



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:12 PM GMT

PDB ID : 1SFC  
Title : NEURONAL SYNAPTIC FUSION COMPLEX  
Authors : Sutton, R.B.; Brunger, A.T.  
Deposited on : 1998-08-24  
Resolution : 2.40 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

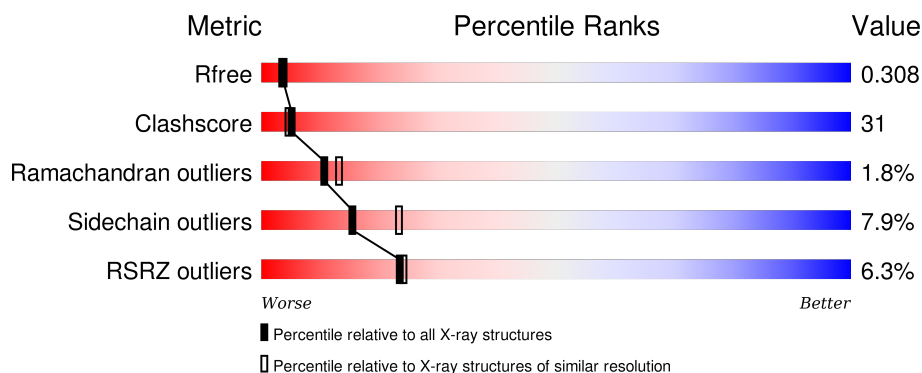
# 1 Overall quality at a glance

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))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	96	 2% 42% 29% 28%
1	E	96	 3% 27% 40% 5% 28%
1	I	96	 9% 40% 29% 28%
2	B	83	 4% 47% 34% 6% 13%
2	F	83	 4% 39% 42% 7% 12%

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Mol	Chain	Length	Quality of chain
2	J	83	
3	C	83	
3	G	83	
3	K	83	
4	D	87	
4	H	87	
4	L	87	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	MPD	A	927	-	-	-	X
6	MPD	F	926	-	-	-	X
6	MPD	I	930	-	-	-	X
6	MPD	K	929	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7105 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 PROTEIN (SYNAPTOBREVIN 2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	69	Total	C	N	O	S	0	0	0
			564	347	106	110	1			
1	E	69	Total	C	N	O	S	0	0	0
			567	349	106	109	3			
1	I	69	Total	C	N	O	S	0	0	0
			565	349	106	109	1			

- Molecule 2 is a protein called PROTEIN (SYNTAXIN 1A).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	72	Total	C	N	O	S	0	0	0
			586	362	100	119	5			
2	F	73	Total	C	N	O	S	0	0	0
			594	368	102	119	5			
2	J	74	Total	C	N	O	S	20	0	0
			600	371	102	122	5			

- Molecule 3 is a protein called PROTEIN (SNAP-25B).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	77	Total	C	N	O	S	0	0	0
			625	371	115	133	6			
3	G	72	Total	C	N	O	S	9	0	0
			581	345	106	125	5			
3	K	73	Total	C	N	O	S	9	0	0
			589	351	107	126	5			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	58	ASP	GLU	SEE REMARK 999	UNP P60881
C	60	VAL	ILE	SEE REMARK 999	UNP P60881

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Chain	Residue	Modelled	Actual	Comment	Reference
C	65	ASN	ASP	SEE REMARK 999	UNP P60881
C	66	HIS	GLN	SEE REMARK 999	UNP P60881
C	69	GLN	LYS	SEE REMARK 999	UNP P60881
C	79	LYS	THR	SEE REMARK 999	UNP P60881
G	58	ASP	GLU	SEE REMARK 999	UNP P60881
G	60	VAL	ILE	SEE REMARK 999	UNP P60881
G	65	ASN	ASP	SEE REMARK 999	UNP P60881
G	66	HIS	GLN	SEE REMARK 999	UNP P60881
G	69	GLN	LYS	SEE REMARK 999	UNP P60881
G	79	LYS	THR	SEE REMARK 999	UNP P60881
K	58	ASP	GLU	SEE REMARK 999	UNP P60881
K	60	VAL	ILE	SEE REMARK 999	UNP P60881
K	65	ASN	ASP	SEE REMARK 999	UNP P60881
K	66	HIS	GLN	SEE REMARK 999	UNP P60881
K	69	GLN	LYS	SEE REMARK 999	UNP P60881
K	79	LYS	THR	SEE REMARK 999	UNP P60881

- Molecule 4 is a protein called PROTEIN (SNAP-25B).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	74	Total	C	N	O	S	11	0	0
			586	346	115	120	5			
4	H	72	Total	C	N	O	S	0	0	0
			578	342	113	118	5			
4	L	73	Total	C	N	O	S	7	0	0
			582	344	114	119	5			

- Molecule 5 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

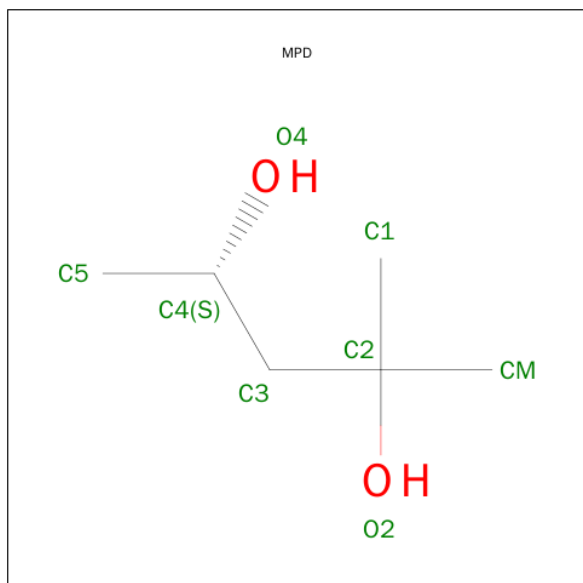
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	3	Total	Sr	0	0
			3	3		
5	J	1	Total	Sr	0	0
			1	1		
5	D	1	Total	Sr	0	0
			1	1		
5	K	1	Total	Sr	0	0
			1	1		
5	B	1	Total	Sr	0	0
			1	1		
5	C	2	Total	Sr	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Sr	0	0
			2	2		
5	F	2	Total	Sr	0	0
			2	2		

- Molecule 6 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:  $C_6H_{14}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	F	1	Total	C	O	0	0
			8	6	2		
6	A	1	Total	C	O	0	0
			8	6	2		
6	A	1	Total	C	O	0	0
			8	6	2		
6	K	1	Total	C	O	0	0
			8	6	2		
6	I	1	Total	C	O	0	0
			8	6	2		
6	K	1	Total	C	O	0	0
			8	6	2		
6	G	1	Total	C	O	0	0
			8	6	2		

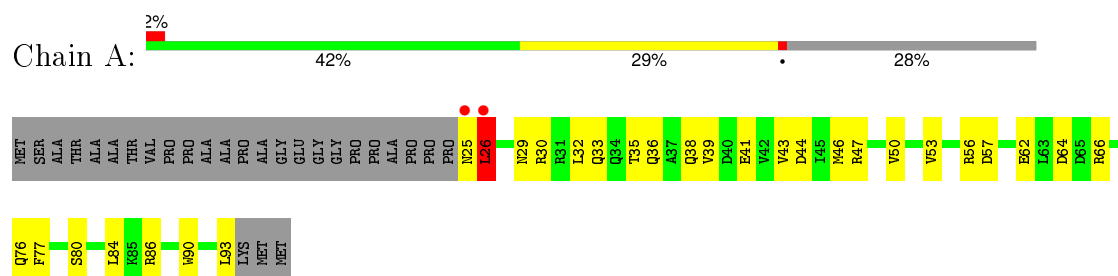
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	2	Total 2	O 2	0	0
7	B	2	Total 2	O 2	0	0
7	C	1	Total 1	O 1	0	0
7	D	1	Total 1	O 1	0	0
7	F	5	Total 5	O 5	0	0
7	G	1	Total 1	O 1	0	0
7	I	3	Total 3	O 3	0	0
7	J	3	Total 3	O 3	0	0
7	K	1	Total 1	O 1	0	0

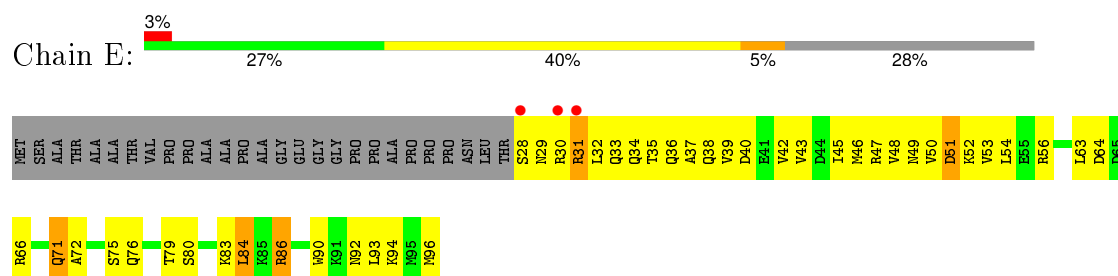
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

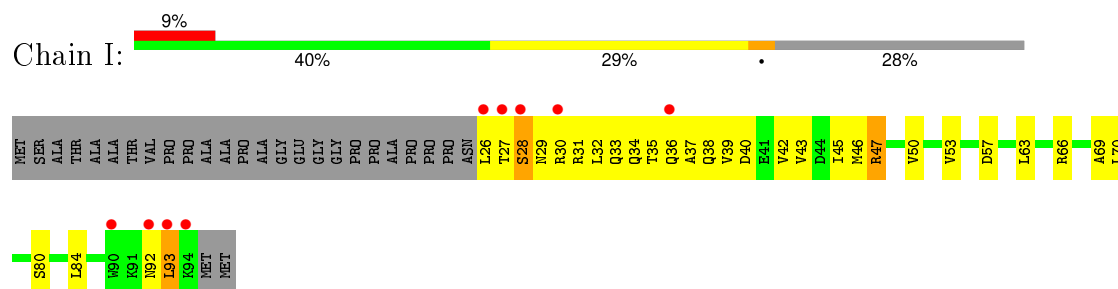
- Molecule 1: PROTEIN (SYNAPTOBREVIN 2)



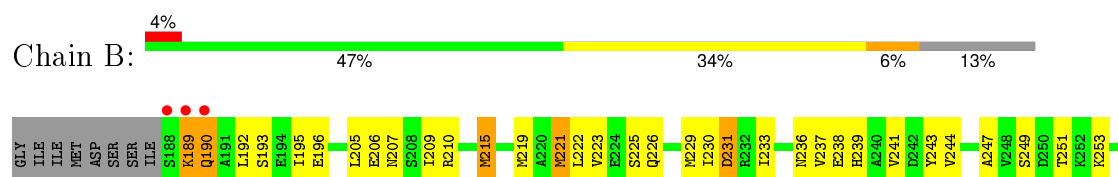
- Molecule 1: PROTEIN (SYNAPTOBREVIN 2)



- Molecule 1: PROTEIN (SYNAPTOBREVIN 2)



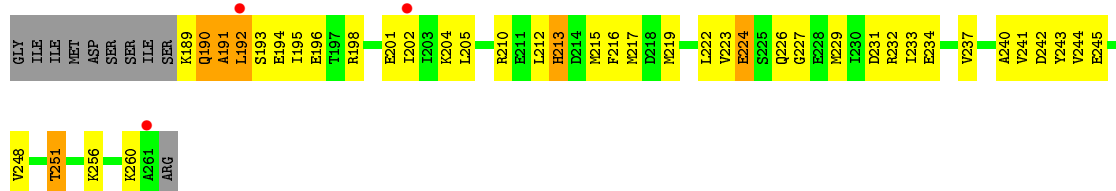
- Molecule 2: PROTEIN (SYNTAXIN 1A)



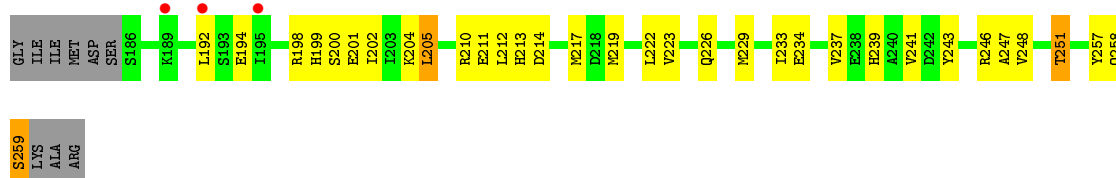




• Molecule 2: PROTEIN (SYNTAXIN 1A)



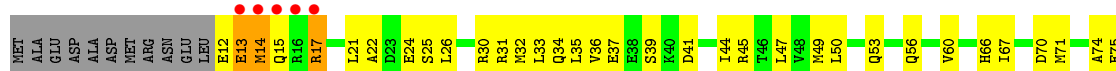
• Molecule 2: PROTEIN (SYNTAXIN 1A)



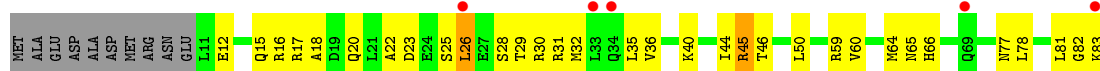
• Molecule 3: PROTEIN (SNAP-25B)



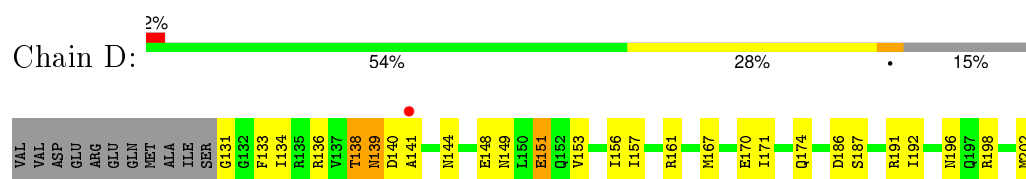
• Molecule 3: PROTEIN (SNAP-25B)



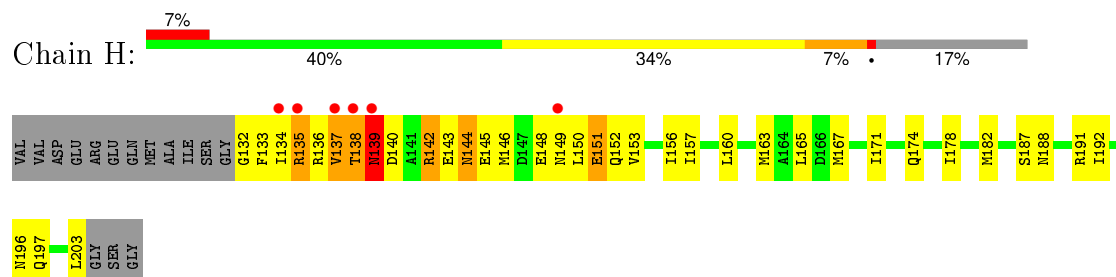
• Molecule 3: PROTEIN (SNAP-25B)



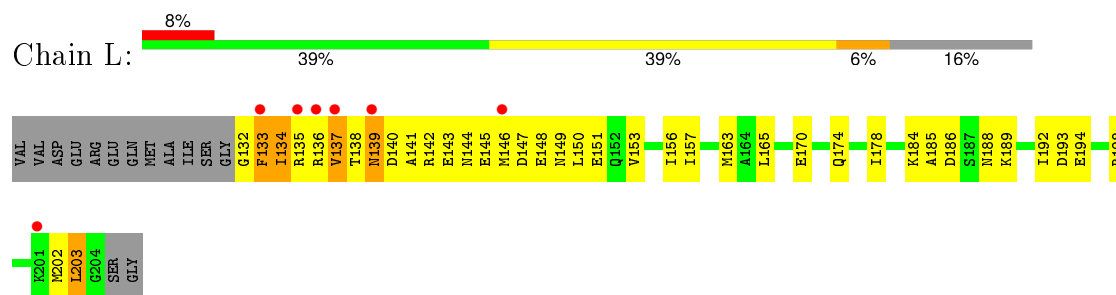
• Molecule 4: PROTEIN (SNAP-25B)



- Molecule 4: PROTEIN (SNAP-25B)



- Molecule 4: PROTEIN (SNAP-25B)



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.72Å 111.07Å 198.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 41.23 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-2.40) 98.9 (41.23-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.47 (at 2.39Å)	Xtriage
Refinement program	CNS 0.3	Depositor
R, $R_{free}$	0.265 , 0.303 0.271 , 0.308	Depositor DCC
$R_{free}$ test set	4177 reflections (9.80%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.3	Xtriage
Anisotropy	0.336	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 61.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.37$ , $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	1 of 82438 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	7105	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% of the height of the origin peak. No significant pseudotranslation is detected.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 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: SR, MPD

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	0.40	0/569	0.63	0/765
1	E	0.39	0/572	0.58	0/764
1	I	0.41	0/570	0.65	1/765 (0.1%)
2	B	0.43	0/592	0.67	0/792
2	F	0.43	0/600	0.62	0/802
2	J	0.42	0/606	0.60	0/811
3	C	0.36	0/625	0.59	0/828
3	G	0.40	0/581	0.68	0/770
3	K	0.41	0/589	0.62	0/781
4	D	0.46	1/587 (0.2%)	0.64	0/782
4	H	0.46	0/579	0.71	0/772
4	L	0.46	0/583	0.71	0/777
All	All	0.42	1/7053 (0.0%)	0.64	1/9409 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	131	GLY	N-CA	5.37	1.54	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	I	28	SER	N-CA-C	5.34	125.41	111.00

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	564	0	565	26	0
1	E	567	0	573	69	0
1	I	565	0	571	52	0
2	B	586	0	575	42	0
2	F	594	0	588	65	0
2	J	600	0	591	47	0
3	C	625	0	614	40	0
3	G	581	0	569	66	0
3	K	589	0	580	50	0
4	D	586	0	573	27	0
4	H	578	0	567	82	0
4	L	582	0	570	71	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
5	D	1	0	0	0	0
5	F	2	0	0	0	0
5	G	3	0	0	0	0
5	J	1	0	0	0	0
5	K	1	0	0	0	0
6	A	16	0	28	0	0
6	F	8	0	14	0	0
6	G	8	0	14	1	0
6	I	8	0	14	2	0
6	K	16	0	28	1	0
7	A	2	0	0	0	0
7	B	2	0	0	2	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	F	5	0	0	0	0
7	G	1	0	0	0	0
7	I	3	0	0	0	0
7	J	3	0	0	0	0
7	K	1	0	0	0	0
All	All	7105	0	7034	430	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 31.

All (430) 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:I:50:VAL:HA	2:J:219:MET:HE3	1.41	1.01
3:G:12:GLU:HG2	3:G:13:GLU:H	1.20	1.01
1:E:53:VAL:HG21	2:F:219:MET:SD	2.03	0.98
1:I:31:ARG:HG2	4:L:132:GLY:HA2	1.47	0.95
2:B:231:ASP:HB3	3:C:56:GLN:HE22	1.36	0.88
2:J:194:GLU:HG2	4:L:135:ARG:NH1	1.87	0.87
2:B:251:THR:HG22	3:C:77:ASN:HB3	1.56	0.85
3:G:12:GLU:C	3:G:14:MET:H	1.77	0.85
4:D:167:MET:O	4:D:171:ILE:HG12	1.77	0.85
1:E:66:ARG:NH1	4:H:182:MET:HB3	1.90	0.85
2:B:210:ARG:HE	3:C:35:LEU:HD21	1.41	0.84
3:G:26:LEU:HD12	4:H:142:ARG:HG3	1.59	0.83
1:E:92:ASN:HD21	2:F:260:LYS:HE3	1.44	0.83
1:E:49:ASN:O	1:E:53:VAL:HG23	1.80	0.82
1:E:29:ASN:H	4:H:135:ARG:HE	1.28	0.81
4:H:139:ASN:C	4:H:139:ASN:HD22	1.82	0.81
1:I:39:VAL:HG22	4:L:157:ILE:HD13	1.62	0.81
1:I:28:SER:O	1:I:29:ASN:HB2	1.81	0.81
3:G:12:GLU:HG2	3:G:13:GLU:N	1.95	0.80
1:E:28:SER:HA	4:H:135:ARG:HD3	1.62	0.80
2:B:189:LYS:HB2	3:C:14:MET:CE	2.11	0.80
4:D:153:VAL:O	4:D:157:ILE:HG12	1.83	0.79
1:E:28:SER:HA	4:H:135:ARG:HB3	1.66	0.78
3:K:40:LYS:HD2	4:L:156:ILE:HG23	1.63	0.78
1:I:39:VAL:CG2	4:L:157:ILE:HD13	2.14	0.77
2:B:207:ASN:O	2:B:210:ARG:HB2	1.84	0.77
4:H:139:ASN:C	4:H:139:ASN:ND2	2.38	0.77
2:F:202:ILE:HD11	4:H:134:ILE:CD1	2.16	0.76
4:L:136:ARG:NH2	4:L:144:ASN:HA	2.01	0.76
4:L:174:GLN:O	4:L:178:ILE:HG13	1.86	0.75
3:G:12:GLU:HA	3:G:15:GLN:HG3	1.68	0.75
3:G:17:ARG:HH11	3:G:17:ARG:HG3	1.51	0.75
1:E:36:GLN:HA	2:F:205:LEU:HD13	1.69	0.74
2:B:251:THR:HG22	3:C:77:ASN:CB	2.17	0.74
2:F:194:GLU:HB3	4:H:137:VAL:HG21	1.70	0.74
4:H:145:GLU:HG2	4:H:149:ASN:HD21	1.52	0.74
1:E:29:ASN:H	4:H:135:ARG:NE	1.86	0.73
3:C:11:LEU:O	3:C:15:GLN:HG2	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:45:ILE:HD13	4:L:165:LEU:HD21	1.69	0.72
1:I:31:ARG:CG	4:L:132:GLY:HA2	2.17	0.72
2:J:205:LEU:HD13	3:K:32:MET:SD	2.30	0.72
2:J:251:THR:HG23	3:K:77:ASN:CB	2.19	0.72
3:G:25:SER:HB3	4:H:146:MET:CE	2.20	0.72
2:F:205:LEU:HG	3:G:32:MET:HE3	1.71	0.71
3:K:65:ASN:HD21	4:L:184:LYS:NZ	1.88	0.71
2:J:258:GLN:O	2:J:258:GLN:HG2	1.90	0.71
1:A:25:ASN:O	1:A:26:LEU:HB2	1.88	0.71
4:H:140:ASP:OD1	4:H:142:ARG:HB3	1.91	0.70
2:J:251:THR:HG23	3:K:77:ASN:HB3	1.73	0.70
4:L:133:PHE:HB3	4:L:147:ASP:OD1	1.91	0.70
4:L:145:GLU:HG2	4:L:149:ASN:HD21	1.56	0.70
4:H:142:ARG:HH11	4:H:142:ARG:CB	2.05	0.70
2:J:247:ALA:O	2:J:251:THR:HB	1.90	0.70
1:E:90:TRP:NE1	1:E:94:LYS:HD2	2.07	0.70
4:H:139:ASN:HA	4:H:143:GLU:OE2	1.91	0.70
1:I:39:VAL:O	1:I:43:VAL:HG23	1.92	0.70
2:B:189:LYS:HB2	3:C:14:MET:HE2	1.73	0.70
4:L:145:GLU:HG2	4:L:149:ASN:ND2	2.07	0.69
3:G:32:MET:HE2	4:H:153:VAL:HG11	1.75	0.69
1:E:93:LEU:HD12	1:E:96:MET:HE3	1.74	0.69
1:E:76:GLN:HG3	4:H:196:ASN:OD1	1.92	0.69
1:A:56:ARG:NH2	3:C:53:GLN:OE1	2.26	0.69
1:I:46:MET:O	1:I:50:VAL:HG23	1.92	0.69
1:E:29:ASN:O	1:E:33:GLN:HG3	1.93	0.68
3:K:29:THR:HA	3:K:32:MET:HE2	1.76	0.68
4:H:136:ARG:HB3	4:H:143:GLU:OE2	1.93	0.68
3:K:26:LEU:HD11	3:K:30:ARG:CZ	2.24	0.68
2:J:194:GLU:HG2	4:L:135:ARG:CZ	2.24	0.67
3:K:44:ILE:N	4:L:163:MET:HE1	2.09	0.67
2:F:231:ASP:HB3	3:G:56:GLN:HE22	1.58	0.67
4:L:135:ARG:HH11	4:L:137:VAL:HG22	1.59	0.67
2:B:210:ARG:NE	3:C:35:LEU:HD21	2.08	0.67
2:F:237:VAL:HG21	3:G:60:VAL:HG13	1.75	0.67
2:B:222:LEU:O	2:B:226:GLN:HG3	1.94	0.67
3:G:71:MET:O	3:G:75:GLU:HG3	1.95	0.67
1:E:45:ILE:HD13	4:H:165:LEU:HD21	1.77	0.67
4:H:174:GLN:O	4:H:178:ILE:HG13	1.94	0.67
3:K:36:VAL:HG12	4:L:156:ILE:HG21	1.75	0.67
4:L:136:ARG:HH22	4:L:144:ASN:HD22	1.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:36:VAL:HG11	4:H:156:ILE:HB	1.77	0.66
1:I:92:ASN:O	1:I:93:LEU:HB2	1.95	0.66
3:G:26:LEU:HD21	4:H:145:GLU:OE1	1.95	0.66
4:L:148:GLU:O	4:L:151:GLU:HB2	1.96	0.65
2:B:221:MET:CE	1:I:93:LEU:HD21	2.27	0.65
3:K:32:MET:HE1	4:L:150:LEU:HD21	1.79	0.64
2:F:194:GLU:CB	4:H:137:VAL:HG21	2.27	0.64
4:H:137:VAL:O	4:H:138:THR:OG1	2.14	0.64
3:G:49:MET:O	3:G:53:GLN:HG3	1.97	0.64
1:A:43:VAL:O	1:A:47:ARG:HG3	1.97	0.64
1:I:36:GLN:NE2	2:J:205:LEU:HA	2.12	0.64
1:I:31:ARG:O	1:I:34:GLN:HG2	1.98	0.63
3:K:36:VAL:HG21	4:L:153:VAL:HG13	1.79	0.63
1:A:64:ASP:HA	2:B:233:ILE:HG12	1.79	0.63
2:J:213:HIS:O	2:J:217:MET:HG2	1.98	0.63
1:E:92:ASN:ND2	2:F:260:LYS:HE3	2.14	0.63
3:G:33:LEU:HD11	4:H:152:GLN:HG2	1.81	0.63
3:K:45:ARG:HH11	3:K:45:ARG:HG2	1.63	0.63
2:F:192:LEU:HG	2:F:196:GLU:CD	2.19	0.63
1:E:29:ASN:N	4:H:135:ARG:HG2	2.14	0.63
1:E:39:VAL:HG22	4:H:157:ILE:HD12	1.81	0.63
4:L:189:LYS:HE3	4:L:193:ASP:OD2	1.99	0.63
1:I:35:THR:O	1:I:39:VAL:HG23	1.98	0.62
1:E:42:VAL:HG12	2:F:212:LEU:HD11	1.81	0.62
1:A:62:GLU:O	1:A:66:ARG:HG3	1.98	0.62
3:G:26:LEU:CD1	4:H:142:ARG:HG3	2.27	0.62
1:A:35:THR:O	1:A:39:VAL:HG23	1.99	0.62
1:I:31:ARG:HH11	1:I:31:ARG:HG2	1.65	0.62
3:G:25:SER:CB	4:H:146:MET:CE	2.78	0.62
3:G:31:ARG:O	3:G:35:LEU:HB2	1.99	0.62
2:F:222:LEU:O	2:F:226:GLN:HG3	2.00	0.62
1:A:90:TRP:O	1:A:93:LEU:HD12	2.00	0.61
2:F:251:THR:CG2	3:G:77:ASN:HB2	2.31	0.61
1:I:57:ASP:HB2	2:J:226:GLN:NE2	2.16	0.61
3:C:70:ASP:OD1	1:E:86:ARG:NH2	2.33	0.61
1:I:31:ARG:HB3	4:L:133:PHE:H	1.64	0.61
3:K:26:LEU:HD11	3:K:30:ARG:NH2	2.15	0.61
3:C:56:GLN:HG2	3:C:59:ARG:HH21	1.65	0.61
3:K:36:VAL:HG12	4:L:156:ILE:CG2	2.31	0.61
2:J:248:VAL:O	2:J:251:THR:HG22	2.01	0.60
2:F:195:ILE:HD11	4:H:137:VAL:HB	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:22:ALA:HB3	4:H:142:ARG:NH2	2.16	0.60
4:D:136:ARG:NH2	4:D:144:ASN:HA	2.17	0.60
1:E:63:LEU:HD13	4:H:182:MET:HG2	1.84	0.60
2:B:189:LYS:HB2	3:C:14:MET:HE1	1.84	0.60
4:L:134:ILE:HG12	4:L:147:ASP:OD2	2.02	0.59
4:L:135:ARG:NH1	4:L:137:VAL:HG22	2.17	0.59
7:B:505:HOH:O	2:J:239:HIS:CD2	2.55	0.59
3:C:40:LYS:O	3:C:44:ILE:HG12	2.01	0.59
1:E:29:ASN:CG	4:H:135:ARG:HG2	2.23	0.59
2:F:198:ARG:HG3	4:H:134:ILE:HD11	1.85	0.59
4:H:140:ASP:OD1	4:H:142:ARG:CB	2.51	0.59
4:H:145:GLU:HG2	4:H:149:ASN:ND2	2.17	0.59
1:I:45:ILE:HD13	4:L:165:LEU:CD2	2.33	0.59
2:B:221:MET:HG3	2:B:222:LEU:N	2.17	0.58
3:C:10:GLU:HA	3:C:10:GLU:OE1	2.03	0.58
1:E:45:ILE:HD13	4:H:165:LEU:CD2	2.33	0.58
3:C:29:THR:HG22	3:C:32:MET:HE3	1.86	0.58
4:D:138:THR:O	4:D:138:THR:HG23	2.04	0.58
2:B:249:SER:O	2:B:253:LYS:HG3	2.04	0.58
3:G:12:GLU:C	3:G:14:MET:N	2.50	0.57
4:L:136:ARG:HH22	4:L:144:ASN:ND2	2.02	0.57
2:J:257:TYR:C	2:J:259:SER:H	2.07	0.57
1:I:92:ASN:HB2	2:J:257:TYR:O	2.04	0.57
1:E:36:GLN:HE22	2:F:205:LEU:HA	1.68	0.57
3:K:64:MET:HE1	4:L:185:ALA:HA	1.85	0.57
4:L:134:ILE:HD12	4:L:146:MET:HE3	1.84	0.57
2:B:253:LYS:HE3	2:F:260:LYS:HZ1	1.69	0.57
4:L:137:VAL:H	4:L:143:GLU:CD	2.07	0.57
4:H:142:ARG:HH11	4:H:142:ARG:HB3	1.69	0.57
1:E:36:GLN:HE22	2:F:205:LEU:CA	2.17	0.57
2:F:242:ASP:CG	2:J:246:ARG:HH21	2.08	0.57
2:F:251:THR:HG23	3:G:77:ASN:CB	2.34	0.57
2:B:231:ASP:HB3	3:C:56:GLN:NE2	2.14	0.57
1:I:32:LEU:HD12	1:I:32:LEU:O	2.04	0.57
2:J:199:HIS:ND1	3:K:25:SER:HB2	2.20	0.57
1:A:57:ASP:HB2	2:B:226:GLN:NE2	2.20	0.56
3:C:81:LEU:C	3:C:83:LYS:H	2.08	0.56
3:K:26:LEU:C	3:K:26:LEU:HD13	2.25	0.56
1:A:36:GLN:OE1	2:B:205:LEU:HA	2.05	0.56
3:K:15:GLN:HG2	6:K:931:MPD:O4	2.04	0.56
2:F:240:ALA:O	2:F:244:VAL:HG23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:143:GLU:HA	4:L:146:MET:HE2	1.88	0.56
4:L:145:GLU:CG	4:L:149:ASN:HD21	2.19	0.56
1:E:29:ASN:H	4:H:135:ARG:CD	2.17	0.56
3:G:25:SER:HB3	4:H:146:MET:HE1	1.86	0.56
1:E:47:ARG:HG3	2:F:215:MET:CE	2.36	0.55
4:L:140:ASP:OD2	4:L:142:ARG:HB2	2.06	0.55
4:L:135:ARG:HH11	4:L:137:VAL:CG2	2.19	0.55
2:B:206:GLU:O	2:B:210:ARG:HG2	2.06	0.55
2:F:210:ARG:HD3	3:G:35:LEU:HD21	1.88	0.55
2:B:190:GLN:O	2:B:193:SER:HB3	2.06	0.55
1:E:80:SER:OG	4:H:196:ASN:ND2	2.38	0.55
3:K:65:ASN:HD21	4:L:184:LYS:HZ2	1.54	0.54
4:D:138:THR:C	4:D:140:ASP:H	2.10	0.54
2:B:251:THR:CG2	3:C:77:ASN:HB2	2.37	0.54
4:L:188:ASN:O	4:L:192:ILE:HG13	2.08	0.54
2:J:237:VAL:HG21	3:K:60:VAL:HG13	1.90	0.54
3:G:26:LEU:HD23	3:G:26:LEU:C	2.28	0.54
1:E:32:LEU:C	1:E:32:LEU:HD23	2.27	0.54
3:G:44:ILE:N	4:H:163:MET:HE1	2.22	0.54
1:I:69:ALA:HA	6:I:930:MPD:HM2	1.90	0.53
2:F:251:THR:CG2	3:G:77:ASN:CB	2.87	0.53
2:B:251:THR:CG2	3:C:77:ASN:CB	2.85	0.53
2:J:210:ARG:CG	3:K:35:LEU:HD21	2.39	0.53
1:I:31:ARG:NH1	1:I:31:ARG:HG2	2.23	0.53
1:E:28:SER:HA	4:H:135:ARG:CB	2.37	0.53
1:E:46:MET:O	1:E:50:VAL:HG23	2.09	0.53
3:K:29:THR:HA	3:K:32:MET:CE	2.38	0.53
3:G:25:SER:CB	4:H:146:MET:HE1	2.39	0.53
1:E:71:GLN:HE21	1:E:72:ALA:N	2.07	0.53
2:J:201:GLU:O	2:J:204:LYS:HB3	2.09	0.52
3:C:72:LYS:HG2	4:D:191:ARG:HH22	1.74	0.52
1:I:30:ARG:O	1:I:33:GLN:HB2	2.08	0.52
3:C:71:MET:CE	4:D:192:ILE:HG12	2.39	0.52
4:L:142:ARG:O	4:L:146:MET:HG3	2.09	0.52
4:D:138:THR:O	4:D:140:ASP:N	2.41	0.52
2:B:221:MET:HE1	1:I:93:LEU:HD21	1.91	0.52
4:H:187:SER:O	4:H:191:ARG:HG3	2.10	0.52
1:I:84:LEU:CD1	4:L:203:LEU:HD22	2.40	0.52
1:A:25:ASN:O	1:A:26:LEU:CB	2.57	0.52
3:G:24:GLU:OE1	3:G:24:GLU:HA	2.10	0.52
3:C:50:LEU:HD21	4:D:171:ILE:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:38:GLN:O	1:I:42:VAL:HG23	2.10	0.51
3:C:29:THR:HA	3:C:32:MET:HE3	1.92	0.51
2:F:224:GLU:HB2	3:G:49:MET:SD	2.50	0.51
2:J:229:MET:O	2:J:233:ILE:HG13	2.10	0.51
3:G:36:VAL:HG12	4:H:156:ILE:HG21	1.92	0.51
1:E:50:VAL:O	1:E:54:LEU:HG	2.11	0.51
1:E:79:THR:O	1:E:83:LYS:HG2	2.11	0.51
3:G:26:LEU:HD23	3:G:26:LEU:O	2.11	0.51
2:B:253:LYS:HE3	2:F:260:LYS:NZ	2.25	0.51
4:D:149:ASN:O	4:D:153:VAL:HG23	2.11	0.51
2:J:233:ILE:O	2:J:237:VAL:HG23	2.11	0.51
1:E:48:VAL:O	1:E:51:ASP:HB2	2.11	0.51
3:G:17:ARG:NH1	3:G:17:ARG:HG3	2.19	0.51
1:E:39:VAL:O	1:E:43:VAL:HG23	2.11	0.51
2:B:192:LEU:O	2:B:192:LEU:HG	2.11	0.51
1:A:32:LEU:HD22	4:D:134:ILE:HG22	1.92	0.51
2:B:229:MET:O	2:B:233:ILE:HG13	2.11	0.51
1:I:36:GLN:NE2	2:J:204:LYS:HZ3	2.08	0.50
1:E:28:SER:CA	4:H:135:ARG:HD3	2.38	0.50
4:L:170:GLU:O	4:L:174:GLN:HG3	2.11	0.50
3:K:31:ARG:O	3:K:35:LEU:HB2	2.11	0.50
2:F:190:GLN:NE2	2:F:191:ALA:N	2.58	0.50
1:E:31:ARG:HA	1:E:34:GLN:HG2	1.93	0.50
1:A:38:GLN:O	1:A:41:GLU:HB3	2.11	0.50
2:F:256:LYS:O	2:F:260:LYS:HG3	2.12	0.50
2:F:229:MET:O	2:F:233:ILE:HG13	2.11	0.50
4:L:194:GLU:O	4:L:198:ARG:HG2	2.11	0.50
1:E:52:LYS:HB3	4:H:171:ILE:HG21	1.94	0.50
1:E:66:ARG:HH11	4:H:182:MET:HB3	1.71	0.50
3:G:36:VAL:CG1	4:H:156:ILE:HB	2.41	0.50
3:K:26:LEU:HD21	4:L:145:GLU:OE1	2.11	0.50
7:B:505:HOH:O	2:J:239:HIS:HD2	1.93	0.49
3:K:64:MET:HE3	3:K:64:MET:HA	1.94	0.49
1:A:56:ARG:NH1	4:D:174:GLN:OE1	2.46	0.49
2:F:192:LEU:O	2:F:196:GLU:HG3	2.12	0.49
4:L:140:ASP:O	4:L:142:ARG:N	2.45	0.49
2:F:198:ARG:CG	4:H:134:ILE:HD11	2.41	0.49
3:C:78:LEU:O	3:C:81:LEU:HB2	2.12	0.49
1:E:47:ARG:HG3	2:F:215:MET:HE1	1.94	0.49
1:I:36:GLN:OE1	2:J:204:LYS:HG3	2.13	0.49
1:A:66:ARG:NH1	4:D:186:ASP:OD1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:192:LEU:HG	2:F:196:GLU:OE1	2.12	0.49
2:J:198:ARG:O	2:J:202:ILE:HG12	2.12	0.49
2:F:251:THR:HG23	3:G:77:ASN:HB3	1.94	0.49
3:C:50:LEU:HD21	4:D:171:ILE:CD1	2.43	0.48
3:K:44:ILE:HG13	4:L:163:MET:CE	2.43	0.48
1:I:27:THR:HB	4:L:135:ARG:HA	1.93	0.48
2:F:216:PHE:CZ	4:H:160:LEU:HG	2.48	0.48
2:J:222:LEU:O	2:J:226:GLN:HG3	2.13	0.48
1:I:29:ASN:ND2	4:L:135:ARG:N	2.61	0.48
4:L:139:ASN:O	4:L:140:ASP:C	2.52	0.48
3:G:45:ARG:HG2	3:G:45:ARG:HH11	1.79	0.48
1:E:28:SER:HA	4:H:135:ARG:CD	2.38	0.48
4:D:186:ASP:O	4:D:187:SER:C	2.51	0.48
1:E:92:ASN:ND2	2:F:260:LYS:HB2	2.28	0.48
3:K:44:ILE:N	4:L:163:MET:CE	2.74	0.48
3:G:44:ILE:HG22	4:H:163:MET:CE	2.43	0.48
1:A:76:GLN:HA	6:I:930:MPD:H51	1.95	0.48
2:F:195:ILE:HD12	2:F:195:ILE:N	2.29	0.48
4:D:170:GLU:OE1	4:D:174:GLN:NE2	2.47	0.48
1:I:39:VAL:O	1:I:39:VAL:HG12	2.14	0.47
3:G:44:ILE:HG13	3:G:45:ARG:N	2.28	0.47
3:K:26:LEU:HD22	3:K:26:LEU:O	2.13	0.47
1:I:66:ARG:NH1	4:L:186:ASP:OD1	2.47	0.47
1:E:53:VAL:CG2	2:F:219:MET:SD	2.91	0.47
1:I:29:ASN:HA	4:L:134:ILE:HA	1.97	0.47
3:C:31:ARG:O	3:C:35:LEU:HB2	2.15	0.47
3:G:25:SER:HB3	4:H:146:MET:HE2	1.92	0.47
2:F:251:THR:HG23	3:G:77:ASN:HB2	1.96	0.47
2:F:251:THR:HG22	3:G:77:ASN:HD22	1.79	0.47
1:I:84:LEU:HD11	4:L:203:LEU:HD22	1.97	0.47
4:L:145:GLU:O	4:L:146:MET:C	2.54	0.47
3:G:36:VAL:HG12	4:H:156:ILE:CG2	2.45	0.47
1:I:42:VAL:HG12	2:J:212:LEU:HD11	1.96	0.46
4:H:142:ARG:C	4:H:144:ASN:H	2.17	0.46
2:F:213:HIS:O	2:F:217:MET:HG2	2.14	0.46
3:K:17:ARG:HH12	3:K:20:GLN:HE22	1.62	0.46
2:F:213:HIS:HA	3:G:39:SER:OG	2.14	0.46
2:F:234:GLU:OE1	3:G:56:GLN:HG2	2.14	0.46
2:F:223:VAL:CG2	3:G:49:MET:HE3	2.44	0.46
2:J:246:ARG:HG3	2:J:246:ARG:HH11	1.80	0.46
3:C:27:GLU:O	3:C:31:ARG:HG3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:198:ARG:HG3	4:H:134:ILE:CD1	2.46	0.46
1:E:30:ARG:C	1:E:32:LEU:H	2.19	0.46
1:A:41:GLU:CD	4:D:161:ARG:HE	2.19	0.46
1:I:28:SER:O	1:I:29:ASN:CB	2.55	0.46
1:I:28:SER:C	1:I:30:ARG:H	2.19	0.46
1:E:35:THR:O	1:E:38:GLN:HG2	2.14	0.46
3:G:56:GLN:O	3:G:60:VAL:HG23	2.15	0.46
1:I:57:ASP:CB	2:J:226:GLN:NE2	2.79	0.46
3:K:64:MET:CE	4:L:185:ALA:HA	2.44	0.46
3:C:81:LEU:HB3	4:D:202:MET:CE	2.46	0.46
1:A:46:MET:O	1:A:50:VAL:HG23	2.15	0.46
1:E:63:LEU:HD22	4:H:178:ILE:HG23	1.97	0.46
1:E:64:ASP:OD2	2:F:232:ARG:NH1	2.46	0.46
1:E:84:LEU:HD13	4:H:203:LEU:HG	1.97	0.46
4:L:132:GLY:O	4:L:150:LEU:HB2	2.15	0.46
3:G:44:ILE:HG22	4:H:163:MET:HE3	1.97	0.46
1:I:39:VAL:HG22	4:L:157:ILE:CD1	2.41	0.46
1:I:33:GLN:O	1:I:36:GLN:HB3	2.15	0.46
4:H:139:ASN:O	4:H:139:ASN:ND2	2.49	0.46
1:A:46:MET:HB3	2:B:215:MET:HG2	1.98	0.46
4:H:163:MET:O	4:H:167:MET:HB2	2.16	0.46
1:E:37:ALA:O	1:E:40:ASP:HB2	2.16	0.46
2:B:243:TYR:OH	2:J:239:HIS:CD2	2.69	0.45
2:J:241:VAL:CG1	3:K:66:HIS:HD2	2.29	0.45
2:F:190:GLN:O	2:F:191:ALA:C	2.54	0.45
2:J:192:LEU:HD13	3:K:18:ALA:HB2	1.98	0.45
3:K:25:SER:O	3:K:28:SER:HB3	2.15	0.45
2:B:237:VAL:O	2:B:241:VAL:HG23	2.15	0.45
3:K:32:MET:HE1	4:L:150:LEU:CD2	2.45	0.45
3:C:81:LEU:HB3	4:D:202:MET:HE2	1.98	0.45
3:G:66:HIS:HE1	6:G:932:MPD:O2	2.00	0.45
2:F:201:GLU:O	2:F:204:LYS:HB3	2.16	0.45
4:H:152:GLN:O	4:H:156:ILE:HG13	2.17	0.45
1:E:30:ARG:O	1:E:32:LEU:N	2.50	0.45
1:E:39:VAL:HG21	2:F:205:LEU:HD11	1.97	0.45
3:K:12:GLU:HA	3:K:15:GLN:NE2	2.31	0.45
4:H:157:ILE:O	4:H:160:LEU:N	2.50	0.45
1:A:41:GLU:O	1:A:44:ASP:N	2.49	0.45
1:E:36:GLN:NE2	2:F:205:LEU:HA	2.31	0.44
2:F:191:ALA:O	2:F:193:SER:N	2.49	0.44
1:I:80:SER:O	1:I:84:LEU:HD13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:52:LYS:CB	4:H:171:ILE:HG21	2.47	0.44
2:J:234:GLU:OE2	3:K:59:ARG:NE	2.45	0.44
1:A:36:GLN:HA	2:B:205:LEU:HD13	1.98	0.44
1:E:71:GLN:NE2	1:E:72:ALA:N	2.65	0.44
3:C:71:MET:HE2	4:D:192:ILE:HG12	1.99	0.44
4:H:188:ASN:O	4:H:192:ILE:HG13	2.16	0.44
1:E:29:ASN:CG	4:H:135:ARG:CG	2.86	0.44
2:J:251:THR:CG2	3:K:77:ASN:HD22	2.31	0.44
3:K:78:LEU:O	3:K:81:LEU:HB2	2.18	0.44
3:C:36:VAL:HG13	4:D:156:ILE:HG21	1.99	0.44
4:L:145:GLU:CG	4:L:149:ASN:ND2	2.79	0.44
1:E:75:SER:HB2	2:F:243:TYR:CE2	2.52	0.44
1:I:29:ASN:HD22	4:L:134:ILE:HA	1.82	0.44
2:B:253:LYS:CE	2:F:260:LYS:NZ	2.81	0.44
1:E:33:GLN:O	1:E:36:GLN:HB3	2.16	0.44
3:C:11:LEU:HD12	3:C:11:LEU:O	2.17	0.44
1:E:93:LEU:HA	1:E:96:MET:HE2	1.99	0.44
2:F:191:ALA:HB1	4:H:137:VAL:HG11	2.00	0.44
3:G:41:ASP:O	3:G:44:ILE:HG12	2.18	0.44
4:L:134:ILE:HD12	4:L:146:MET:CE	2.48	0.44
3:G:30:ARG:NH1	4:H:145:GLU:OE1	2.51	0.44
4:H:156:ILE:HG22	4:H:156:ILE:O	2.18	0.43
1:A:80:SER:O	1:A:84:LEU:HB2	2.18	0.43
1:I:29:ASN:HD21	2:J:198:ARG:HG3	1.83	0.43
2:F:227:GLY:CA	3:G:53:GLN:NE2	2.81	0.43
2:F:195:ILE:HD11	4:H:137:VAL:CB	2.46	0.43
1:E:35:THR:HA	1:E:38:GLN:HG2	2.00	0.43
2:J:257:TYR:CD1	2:J:257:TYR:N	2.86	0.43
3:C:29:THR:HA	3:C:32:MET:CE	2.48	0.43
2:J:210:ARG:HG3	3:K:35:LEU:HD21	1.99	0.43
1:I:63:LEU:HD22	4:L:178:ILE:HG23	1.99	0.43
2:B:230:ILE:HD12	3:C:53:GLN:OE1	2.19	0.43
1:E:47:ARG:HG3	2:F:215:MET:HE2	1.99	0.43
2:J:211:GLU:O	2:J:214:ASP:HB2	2.18	0.43
1:E:35:THR:O	1:E:39:VAL:HG23	2.19	0.43
1:I:50:VAL:HG22	2:J:219:MET:HE2	1.99	0.43
1:A:56:ARG:NE	2:B:226:GLN:OE1	2.51	0.43
2:J:200:SER:O	2:J:204:LYS:N	2.47	0.43
3:K:45:ARG:NH1	3:K:45:ARG:HG2	2.33	0.43
3:G:15:GLN:C	3:G:17:ARG:H	2.21	0.42
2:F:192:LEU:HD22	3:G:14:MET:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:36:GLN:HE22	2:F:205:LEU:N	2.17	0.42
1:A:32:LEU:HB2	4:D:133:PHE:O	2.19	0.42
3:K:36:VAL:HG11	4:L:156:ILE:HB	2.01	0.42
3:G:17:ARG:HH12	3:G:21:LEU:HD21	1.84	0.42
2:F:248:VAL:HG22	3:G:74:ALA:HB2	2.01	0.42
4:D:141:ALA:HA	4:D:144:ASN:HB2	2.00	0.42
2:F:251:THR:HG21	3:G:74:ALA:HA	2.02	0.42
1:A:29:ASN:O	1:A:33:GLN:HG3	2.19	0.42
4:H:156:ILE:O	4:H:160:LEU:HB2	2.19	0.42
2:F:244:VAL:HG21	3:G:67:ILE:HG23	2.02	0.42
3:G:33:LEU:HD13	4:H:153:VAL:HG23	2.01	0.42
4:L:136:ARG:HH22	4:L:144:ASN:HA	1.79	0.42
3:G:25:SER:HB2	4:H:146:MET:CE	2.49	0.42
1:E:31:ARG:HB3	4:H:132:GLY:HA2	2.02	0.42
1:A:86:ARG:HH11	1:A:86:ARG:HG3	1.84	0.42
1:I:31:ARG:CB	4:L:133:PHE:H	2.32	0.42
1:E:38:GLN:HG3	4:H:157:ILE:HG21	2.01	0.42
3:C:71:MET:HE3	4:D:192:ILE:HG12	2.01	0.42
2:B:244:VAL:HG21	3:C:67:ILE:HG23	2.02	0.42
4:H:136:ARG:HH22	4:H:144:ASN:ND2	2.17	0.41
3:K:44:ILE:HG13	4:L:163:MET:HE1	2.02	0.41
3:K:17:ARG:NH1	3:K:20:GLN:NE2	2.67	0.41
3:K:17:ARG:HH12	3:K:20:GLN:NE2	2.18	0.41
3:G:17:ARG:NH1	3:G:17:ARG:CG	2.83	0.41
3:K:64:MET:HA	3:K:64:MET:CE	2.50	0.41
2:B:195:ILE:HD12	3:C:18:ALA:HB1	2.02	0.41
3:G:15:GLN:C	3:G:17:ARG:N	2.71	0.41
3:G:36:VAL:O	3:G:39:SER:HB2	2.20	0.41
1:E:84:LEU:HA	1:E:84:LEU:HD12	1.90	0.41
4:L:198:ARG:O	4:L:202:MET:HG2	2.21	0.41
2:F:241:VAL:O	2:F:245:GLU:HG3	2.20	0.41
2:J:198:ARG:NH1	4:L:143:GLU:OE2	2.53	0.41
2:J:257:TYR:C	2:J:259:SER:N	2.72	0.41
2:B:209:ILE:HD11	4:D:153:VAL:HG11	2.03	0.41
2:F:189:LYS:HB2	2:F:190:GLN:H	1.15	0.41
2:B:219:MET:HE2	4:D:167:MET:SD	2.61	0.41
1:E:29:ASN:N	4:H:135:ARG:CG	2.83	0.41
1:I:57:ASP:HB2	2:J:226:GLN:HE22	1.85	0.41
3:G:17:ARG:HA	3:G:17:ARG:HD2	1.76	0.41
3:G:44:ILE:CG1	3:G:45:ARG:N	2.83	0.41
3:K:78:LEU:HD13	4:L:198:ARG:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:PHE:CE2	2:B:247:ALA:HB1	2.56	0.41
4:D:148:GLU:O	4:D:151:GLU:HB2	2.21	0.41
3:G:12:GLU:O	3:G:14:MET:N	2.54	0.41
2:B:239:HIS:HD2	2:J:243:TYR:OH	2.04	0.41
4:H:148:GLU:O	4:H:151:GLU:HB2	2.19	0.41
3:C:70:ASP:CG	1:E:86:ARG:NH2	2.75	0.40
1:I:84:LEU:HD12	4:L:203:LEU:HD13	2.02	0.40
3:K:20:GLN:C	3:K:22:ALA:H	2.24	0.40
1:I:36:GLN:NE2	2:J:204:LYS:NZ	2.69	0.40
2:B:251:THR:HG21	3:C:77:ASN:HB2	2.03	0.40
2:B:190:GLN:O	2:B:193:SER:N	2.53	0.40
1:I:37:ALA:O	1:I:40:ASP:HB2	2.22	0.40
4:L:140:ASP:O	4:L:143:GLU:N	2.55	0.40
2:B:192:LEU:HD12	3:C:18:ALA:HB2	2.03	0.40
1:E:31:ARG:HD3	4:H:133:PHE:CD2	2.57	0.40
1:I:42:VAL:O	1:I:46:MET:HG2	2.21	0.40
4:L:134:ILE:HG23	4:L:150:LEU:HD12	2.04	0.40
4:L:143:GLU:HA	4:L:146:MET:CE	2.51	0.40
1:I:47:ARG:HG2	1:I:47:ARG:HH11	1.86	0.40
1:E:56:ARG:NH1	4:H:174:GLN:OE1	2.55	0.40
3:K:45:ARG:HH11	3:K:45:ARG:CG	2.33	0.40
2:J:223:VAL:HG21	3:K:46:THR:HG23	2.03	0.40
3:K:82:GLY:O	3:K:83:LYS:OXT	2.40	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	67/96 (70%)	64 (96%)	2 (3%)	1 (2%)	13	17
1	E	67/96 (70%)	63 (94%)	3 (4%)	1 (2%)	13	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	67/96 (70%)	63 (94%)	3 (4%)	1 (2%)	13	17
2	B	70/83 (84%)	68 (97%)	2 (3%)	0	100	100
2	F	71/83 (86%)	67 (94%)	2 (3%)	2 (3%)	6	5
2	J	72/83 (87%)	68 (94%)	4 (6%)	0	100	100
3	C	75/83 (90%)	73 (97%)	2 (3%)	0	100	100
3	G	70/83 (84%)	67 (96%)	3 (4%)	0	100	100
3	K	71/83 (86%)	68 (96%)	3 (4%)	0	100	100
4	D	72/87 (83%)	63 (88%)	7 (10%)	2 (3%)	6	5
4	H	70/87 (80%)	61 (87%)	6 (9%)	3 (4%)	3	2
4	L	71/87 (82%)	62 (87%)	4 (6%)	5 (7%)	1	0
All	All	843/1047 (80%)	787 (93%)	41 (5%)	15 (2%)	11	13

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
4	H	139	ASN
1	I	93	LEU
4	L	138	THR
4	D	139	ASN
1	E	31	ARG
2	F	192	LEU
4	H	138	THR
4	L	141	ALA
2	F	191	ALA
4	L	134	ILE
4	L	137	VAL
4	D	198	ARG
4	L	139	ASN
4	H	137	VAL

### 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	61/78 (78%)	58 (95%)	3 (5%)	31	48
1	E	61/78 (78%)	57 (93%)	4 (7%)	21	32
1	I	61/78 (78%)	57 (93%)	4 (7%)	21	32
2	B	66/75 (88%)	56 (85%)	10 (15%)	3	4
2	F	66/75 (88%)	62 (94%)	4 (6%)	23	36
2	J	68/75 (91%)	65 (96%)	3 (4%)	35	53
3	C	69/73 (94%)	62 (90%)	7 (10%)	9	13
3	G	64/73 (88%)	56 (88%)	8 (12%)	6	7
3	K	65/73 (89%)	60 (92%)	5 (8%)	16	24
4	D	63/74 (85%)	59 (94%)	4 (6%)	22	35
4	H	63/74 (85%)	56 (89%)	7 (11%)	8	10
4	L	63/74 (85%)	61 (97%)	2 (3%)	46	68
All	All	770/900 (86%)	709 (92%)	61 (8%)	15	23

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	30	ARG
1	A	53	VAL
2	B	189	LYS
2	B	190	GLN
2	B	196	GLU
2	B	215	MET
2	B	221	MET
2	B	223	VAL
2	B	225	SER
2	B	231	ASP
2	B	236	ASN
2	B	238	GLU
3	C	8	ARG
3	C	10	GLU
3	C	19	ASP
3	C	26	LEU
3	C	36	VAL
3	C	52	GLU
3	C	68	ASN
4	D	138	THR
4	D	139	ASN

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Mol	Chain	Res	Type
4	D	151	GLU
4	D	196	ASN
1	E	51	ASP
1	E	71	GLN
1	E	84	LEU
1	E	86	ARG
2	F	190	GLN
2	F	213	HIS
2	F	224	GLU
2	F	251	THR
3	G	13	GLU
3	G	14	MET
3	G	17	ARG
3	G	34	GLN
3	G	37	GLU
3	G	47	LEU
3	G	50	LEU
3	G	70	ASP
4	H	135	ARG
4	H	139	ASN
4	H	142	ARG
4	H	144	ASN
4	H	150	LEU
4	H	151	GLU
4	H	197	GLN
1	I	26	LEU
1	I	47	ARG
1	I	53	VAL
1	I	70	LEU
2	J	205	LEU
2	J	251	THR
2	J	259	SER
3	K	16	ARG
3	K	23	ASP
3	K	26	LEU
3	K	45	ARG
3	K	50	LEU
4	L	133	PHE
4	L	203	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	76	GLN
2	B	236	ASN
2	B	239	HIS
2	B	258	GLN
3	C	34	GLN
3	C	56	GLN
4	D	159	ASN
4	D	169	ASN
4	D	196	ASN
1	E	36	GLN
1	E	49	ASN
1	E	71	GLN
1	E	92	ASN
2	F	190	GLN
2	F	236	ASN
3	G	66	HIS
3	G	69	GLN
3	G	77	ASN
4	H	139	ASN
4	H	144	ASN
4	H	149	ASN
4	H	196	ASN
1	I	29	ASN
1	I	33	GLN
1	I	36	GLN
1	I	49	ASN
1	I	76	GLN
1	I	92	ASN
2	J	239	HIS
3	K	15	GLN
3	K	20	GLN
3	K	65	ASN
3	K	66	HIS
3	K	68	ASN
3	K	77	ASN
4	L	144	ASN
4	L	149	ASN
4	L	196	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 13 are monoatomic - leaving 7 for Mogul analysis.

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	MPD	A	927	-	6,7,7	1.05	1 (16%)	7,10,10	2.90	2 (28%)
6	MPD	A	928	-	6,7,7	1.02	1 (16%)	7,10,10	3.02	2 (28%)
6	MPD	F	926	-	6,7,7	1.08	1 (16%)	7,10,10	3.12	2 (28%)
6	MPD	G	932	-	6,7,7	0.97	1 (16%)	7,10,10	3.01	2 (28%)
6	MPD	I	930	-	6,7,7	1.02	1 (16%)	7,10,10	3.13	2 (28%)
6	MPD	K	929	-	6,7,7	1.07	1 (16%)	7,10,10	3.17	2 (28%)
6	MPD	K	931	-	6,7,7	1.04	1 (16%)	7,10,10	3.00	2 (28%)

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
6	MPD	A	927	-	-	0/5/5/5	0/0/0/0
6	MPD	A	928	-	-	0/5/5/5	0/0/0/0
6	MPD	F	926	-	-	0/5/5/5	0/0/0/0
6	MPD	G	932	-	-	0/5/5/5	0/0/0/0
6	MPD	I	930	-	-	0/5/5/5	0/0/0/0
6	MPD	K	929	-	-	0/5/5/5	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MPD	K	931	-	-	0/5/5/5	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	G	932	MPD	O2-C2	2.14	1.50	1.44
6	F	926	MPD	O2-C2	2.20	1.50	1.44
6	I	930	MPD	O2-C2	2.25	1.50	1.44
6	A	928	MPD	O2-C2	2.25	1.50	1.44
6	A	927	MPD	O2-C2	2.33	1.51	1.44
6	K	931	MPD	O2-C2	2.34	1.51	1.44
6	K	929	MPD	O2-C2	2.37	1.51	1.44

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	K	929	MPD	O2-C2-CM	-3.35	95.80	108.09
6	I	930	MPD	O2-C2-CM	-3.32	95.91	108.09
6	K	931	MPD	O2-C2-CM	-3.15	96.56	108.09
6	G	932	MPD	O2-C2-CM	-3.14	96.59	108.09
6	F	926	MPD	O2-C2-CM	-3.09	96.77	108.09
6	A	928	MPD	O2-C2-CM	-3.07	96.83	108.09
6	A	927	MPD	O2-C2-CM	-3.01	97.08	108.09
6	A	927	MPD	CM-C2-C1	6.85	125.16	110.24
6	G	932	MPD	CM-C2-C1	7.08	125.66	110.24
6	K	931	MPD	CM-C2-C1	7.08	125.67	110.24
6	A	928	MPD	CM-C2-C1	7.10	125.71	110.24
6	I	930	MPD	CM-C2-C1	7.30	126.16	110.24
6	K	929	MPD	CM-C2-C1	7.39	126.35	110.24
6	F	926	MPD	CM-C2-C1	7.43	126.43	110.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	G	932	MPD	1	0
6	I	930	MPD	2	0
6	K	931	MPD	1	0

## 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 ⓘ

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	69/96 (71%)	0.33	2 (2%) 55 54	28, 39, 57, 64	0
1	E	69/96 (71%)	0.27	3 (4%) 39 40	23, 41, 73, 84	0
1	I	69/96 (71%)	0.51	9 (13%) 5 4	19, 39, 76, 80	0
2	B	72/83 (86%)	0.23	3 (4%) 40 41	20, 36, 60, 74	0
2	F	73/83 (87%)	0.35	3 (4%) 41 42	22, 41, 82, 89	0
2	J	71/83 (85%)	0.46	3 (4%) 40 41	20, 38, 76, 82	0
3	C	77/83 (92%)	0.31	6 (7%) 16 15	22, 39, 73, 79	0
3	G	72/83 (86%)	0.54	5 (6%) 20 19	0, 42, 91, 94	1 (1%)
3	K	72/83 (86%)	0.53	5 (6%) 20 19	20, 42, 70, 74	0
4	D	73/87 (83%)	0.26	2 (2%) 58 57	24, 40, 63, 70	0
4	H	72/87 (82%)	0.56	6 (8%) 14 14	26, 45, 83, 86	0
4	L	72/87 (82%)	0.61	7 (9%) 10 9	22, 44, 70, 72	0
All	All	861/1047 (82%)	0.41	54 (6%) 23 24	0, 41, 76, 94	1 (0%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	H	137	VAL	7.8
4	L	137	VAL	4.9
2	J	189	LYS	4.4
3	G	15	GLN	4.3
1	I	93	LEU	4.1
4	H	134	ILE	4.0
2	B	189	LYS	3.9
4	L	136	ARG	3.9
1	I	26	LEU	3.8
4	H	138	THR	3.6
4	L	133	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
3	C	18	ALA	3.5
3	G	16	ARG	3.5
1	E	30	ARG	3.4
1	I	27	THR	3.3
3	C	83	LYS	3.2
1	I	94	LYS	3.1
2	B	188	SER	3.1
4	H	135	ARG	3.1
1	A	25	ASN	3.0
4	D	204	GLY	3.0
1	I	28	SER	3.0
3	K	34	GLN	2.9
3	G	13	GLU	2.8
2	B	190	GLN	2.8
3	G	17	ARG	2.8
3	G	14	MET	2.7
3	C	10	GLU	2.7
1	A	26	LEU	2.7
1	E	28	SER	2.7
4	H	149	ASN	2.5
2	J	195	ILE	2.4
3	C	7	MET	2.4
4	L	146	MET	2.4
1	E	31	ARG	2.3
3	K	26	LEU	2.3
3	K	33	LEU	2.3
2	F	202	ILE	2.3
3	C	45	ARG	2.3
4	D	141	ALA	2.2
1	I	30	ARG	2.2
4	H	139	ASN	2.2
3	K	83	LYS	2.2
4	L	139	ASN	2.2
2	F	192	LEU	2.1
2	J	192	LEU	2.1
3	K	69	GLN	2.1
3	C	16	ARG	2.1
1	I	92	ASN	2.1
2	F	261	ALA	2.1
4	L	135	ARG	2.1
1	I	90	TRP	2.0
1	I	36	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
4	L	201	LYS	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
6	MPD	K	929	8/8	-0.00	0.68	15.88	79,80,80,81	0
6	MPD	I	930	8/8	0.75	0.40	6.59	65,69,70,72	0
6	MPD	A	927	8/8	0.89	0.31	4.38	74,75,75,75	0
6	MPD	F	926	8/8	0.87	0.28	2.83	44,46,50,52	0
6	MPD	A	928	8/8	0.89	0.29	1.81	51,54,55,56	0
6	MPD	G	932	8/8	0.84	0.30	1.81	70,71,72,72	0
5	SR	D	288	1/1	0.94	0.17	1.43	58,58,58,58	0
5	SR	A	290	1/1	0.97	0.14	-0.43	50,50,50,50	0
6	MPD	K	931	8/8	0.86	0.22	-0.82	70,71,71,72	0
5	SR	A	289	1/1	0.99	0.12	-1.76	30,30,30,30	0
5	SR	K	293	1/1	0.91	0.05	-	96,96,96,96	1
5	SR	C	295	1/1	0.75	0.23	-	87,87,87,87	1
5	SR	J	292	1/1	0.88	0.14	-	96,96,96,96	0
5	SR	C	296	1/1	0.91	0.06	-	96,96,96,96	1
5	SR	G	298	1/1	0.97	0.15	-	63,63,63,63	0
5	SR	G	299	1/1	0.94	0.14	-	92,92,92,92	0
5	SR	G	300	1/1	0.87	0.15	-	81,81,81,81	0
5	SR	B	294	1/1	0.95	0.21	-	96,96,96,96	1
5	SR	F	297	1/1	0.76	0.06	-	95,95,95,95	0
5	SR	F	291	1/1	0.98	0.17	-	63,63,63,63	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.