



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 22, 2023 – 10:44 AM JST

PDB ID : 7DF1  
Title : Crystal structure of human CD98 heavy chain extracellular domain in complex with S1-F4 scFv  
Authors : Liu, X.; Ding, J.; Sui, J.; Tian, X.  
Deposited on : 2020-11-06  
Resolution : 2.81 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](mailto: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>.

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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 : 2.36  
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) : 2.36

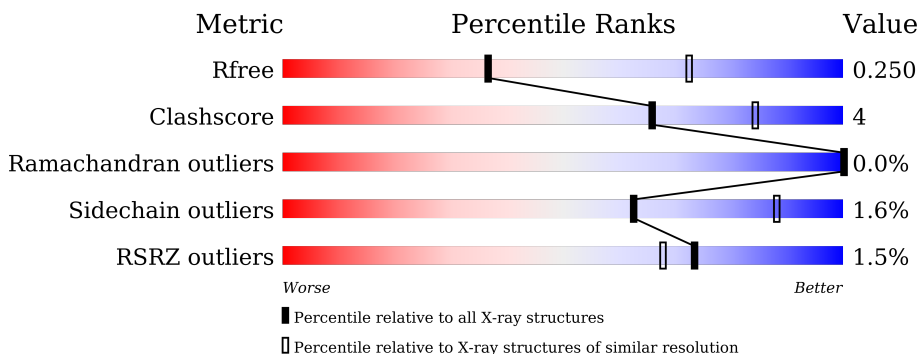
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.81 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.



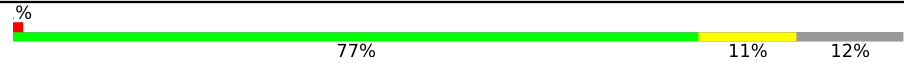


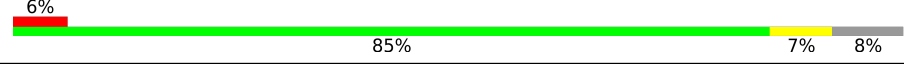


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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  $\geq 3$ , 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	420	
1	B	420	
1	C	420	
1	D	420	
2	E	140	
2	F	140	

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Mol	Chain	Length	Quality of chain
2	G	140	 <p>77% 11% 12%</p>
2	H	140	 <p>79% 9% 12%</p>
3	I	122	 <p>2% 87% 5% 8%</p>
3	J	122	 <p>6% 85% 7% 8%</p>
3	K	122	 <p>2% 84% 7% 8%</p>
3	L	122	 <p>2% 87% 8%</p>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 19740 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 4F2 cell-surface antigen heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	400	Total 3130	C 1992	N 535	O 598	S 5	0	0	0
1	B	400	Total 3130	C 1992	N 535	O 598	S 5	0	0	0
1	C	394	Total 3090	C 1970	N 527	O 588	S 5	0	0	0
1	D	394	Total 3090	C 1970	N 527	O 588	S 5	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	110	SER	-	expression tag	UNP P08195
B	110	SER	-	expression tag	UNP P08195
C	110	SER	-	expression tag	UNP P08195
D	110	SER	-	expression tag	UNP P08195

- Molecule 2 is a protein called S1-F4 VH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	123	Total 952	C 603	N 159	O 183	S 7	0	0	0
2	E	123	Total 952	C 603	N 159	O 183	S 7	0	0	0
2	F	123	Total 952	C 603	N 159	O 183	S 7	0	0	0
2	G	123	Total 952	C 603	N 159	O 183	S 7	0	0	0

- Molecule 3 is a protein called IGL c2062\_light\_IGKV4-1\_IGKJ5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	112	873	550	144	176	3	0	0	0
3	I	112	873	550	144	176	3	0	0	0
3	J	112	873	550	144	176	3	0	0	0
3	K	112	873	550	144	176	3	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	93	ASN	SER	conflict	UNP A0A5C2G3X0
L	108	ALA	-	expression tag	UNP A0A5C2G3X0
L	109	ALA	-	expression tag	UNP A0A5C2G3X0
L	110	ALA	-	expression tag	UNP A0A5C2G3X0
L	111	HIS	-	expression tag	UNP A0A5C2G3X0
L	112	HIS	-	expression tag	UNP A0A5C2G3X0
L	113	HIS	-	expression tag	UNP A0A5C2G3X0
L	114	HIS	-	expression tag	UNP A0A5C2G3X0
L	115	HIS	-	expression tag	UNP A0A5C2G3X0
L	116	HIS	-	expression tag	UNP A0A5C2G3X0
I	93	ASN	SER	conflict	UNP A0A5C2G3X0
I	108	ALA	-	expression tag	UNP A0A5C2G3X0
I	109	ALA	-	expression tag	UNP A0A5C2G3X0
I	110	ALA	-	expression tag	UNP A0A5C2G3X0
I	111	HIS	-	expression tag	UNP A0A5C2G3X0
I	112	HIS	-	expression tag	UNP A0A5C2G3X0
I	113	HIS	-	expression tag	UNP A0A5C2G3X0
I	114	HIS	-	expression tag	UNP A0A5C2G3X0
I	115	HIS	-	expression tag	UNP A0A5C2G3X0
I	116	HIS	-	expression tag	UNP A0A5C2G3X0
J	93	ASN	SER	conflict	UNP A0A5C2G3X0
J	108	ALA	-	expression tag	UNP A0A5C2G3X0
J	109	ALA	-	expression tag	UNP A0A5C2G3X0
J	110	ALA	-	expression tag	UNP A0A5C2G3X0
J	111	HIS	-	expression tag	UNP A0A5C2G3X0
J	112	HIS	-	expression tag	UNP A0A5C2G3X0
J	113	HIS	-	expression tag	UNP A0A5C2G3X0
J	114	HIS	-	expression tag	UNP A0A5C2G3X0
J	115	HIS	-	expression tag	UNP A0A5C2G3X0
J	116	HIS	-	expression tag	UNP A0A5C2G3X0
K	93	ASN	SER	conflict	UNP A0A5C2G3X0

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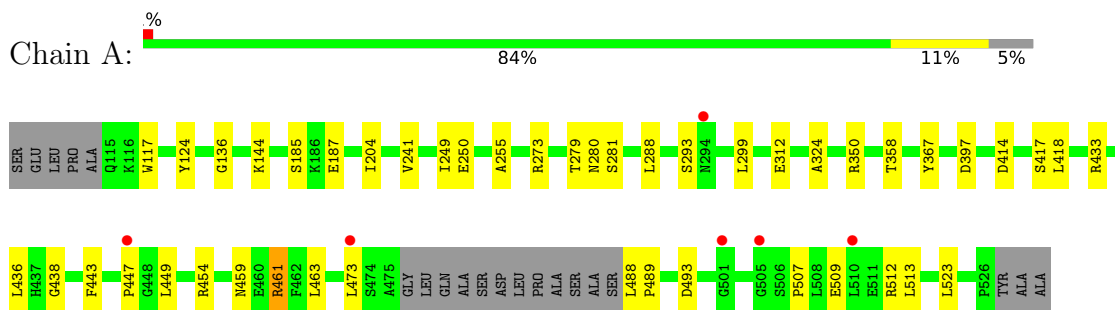
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<b>Chain</b>	<b>Residue</b>	<b>Modelled</b>	<b>Actual</b>	<b>Comment</b>	<b>Reference</b>
K	108	ALA	-	expression tag	UNP A0A5C2G3X0
K	109	ALA	-	expression tag	UNP A0A5C2G3X0
K	110	ALA	-	expression tag	UNP A0A5C2G3X0
K	111	HIS	-	expression tag	UNP A0A5C2G3X0
K	112	HIS	-	expression tag	UNP A0A5C2G3X0
K	113	HIS	-	expression tag	UNP A0A5C2G3X0
K	114	HIS	-	expression tag	UNP A0A5C2G3X0
K	115	HIS	-	expression tag	UNP A0A5C2G3X0
K	116	HIS	-	expression tag	UNP A0A5C2G3X0

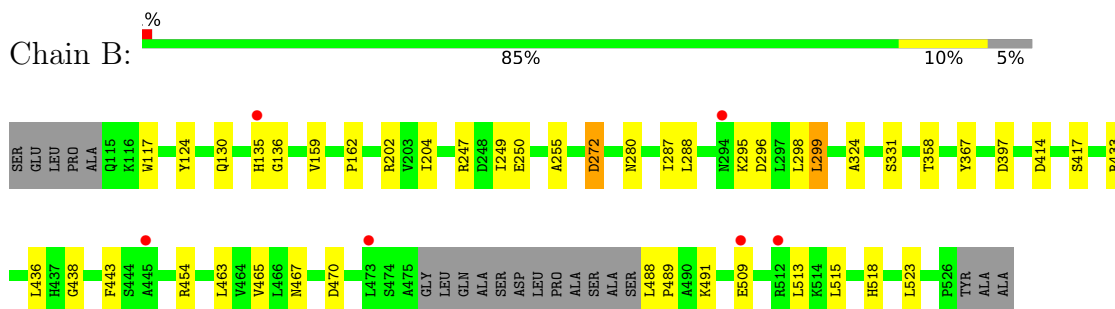
### 3 Residue-property plots [i](#)

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.

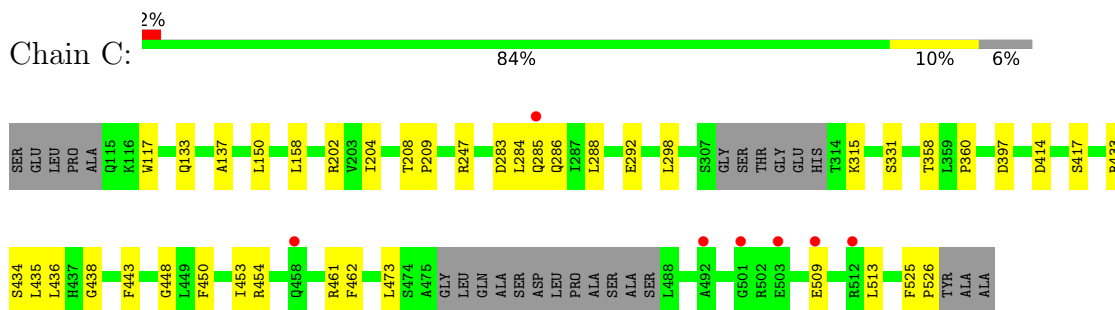
- Molecule 1: 4F2 cell-surface antigen heavy chain



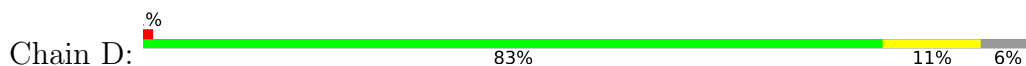
- Molecule 1: 4F2 cell-surface antigen heavy chain

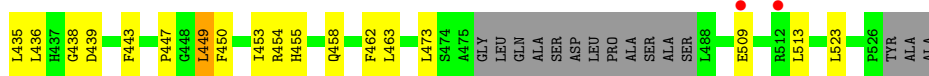
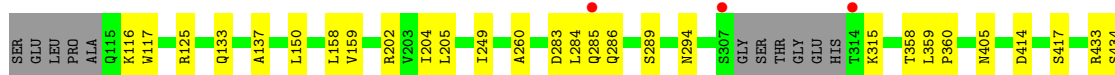


- Molecule 1: 4F2 cell-surface antigen heavy chain

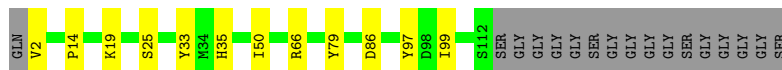
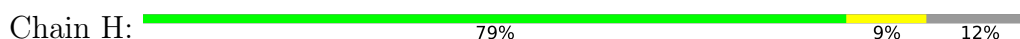


- Molecule 1: 4F2 cell-surface antigen heavy chain

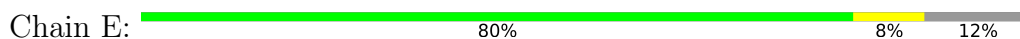




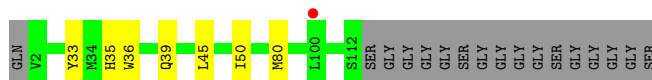
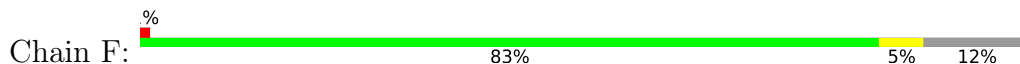
- Molecule 2: S1-F4 VH



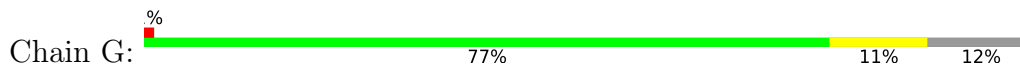
- Molecule 2: S1-F4 VH



- Molecule 2: S1-F4 VH



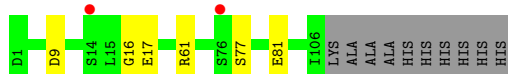
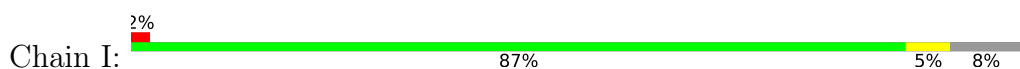
- Molecule 2: S1-F4 VH



- Molecule 3: IGL c2062\_light\_IGKV4-1\_IGKJ5




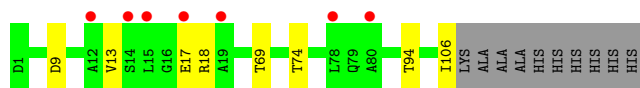
- Molecule 3: IGL c2062\_light\_IGKV4-1\_IGKJ5






- Molecule 3: IGL c2062\_light\_IGKV4-1\_IGKJ5

Chain J: 



- Molecule 3: IGL c2062\_light\_IGKV4-1\_IGKJ5

Chain K: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	125.80Å 165.21Å 176.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.04 – 2.81 50.04 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.04-2.81) 93.2 (50.04-2.81)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.59 (at 2.81Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.217 , 0.249 0.217 , 0.250	Depositor DCC
$R_{free}$ test set	2013 reflections (2.23%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.8	Xtrriage
Anisotropy	0.489	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 32.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	19740	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	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 51.15 % 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 5.8437e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.24	0/3199	0.43	0/4335
1	B	0.25	0/3199	0.44	0/4335
1	C	0.25	0/3157	0.44	0/4277
1	D	0.25	0/3157	0.44	0/4277
2	E	0.25	0/975	0.47	0/1321
2	F	0.27	0/975	0.46	0/1321
2	G	0.25	0/975	0.46	0/1321
2	H	0.25	0/975	0.47	0/1321
3	I	0.25	0/893	0.46	0/1216
3	J	0.25	0/893	0.45	0/1216
3	K	0.25	0/893	0.47	0/1216
3	L	0.25	0/893	0.45	0/1216
All	All	0.25	0/20184	0.45	0/27372

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	3130	0	3095	25	0
1	B	3130	0	3095	27	0
1	C	3090	0	3063	26	0
1	D	3090	0	3063	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	952	0	921	7	0
2	F	952	0	921	6	0
2	G	952	0	921	8	0
2	H	952	0	921	9	0
3	I	873	0	841	2	0
3	J	873	0	841	3	0
3	K	873	0	841	6	0
3	L	873	0	841	2	0
All	All	19740	0	19364	145	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 (145) 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:E:33:TYR:HB3	2:E:50:ILE:HD11	1.52	0.92
2:H:33:TYR:HB3	2:H:50:ILE:HD11	1.56	0.88
1:A:136:GLY:HA3	1:B:136:GLY:HA3	1.58	0.84
2:G:33:TYR:HB3	2:G:50:ILE:HD11	1.59	0.83
2:F:33:TYR:HB3	2:F:50:ILE:HD11	1.64	0.79
1:D:283:ASP:HB3	1:D:286:GLN:OE1	1.97	0.65
1:B:288:LEU:HD21	1:B:324:ALA:HB1	1.80	0.64
1:D:360:PRO:HB3	1:D:454:ARG:HH21	1.63	0.63
1:B:470:ASP:OD1	1:B:518:HIS:NE2	2.31	0.62
1:B:465:VAL:HG12	1:B:515:LEU:HD11	1.81	0.62
1:C:360:PRO:HB3	1:C:454:ARG:HH21	1.64	0.61
1:C:434:SER:O	1:C:454:ARG:NH1	2.34	0.61
1:D:133:GLN:NE2	1:D:137:ALA:O	2.33	0.60
1:C:133:GLN:NE2	1:C:137:ALA:O	2.34	0.60
1:D:283:ASP:OD1	1:D:284:LEU:N	2.34	0.60
1:C:433:ARG:HA	1:C:436:LEU:HD12	1.83	0.59
1:C:461:ARG:NH1	1:C:526:PRO:O	2.36	0.59
1:C:283:ASP:HB3	1:C:286:GLN:OE1	2.03	0.58
1:B:463:LEU:HD23	1:B:523:LEU:HD13	1.85	0.58
3:K:18:ARG:HH11	3:K:74:THR:HG21	1.69	0.58
1:C:283:ASP:OD1	1:C:284:LEU:N	2.37	0.57
1:D:414:ASP:HB3	1:D:417:SER:HB3	1.85	0.57
1:D:447:PRO:HD2	1:D:473:LEU:HD21	1.86	0.57
1:D:433:ARG:HA	1:D:436:LEU:HD12	1.86	0.57
1:A:509:GLU:N	1:A:509:GLU:OE1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:46:GLU:OE2	2:G:62:LYS:NZ	2.34	0.57
3:K:35:TRP:CD1	3:K:48:ILE:HD11	2.38	0.57
1:D:434:SER:O	1:D:454:ARG:NH1	2.38	0.57
1:C:438:GLY:HA2	1:C:454:ARG:HH22	1.71	0.56
1:A:250:GLU:OE1	1:A:280:ASN:ND2	2.35	0.55
1:D:358:THR:O	1:D:454:ARG:HD2	2.06	0.55
3:K:35:TRP:HB2	3:K:48:ILE:HG12	1.89	0.55
1:A:288:LEU:HD11	1:A:324:ALA:HB1	1.89	0.55
1:A:447:PRO:HD2	1:A:473:LEU:HD21	1.89	0.55
1:B:117:TRP:CG	1:B:202:ARG:HD2	2.41	0.55
1:B:414:ASP:HB3	1:B:417:SER:HB3	1.89	0.54
1:A:358:THR:O	1:A:454:ARG:HD2	2.08	0.53
1:C:315:LYS:HG3	1:C:450:PHE:CD2	2.44	0.53
1:D:509:GLU:N	1:D:509:GLU:OE1	2.41	0.53
2:H:66:ARG:NH2	2:H:86:ASP:OD2	2.42	0.53
1:C:358:THR:O	1:C:454:ARG:HD2	2.09	0.53
1:C:509:GLU:N	1:C:509:GLU:OE1	2.43	0.52
1:B:509:GLU:OE1	1:B:509:GLU:N	2.43	0.52
1:A:488:LEU:HD12	1:A:489:PRO:HD2	1.92	0.52
1:B:467:ASN:HB2	1:B:515:LEU:HD13	1.92	0.52
1:D:117:TRP:CG	1:D:202:ARG:HD2	2.45	0.52
1:D:285:GLN:O	1:D:289:SER:N	2.35	0.51
1:A:433:ARG:HA	1:A:436:LEU:HD12	1.92	0.51
2:E:35:HIS:CE1	2:E:50:ILE:HD13	2.46	0.51
2:G:35:HIS:CE1	2:G:50:ILE:HD13	2.46	0.51
1:B:117:TRP:HD1	1:B:272:ASP:OD2	1.94	0.50
1:C:117:TRP:CG	1:C:202:ARG:HD2	2.45	0.50
2:F:39:GLN:HB2	2:F:45:LEU:HD23	1.93	0.50
1:A:241:VAL:O	1:A:273:ARG:NH2	2.45	0.50
1:A:312:GLU:HB2	1:A:447:PRO:O	2.10	0.50
1:A:414:ASP:HB3	1:A:417:SER:HB3	1.94	0.50
1:C:448:GLY:H	1:C:473:LEU:HD21	1.77	0.50
1:C:117:TRP:HH2	1:C:204:ILE:HD11	1.76	0.50
1:A:459:ASN:O	1:A:461:ARG:HD3	2.12	0.50
2:F:33:TYR:HB3	2:F:50:ILE:CD1	2.40	0.50
1:A:279:THR:HG22	1:A:281:SER:H	1.77	0.49
2:E:2:VAL:HA	2:E:25:SER:O	2.12	0.49
1:A:463:LEU:HD23	1:A:523:LEU:HD13	1.93	0.49
1:A:438:GLY:HA2	1:A:454:ARG:NH2	2.28	0.49
1:B:117:TRP:CD2	1:B:202:ARG:HD2	2.47	0.49
1:B:358:THR:O	1:B:454:ARG:HD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:35:HIS:CE1	2:H:50:ILE:HD13	2.46	0.49
1:C:150:LEU:HD13	1:C:158:LEU:HD21	1.93	0.49
1:A:509:GLU:OE2	1:A:512:ARG:NH2	2.45	0.49
1:C:414:ASP:HB3	1:C:417:SER:HB3	1.93	0.49
2:F:35:HIS:CE1	2:F:50:ILE:HD13	2.48	0.48
1:B:438:GLY:HA2	1:B:454:ARG:NH2	2.28	0.48
1:D:117:TRP:CD2	1:D:202:ARG:HD2	2.48	0.48
2:H:2:VAL:HA	2:H:25:SER:O	2.14	0.48
1:D:150:LEU:HD13	1:D:158:LEU:HD21	1.97	0.47
1:C:117:TRP:CD2	1:C:202:ARG:HD2	2.49	0.47
1:D:435:LEU:HA	1:D:454:ARG:NH1	2.30	0.47
3:J:17:GLU:HG2	3:J:18:ARG:H	1.79	0.47
1:A:249:ILE:HG23	1:A:255:ALA:HB1	1.98	0.46
2:G:33:TYR:HB3	2:G:50:ILE:CD1	2.38	0.46
1:B:250:GLU:OE1	1:B:280:ASN:ND2	2.49	0.46
1:A:438:GLY:HA2	1:A:454:ARG:HH22	1.80	0.46
1:D:125:ARG:HA	1:D:159:VAL:HB	1.97	0.46
3:J:18:ARG:HH11	3:J:74:THR:HG21	1.80	0.45
1:A:117:TRP:CH2	1:A:204:ILE:HD11	2.51	0.45
1:B:130:GLN:OE1	1:B:135:HIS:ND1	2.50	0.45
1:B:433:ARG:HA	1:B:436:LEU:HD12	1.98	0.45
3:I:61:ARG:NH2	3:I:81:GLU:OE1	2.49	0.45
1:C:435:LEU:HA	1:C:454:ARG:NH1	2.32	0.45
1:B:249:ILE:HG23	1:B:255:ALA:HB1	1.99	0.44
1:D:405:ASN:ND2	2:H:14:PRO:O	2.47	0.44
1:C:288:LEU:O	1:C:292:GLU:HG2	2.18	0.44
1:C:461:ARG:HD2	1:C:525:PHE:CE2	2.52	0.44
1:B:159:VAL:HA	1:B:204:ILE:HB	1.99	0.44
3:K:18:ARG:NH1	3:K:74:THR:HG21	2.31	0.43
1:A:124:TYR:CZ	1:A:367:TYR:HA	2.53	0.43
1:D:249:ILE:HD13	1:D:249:ILE:HA	1.89	0.43
2:G:19:LYS:HE3	2:G:79:TYR:HB3	2.01	0.43
1:D:463:LEU:HD23	1:D:523:LEU:HD13	1.99	0.43
1:D:315:LYS:HG3	1:D:450:PHE:CE1	2.53	0.43
1:D:439:ASP:HB2	1:D:455:HIS:O	2.19	0.42
1:C:247:ARG:HE	1:C:247:ARG:HB2	1.49	0.42
3:L:33:LEU:HD13	3:L:71:PHE:CD1	2.54	0.42
3:I:16:GLY:HA2	3:I:77:SER:HB2	2.02	0.42
2:H:33:TYR:HB3	2:H:50:ILE:CD1	2.39	0.42
1:A:350:ARG:HG2	1:A:418:LEU:HD13	2.01	0.42
1:B:491:LYS:HE2	1:B:509:GLU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:315:LYS:HG3	1:D:450:PHE:CD1	2.55	0.42
2:G:40:ALA:HB3	2:G:43:GLN:HB2	2.01	0.42
3:K:16:GLY:HA2	3:K:77:SER:OG	2.19	0.42
1:B:124:TYR:CZ	1:B:367:TYR:HA	2.54	0.42
2:E:19:LYS:HE3	2:E:79:TYR:HB3	2.01	0.42
2:H:99:ILE:HG23	2:E:97:TYR:CZ	2.54	0.42
1:B:509:GLU:O	1:B:513:LEU:HD13	2.20	0.42
1:B:117:TRP:CH2	1:B:204:ILE:HD11	2.55	0.42
2:G:35:HIS:NE2	2:G:50:ILE:HD13	2.35	0.42
1:A:493:ASP:HA	1:A:507:PRO:HA	2.02	0.41
1:D:438:GLY:HA2	1:D:454:ARG:HH22	1.84	0.41
3:J:13:VAL:O	3:J:106:ILE:HA	2.20	0.41
1:D:117:TRP:HH2	1:D:204:ILE:HD11	1.85	0.41
3:L:16:GLY:HA2	3:L:77:SER:HB2	2.03	0.41
3:K:33:LEU:HD22	3:K:71:PHE:CG	2.55	0.41
1:A:185:SER:OG	1:A:187:GLU:HG2	2.21	0.41
1:B:287:ILE:HG23	1:B:299:LEU:HD22	2.02	0.41
1:C:513:LEU:HD12	1:C:513:LEU:HA	1.88	0.41
1:B:162:PRO:HD3	1:B:247:ARG:HH12	1.85	0.41
1:D:449:LEU:HD23	1:D:473:LEU:HD23	2.02	0.41
1:D:453:ILE:HD12	1:D:462:PHE:O	2.20	0.41
1:B:249:ILE:HD13	1:B:249:ILE:HA	1.87	0.41
1:A:449:LEU:HG	1:A:473:LEU:HD23	2.02	0.41
2:E:66:ARG:NH2	2:E:86:ASP:OD1	2.52	0.41
2:F:35:HIS:NE2	2:F:50:ILE:HD13	2.36	0.41
2:G:34:MET:HG2	2:G:78:VAL:HG21	2.01	0.41
1:C:453:ILE:HD12	1:C:462:PHE:O	2.21	0.41
1:C:298:LEU:HG	1:C:331:SER:HB3	2.03	0.40
1:D:359:LEU:HD23	1:D:359:LEU:HA	1.94	0.40
2:H:19:LYS:HE3	2:H:79:TYR:HB3	2.02	0.40
1:A:117:TRP:HH2	1:A:204:ILE:HD11	1.85	0.40
2:F:36:TRP:CE2	2:F:80:MET:HB2	2.57	0.40
1:C:208:THR:HA	1:C:209:PRO:HD3	1.95	0.40
2:H:97:TYR:CZ	2:E:99:ILE:HG23	2.57	0.40
1:B:298:LEU:HG	1:B:331:SER:HB3	2.03	0.40
1:B:488:LEU:HA	1:B:489:PRO:HD3	1.98	0.40
1:C:315:LYS:HD2	1:C:450:PHE:HA	2.04	0.40
1:D:260:ALA:HA	1:D:294:ASN:OD1	2.21	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	396/420 (94%)	381 (96%)	15 (4%)	0	100	100
1	B	396/420 (94%)	381 (96%)	14 (4%)	1 (0%)	41	72
1	C	388/420 (92%)	374 (96%)	14 (4%)	0	100	100
1	D	388/420 (92%)	373 (96%)	15 (4%)	0	100	100
2	E	121/140 (86%)	120 (99%)	1 (1%)	0	100	100
2	F	121/140 (86%)	120 (99%)	1 (1%)	0	100	100
2	G	121/140 (86%)	120 (99%)	1 (1%)	0	100	100
2	H	121/140 (86%)	120 (99%)	1 (1%)	0	100	100
3	I	110/122 (90%)	104 (94%)	6 (6%)	0	100	100
3	J	110/122 (90%)	105 (96%)	5 (4%)	0	100	100
3	K	110/122 (90%)	104 (94%)	6 (6%)	0	100	100
3	L	110/122 (90%)	104 (94%)	6 (6%)	0	100	100
All	All	2492/2728 (91%)	2406 (96%)	85 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	296	ASP

### 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	341/354 (96%)	334 (98%)	7 (2%)	53	84
1	B	341/354 (96%)	336 (98%)	5 (2%)	65	89
1	C	337/354 (95%)	334 (99%)	3 (1%)	78	94
1	D	337/354 (95%)	331 (98%)	6 (2%)	59	86
2	E	103/108 (95%)	103 (100%)	0	100	100
2	F	103/108 (95%)	103 (100%)	0	100	100
2	G	103/108 (95%)	99 (96%)	4 (4%)	32	66
2	H	103/108 (95%)	103 (100%)	0	100	100
3	I	98/105 (93%)	96 (98%)	2 (2%)	55	84
3	J	98/105 (93%)	95 (97%)	3 (3%)	40	74
3	K	98/105 (93%)	97 (99%)	1 (1%)	76	93
3	L	98/105 (93%)	95 (97%)	3 (3%)	40	74
All	All	2160/2268 (95%)	2126 (98%)	34 (2%)	62	88

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	LYS
1	A	293	SER
1	A	299	LEU
1	A	397	ASP
1	A	443	PHE
1	A	461	ARG
1	A	513	LEU
1	B	272	ASP
1	B	295	LYS
1	B	299	LEU
1	B	397	ASP
1	B	443	PHE
1	C	285	GLN
1	C	397	ASP
1	C	443	PHE
1	D	116	LYS
1	D	205	LEU
1	D	443	PHE
1	D	449	LEU
1	D	458	GLN
1	D	513	LEU
3	L	9	ASP

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Mol	Chain	Res	Type
3	L	33	LEU
3	L	48	ILE
3	I	9	ASP
3	I	17	GLU
3	J	9	ASP
3	J	69	THR
3	J	94	THR
2	G	71	ARG
2	G	73	THR
2	G	83	ARG
2	G	99	ILE
3	K	9	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	400/420 (95%)	-0.06	6 (1%) 73 68	32, 48, 89, 113	0
1	B	400/420 (95%)	-0.09	6 (1%) 73 68	30, 47, 87, 108	0
1	C	394/420 (93%)	-0.08	7 (1%) 68 61	32, 50, 90, 118	0
1	D	394/420 (93%)	-0.03	5 (1%) 77 72	35, 51, 92, 118	0
2	E	123/140 (87%)	-0.32	0 100 100	31, 45, 60, 80	0
2	F	123/140 (87%)	-0.08	1 (0%) 86 81	37, 55, 71, 87	0
2	G	123/140 (87%)	-0.10	1 (0%) 86 81	37, 54, 70, 89	0
2	H	123/140 (87%)	-0.35	0 100 100	33, 45, 57, 79	0
3	I	112/122 (91%)	0.12	2 (1%) 68 61	35, 49, 77, 84	0
3	J	112/122 (91%)	0.30	7 (6%) 20 12	47, 68, 100, 111	0
3	K	112/122 (91%)	0.36	3 (2%) 54 44	48, 69, 92, 104	0
3	L	112/122 (91%)	0.08	0 100 100	35, 49, 78, 85	0
All	All	2528/2728 (92%)	-0.04	38 (1%) 73 68	30, 51, 88, 118	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	100	LEU	4.3
1	D	509	GLU	3.7
3	J	17	GLU	3.6
1	C	512	ARG	3.6
1	A	473	LEU	3.5
1	A	510	LEU	3.5
1	A	501	GLY	3.5
3	J	80	ALA	3.4
1	D	307	SER	3.0
1	D	512	ARG	2.8
1	B	512	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
3	I	14	SER	2.7
3	J	78	LEU	2.7
1	D	285	GLN	2.7
3	K	80	ALA	2.7
3	I	76	SER	2.6
1	B	445	ALA	2.6
3	J	19	ALA	2.5
1	B	509	GLU	2.5
3	K	10	SER	2.5
1	C	509	GLU	2.5
3	J	12	ALA	2.5
2	F	100	LEU	2.5
1	C	285	GLN	2.5
1	C	503	GLU	2.4
1	B	294	ASN	2.4
1	D	314	THR	2.4
1	A	505	GLY	2.4
1	A	294	ASN	2.3
1	B	473	LEU	2.3
3	J	14	SER	2.3
1	C	492	ALA	2.3
1	B	135	HIS	2.3
3	K	105	GLU	2.2
3	J	15	LEU	2.2
1	C	458	GLN	2.2
1	A	447	PRO	2.1
1	C	501	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 monosaccharides 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.