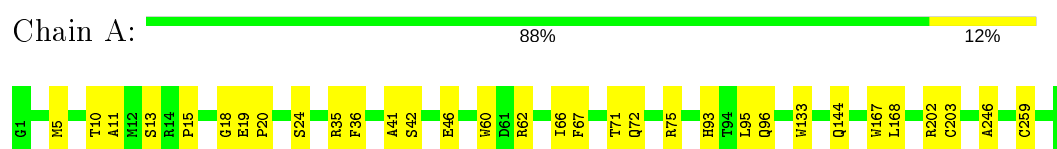
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	D	5	Total O 5 5	0	0
8	E	9	Total O 9 9	0	0
8	F	10	Total O 10 10	0	0
8	G	6	Total O 6 6	0	0
8	H	1	Total O 1 1	0	0
8	I	3	Total O 3 3	0	0
8	J	3	Total O 3 3	0	0
8	K	14	Total O 14 14	0	0
8	L	5	Total O 5 5	0	0

3 Residue-property plots [i](#)

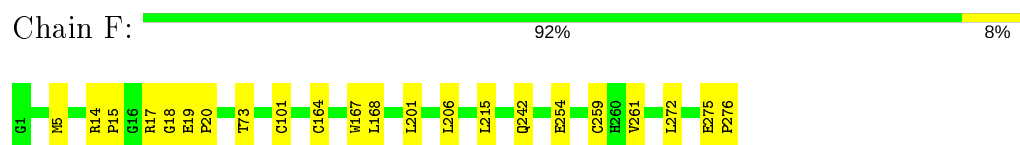
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS failed to run properly.

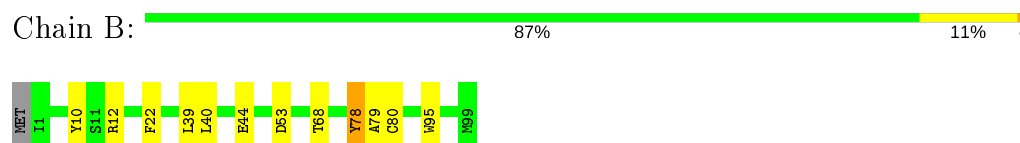
- Molecule 1: HLA class I histocompatibility antigen, B-8 alpha chain



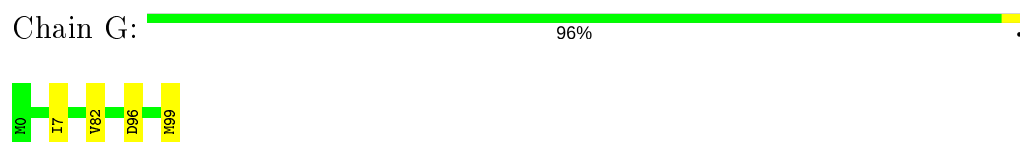
- Molecule 1: HLA class I histocompatibility antigen, B-8 alpha chain



- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 3: NS3-4A protein



There are no outlier residues recorded for this chain.

- Molecule 3: NS3-4A protein





- Molecule 4: DD31 TCR alpha chain

Chain D: 90% 9% .



- Molecule 4: DD31 TCR alpha chain

Chain J: 92% 7% .



- Molecule 4: DD31 TCR alpha chain

Chain K: 88% 10% .



- Molecule 5: DD31 TCR beta chain

Chain E: 94% 5% .



- Molecule 5: DD31 TCR beta chain

Chain I: 89% 10% .



- Molecule 5: DD31 TCR beta chain

Chain L: 88% 11% .



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.16Å 252.19Å 79.45Å 90.00° 101.97° 90.00°	Depositor
Resolution (Å)	19.85 – 2.90	Depositor
% Data completeness (in resolution range)	99.9 (19.85-2.90)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 2.88Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.10.0, BUSTER 2.10.0	Depositor
R, R_{free}	0.206 , 0.248	Depositor
Wilson B-factor (Å ²)	49.0	Xtriage
Anisotropy	0.297	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16924	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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: NA, IOD

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	0.37	0/2313	0.60	1/3146 (0.0%)
1	F	0.36	0/2313	0.61	0/3146
2	B	0.41	0/852	0.74	1/1152 (0.1%)
2	G	0.36	0/860	0.61	0/1162
3	C	0.32	0/75	0.52	0/95
3	H	0.34	0/75	0.56	0/95
4	D	0.37	0/1608	0.63	0/2182
4	J	0.38	0/1608	0.61	0/2182
4	K	0.37	0/1613	0.65	1/2189 (0.0%)
5	E	0.36	0/1988	0.62	0/2702
5	I	0.35	0/1988	0.61	0/2702
5	L	0.35	0/1988	0.58	0/2702
All	All	0.36	0/17281	0.62	3/23455 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	78	TYR	C-N-CA	7.88	141.40	121.70
4	K	143	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	20	PRO	N-CA-C	5.17	125.55	112.10

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	2251	0	2097	26	0
1	F	2251	0	2097	30	0
2	B	829	0	796	8	0
2	G	837	0	805	2	0
3	C	75	0	79	0	0
3	H	75	0	79	1	0
4	D	1573	0	1498	10	0
4	J	1573	0	1498	8	0
4	K	1578	0	1498	12	0
5	E	1937	0	1875	11	0
5	I	1937	0	1875	14	0
5	L	1937	0	1875	18	0
6	D	1	0	0	0	0
6	E	2	0	0	0	0
6	G	1	0	0	0	0
6	I	2	0	0	0	0
6	J	1	0	0	0	0
6	K	2	0	0	1	0
6	L	3	0	0	0	0
7	E	1	0	0	0	0
7	G	1	0	0	0	0
7	L	1	0	0	0	0
8	D	5	0	0	0	0
8	E	9	0	0	0	0
8	F	10	0	0	0	0
8	G	6	0	0	0	0
8	H	1	0	0	0	0
8	I	3	0	0	0	0
8	J	3	0	0	0	0
8	K	14	0	0	0	0
8	L	5	0	0	0	0
All	All	16924	0	16072	128	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.

All (128) 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)
1:F:254:GLU:CB	1:F:275:GLU:OE1	1.79	1.30
1:F:201:LEU:HD11	1:F:275:GLU:OE2	1.13	1.30
1:A:19:GLU:OE1	1:A:75:ARG:NH1	1.74	1.19
2:B:78:TYR:HB2	2:B:79:ALA:HB2	1.13	1.12
1:F:254:GLU:HB2	1:F:275:GLU:OE1	1.43	1.11
1:F:254:GLU:HB2	1:F:275:GLU:CD	1.76	1.06
1:F:201:LEU:CD1	1:F:275:GLU:OE2	2.03	1.05
1:F:201:LEU:HD21	1:F:275:GLU:HG2	1.40	1.00
1:A:19:GLU:CG	1:A:75:ARG:HG2	1.91	0.99
1:F:254:GLU:HB3	1:F:275:GLU:OE1	1.63	0.97
1:A:19:GLU:HG2	1:A:75:ARG:HG2	1.46	0.97
2:B:78:TYR:HB2	2:B:79:ALA:CB	1.98	0.92
1:A:19:GLU:CD	1:A:75:ARG:HG2	1.91	0.89
1:F:201:LEU:HD21	1:F:275:GLU:CG	2.08	0.82
5:E:23:CYS:HG	5:E:104:CYS:HG	1.21	0.80
4:D:0:MET:HG2	4:D:1:GLY:H	1.53	0.73
5:I:22:TRP:CH2	5:I:24:ASN:HB2	2.26	0.70
4:K:174:LEU:HB3	5:L:184:CYS:HB2	1.73	0.70
5:L:9:ARG:H	5:L:9:ARG:HE	1.41	0.68
1:F:254:GLU:CG	1:F:275:GLU:OE1	2.42	0.67
1:F:254:GLU:CD	1:F:275:GLU:OE1	2.34	0.66
1:F:201:LEU:CD2	1:F:275:GLU:HG2	2.21	0.65
4:K:32:LEU:HD13	4:K:86:PHE:HB2	1.81	0.61
5:L:40:TYR:HB2	5:L:105:ALA:HB3	1.82	0.61
5:E:92:GLN:HB3	5:E:93:PRO:HD2	1.83	0.61
1:A:46:GLU:HB3	1:A:60:TRP:HE1	1.67	0.59
4:J:40:PHE:HB2	4:J:105:ALA:HB3	1.84	0.59
1:A:13:SER:HB2	1:A:93:HIS:H	1.67	0.59
1:A:19:GLU:CD	1:A:75:ARG:CG	2.71	0.58
1:F:201:LEU:HD21	1:F:275:GLU:CD	2.24	0.58
1:A:18:GLY:O	1:A:19:GLU:HG3	2.04	0.58
4:D:108:ASP:HB2	4:D:109:PRO:HD2	1.85	0.58
5:L:143:PRO:HD3	5:L:156:LEU:HG	1.86	0.57
4:K:22:CYS:HG	4:K:103:CYS:HG	0.63	0.57
5:E:158:CYS:CB	5:E:223:CYS:HG	2.18	0.56
5:I:170:LEU:HG	5:I:225:VAL:HG22	1.87	0.56
2:B:39:LEU:HA	2:B:80:CYS:HA	1.88	0.56
1:F:215:LEU:HD22	1:F:261:VAL:HG12	1.88	0.55
4:K:172:CYS:HB3	5:L:184:CYS:SG	2.46	0.55
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.87	0.55
5:I:175:ASN:HD21	5:I:219:ASN:HD22	1.54	0.54
2:G:7:ILE:HG12	2:G:82:VAL:HG21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:GLU:OE2	1:A:75:ARG:HB3	2.08	0.53
1:F:201:LEU:HD21	1:F:275:GLU:OE2	2.08	0.53
5:L:54:ILE:HB	5:L:71:LEU:HD13	1.90	0.53
5:I:92:GLN:HG3	5:I:93:PRO:HD2	1.90	0.53
4:J:108:ASP:HB2	4:J:109:PRO:HD2	1.91	0.53
4:D:21:ILE:HD12	4:D:89:LEU:HD23	1.90	0.53
5:E:247:ILE:H	1:F:17:ARG:HH21	1.57	0.53
5:E:92:GLN:O	5:E:93:PRO:C	2.48	0.53
4:K:192:LYS:HE3	4:K:194:ASP:HB2	1.90	0.52
4:D:40:PHE:HB2	4:D:105:ALA:HB3	1.91	0.52
1:A:11:ALA:HB3	1:A:95:LEU:HB3	1.92	0.52
1:A:167:TRP:HZ2	4:D:0:MET:HB2	1.75	0.51
1:A:35:ARG:CZ	2:B:53:ASP:HB2	2.40	0.51
5:E:247:ILE:HD12	1:F:17:ARG:HG3	1.92	0.51
4:D:23:CYS:H	4:D:88:HIS:HD2	1.59	0.51
1:A:24:SER:HB3	1:A:36:PHE:HB2	1.93	0.50
2:G:96:ASP:HB3	2:G:99:MET:HB2	1.92	0.50
1:A:72:GLN:HA	1:A:75:ARG:HD2	1.94	0.49
5:L:158:CYS:HG	5:L:223:CYS:HG	1.53	0.49
4:K:153:ASP:HB2	6:K:301:IOD:I	2.82	0.49
2:B:39:LEU:HD11	2:B:68:THR:HG22	1.95	0.49
1:A:62:ARG:O	1:A:66:ILE:HG12	2.13	0.49
4:K:141:SER:HB2	4:K:142:SER:HA	1.95	0.49
1:A:19:GLU:CD	1:A:75:ARG:HH11	2.09	0.48
5:I:228:TYR:HA	5:I:245:THR:HG23	1.95	0.48
5:L:158:CYS:SG	5:L:223:CYS:SG	3.09	0.48
1:F:259:CYS:HB3	1:F:272:LEU:HB2	1.95	0.48
1:A:10:THR:HG22	1:A:96:GLN:HG2	1.96	0.47
1:A:41:ALA:HA	1:A:42:SER:HA	1.68	0.47
1:F:5:MET:HB2	1:F:168:LEU:HD13	1.96	0.47
4:D:148:CYS:HB2	4:D:189:ALA:HB3	1.97	0.47
5:L:158:CYS:CB	5:L:223:CYS:HG	2.28	0.47
5:L:22:TRP:HE1	5:L:86:ASP:HB3	1.80	0.47
4:D:58:LYS:O	4:D:61:ASP:HB2	2.15	0.47
5:E:78:ALA:HB2	5:E:89:LEU:HD12	1.97	0.46
5:L:184:CYS:HB3	5:L:206:ARG:HB2	1.97	0.46
5:L:192:GLU:HG3	5:L:200:ARG:HB2	1.96	0.46
1:A:19:GLU:HG2	1:A:75:ARG:CG	2.31	0.46
1:F:254:GLU:CB	1:F:275:GLU:CD	2.52	0.46
1:A:133:TRP:HB2	1:A:144:GLN:HG3	1.97	0.46
5:E:21:PHE:HZ	5:E:124:LEU:HD22	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:247:ILE:HD13	1:F:15:PRO:HB2	1.98	0.45
1:F:254:GLU:HB2	1:F:275:GLU:OE2	2.14	0.45
1:A:203:CYS:HG	1:A:259:CYS:HG	1.65	0.45
5:L:75:ARG:HA	5:L:93:PRO:HD2	1.99	0.45
5:L:78:ALA:HB2	5:L:89:LEU:HD12	1.98	0.45
2:B:10:TYR:HA	2:B:95:TRP:CZ3	2.52	0.45
5:I:92:GLN:O	5:I:93:PRO:C	2.54	0.44
5:E:193:GLN:HG3	5:E:196:LEU:HD13	2.00	0.44
5:I:158:CYS:SG	5:I:223:CYS:SG	3.03	0.44
1:F:206:LEU:HD23	1:F:242:GLN:HG2	2.01	0.43
5:L:101:VAL:HG22	5:L:123:ARG:HD2	2.00	0.43
1:A:18:GLY:C	1:A:19:GLU:HG3	2.38	0.43
5:I:135:PRO:HD3	5:I:243:PRO:HB3	1.99	0.43
4:J:8:GLU:HG2	4:J:9:GLY:N	2.33	0.43
5:L:31:THR:HG21	5:L:110:GLY:HA3	2.01	0.43
4:D:159:VAL:HG21	4:D:187:ALA:HB2	2.01	0.43
4:K:85:SER:HB2	4:K:87:HIS:CE1	2.54	0.43
4:D:54:LEU:HD11	4:D:78:ALA:HB3	1.99	0.43
5:L:12:ILE:HG23	5:L:127:LEU:HD13	2.00	0.43
5:I:140:VAL:HG23	5:I:250:ALA:HB3	2.00	0.43
4:K:163:ASP:HB3	4:K:166:VAL:HG22	2.00	0.43
5:I:21:PHE:HZ	5:I:124:LEU:HD22	1.84	0.42
1:A:202:ARG:HG3	1:A:246:ALA:HB2	2.02	0.42
1:F:19:GLU:HA	1:F:20:PRO:HD3	1.94	0.42
4:K:195:PHE:HA	4:K:199:ASN:HD21	1.84	0.42
5:I:78:ALA:HB2	5:I:89:LEU:HD12	2.01	0.42
1:F:73:THR:HG21	3:H:6:CYS:HA	2.01	0.42
4:J:124:LYS:HD2	4:J:155:SER:HB3	2.01	0.42
1:A:67:PHE:O	1:A:71:THR:HG23	2.20	0.41
5:L:224:GLN:HG3	5:L:247:ILE:HG23	2.03	0.41
5:I:184:CYS:SG	4:J:175:LEU:HB3	2.60	0.41
1:F:167:TRP:HZ2	4:J:0:MET:HB2	1.86	0.41
1:F:14:ARG:HG3	1:F:18:GLY:H	1.85	0.41
2:B:12:ARG:HB2	2:B:22:PHE:HB2	2.02	0.41
1:A:15:PRO:HB2	5:I:247:ILE:HD11	2.01	0.41
1:F:101:CYS:SG	1:F:164:CYS:SG	3.13	0.41
4:J:32:SER:HA	4:J:57:THR:HA	2.02	0.41
2:B:40:LEU:HD11	2:B:44:GLU:C	2.41	0.41
5:E:247:ILE:H	1:F:17:ARG:HE	1.68	0.41
5:I:23:CYS:CB	5:I:104:CYS:HG	2.33	0.40
4:K:192:LYS:HE2	4:K:195:PHE:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:201:LEU:CD2	1:F:275:GLU:OE2	2.69	0.40
4:J:41:TRP:CE2	4:J:89:LEU:HB2	2.56	0.40
4:K:1:ASP:O	4:K:113:ARG:HD2	2.21	0.40
1:F:275:GLU:H	1:F:276:PRO:CD	2.33	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 15 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section is therefore empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section is therefore empty.