



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 05:19 AM GMT

PDB ID : 3L2Y
Title : The structure of C-reactive protein bound to phosphoethanolamine
Authors : Mikolajek, H.; Kolstoe, S.E.; Wood, S.P.; Pepys, M.B.
Deposited on : 2009-12-15
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

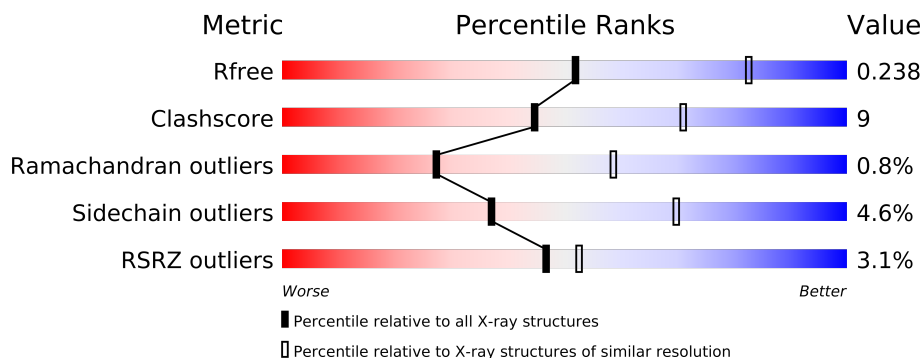
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 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}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	206	
1	B	206	
1	C	206	
1	D	206	
1	E	206	
1	F	206	
1	G	206	
1	H	206	
1	I	206	
1	J	206	
1	K	206	
1	L	206	
1	M	206	
1	N	206	

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Mol	Chain	Length	Quality of chain
1	O	206	
1	P	206	
1	Q	206	
1	R	206	
1	S	206	
1	T	206	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 32993 atoms, of which 0 are hydrogen and 0 are deuterium.

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 C-reactive protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	B	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	C	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	D	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	E	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	F	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	G	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	H	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	I	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	J	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	K	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	L	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	M	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	N	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	O	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			
1	P	206	Total	C	N	O	S	0	0	0
			1632	1058	261	309	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	206	Total 1632	C 1058	N 261	O 309	S 4	0	0	0
1	R	206	Total 1632	C 1058	N 261	O 309	S 4	0	0	0
1	S	206	Total 1632	C 1058	N 261	O 309	S 4	0	0	0
1	T	206	Total 1632	C 1058	N 261	O 309	S 4	0	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

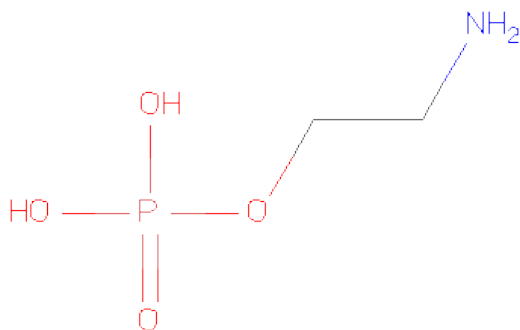
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	P	2	Total 2	Ca 2	0	0
2	G	2	Total 2	Ca 2	0	0
2	J	2	Total 2	Ca 2	0	0
2	Q	2	Total 2	Ca 2	0	0
2	D	2	Total 2	Ca 2	0	0
2	K	2	Total 2	Ca 2	0	0
2	E	2	Total 2	Ca 2	0	0
2	H	2	Total 2	Ca 2	0	0
2	B	2	Total 2	Ca 2	0	0
2	I	2	Total 2	Ca 2	0	0
2	C	2	Total 2	Ca 2	0	0
2	A	2	Total 2	Ca 2	0	0
2	T	2	Total 2	Ca 2	0	0
2	N	2	Total 2	Ca 2	0	0
2	O	2	Total 2	Ca 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	R	2	Total	Ca	0	0
			2	2		
2	L	2	Total	Ca	0	0
			2	2		
2	S	2	Total	Ca	0	0
			2	2		
2	F	2	Total	Ca	0	0
			2	2		
2	M	2	Total	Ca	0	0
			2	2		

- Molecule 3 is PHOSPHORIC ACID MONO-(2-AMINO-ETHYL) ESTER (three-letter code: OPE) (formula: $C_2H_8NO_4P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	B	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	C	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	D	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	E	1	Total	C	N	O	P	0	0
			8	2	1	4	1		
3	F	1	Total	C	N	O	P	0	0
			8	2	1	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	G	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	H	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	I	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	J	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	K	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	L	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	M	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	N	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	O	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	P	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	Q	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	R	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	S	1	Total 8	C 2	N 1	O 4	P 1	0	0
3	T	1	Total 8	C 2	N 1	O 4	P 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	11	Total 11	O 11	0	0
4	B	13	Total 13	O 13	0	0
4	C	12	Total 12	O 12	0	0
4	D	8	Total 8	O 8	0	0
4	E	12	Total 12	O 12	0	0

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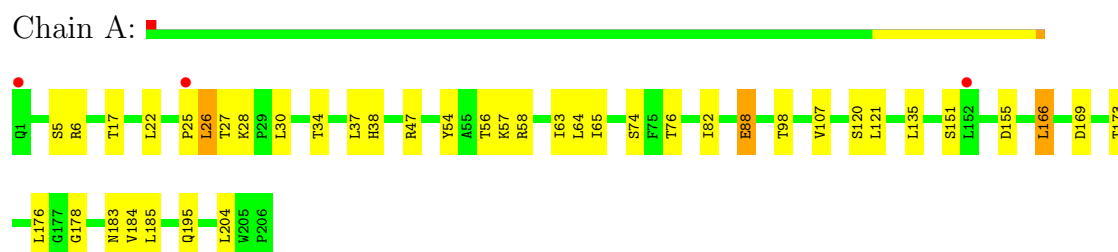
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	2	Total O 2 2	0	0
4	G	7	Total O 7 7	0	0
4	H	12	Total O 12 12	0	0
4	I	7	Total O 7 7	0	0
4	J	7	Total O 7 7	0	0
4	K	7	Total O 7 7	0	0
4	L	2	Total O 2 2	0	0
4	M	6	Total O 6 6	0	0
4	N	6	Total O 6 6	0	0
4	O	7	Total O 7 7	0	0
4	P	10	Total O 10 10	0	0
4	Q	2	Total O 2 2	0	0
4	R	3	Total O 3 3	0	0
4	S	4	Total O 4 4	0	0
4	T	15	Total O 15 15	0	0

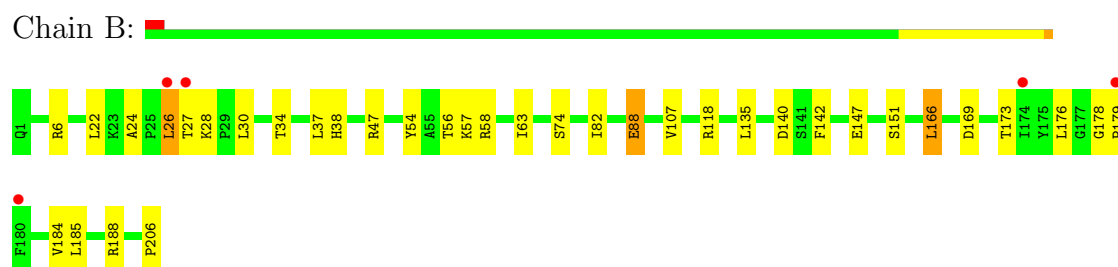
3 Residue-property plots

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.

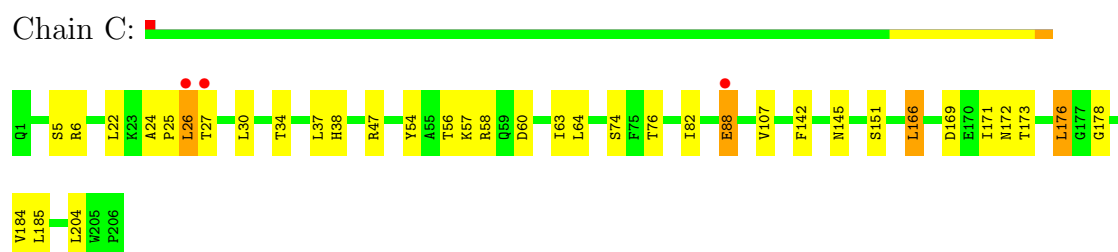
• Molecule 1: C-reactive protein



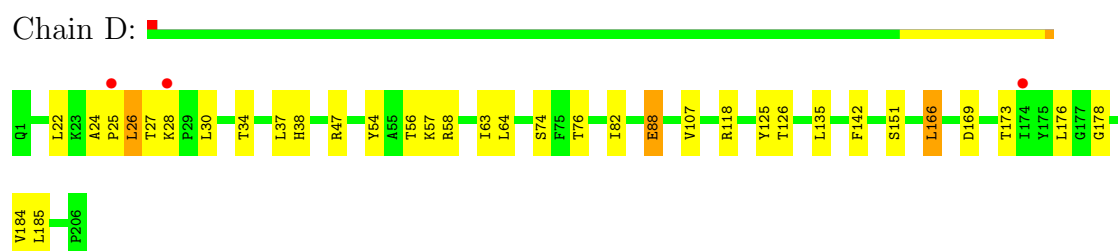
• Molecule 1: C-reactive protein



• Molecule 1: C-reactive protein

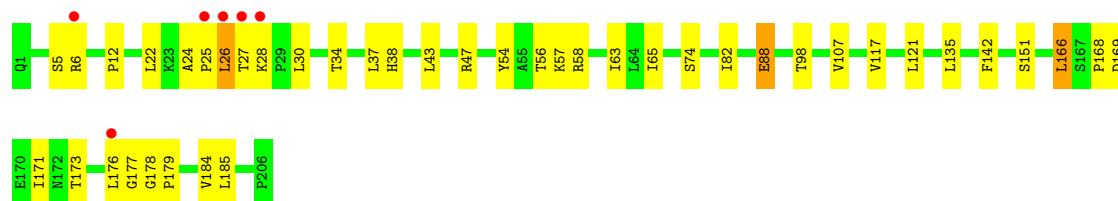


• Molecule 1: C-reactive protein



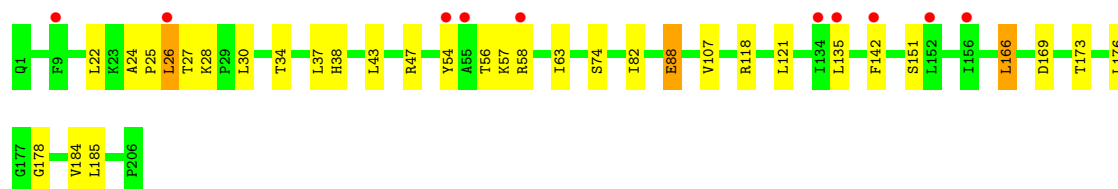
- Molecule 1: C-reactive protein

Chain E:



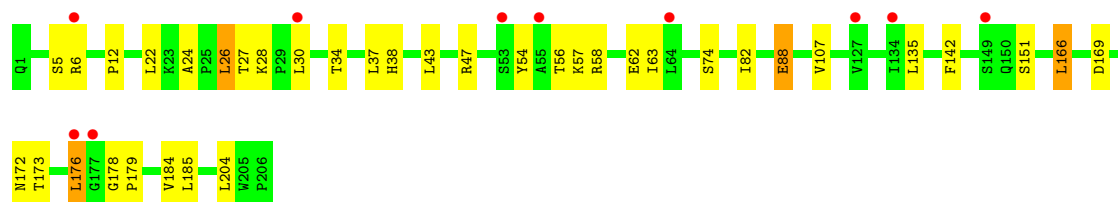
- Molecule 1: C-reactive protein

Chain F:



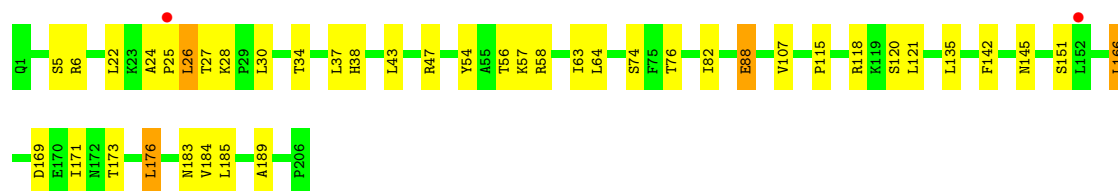
- Molecule 1: C-reactive protein

Chain G:



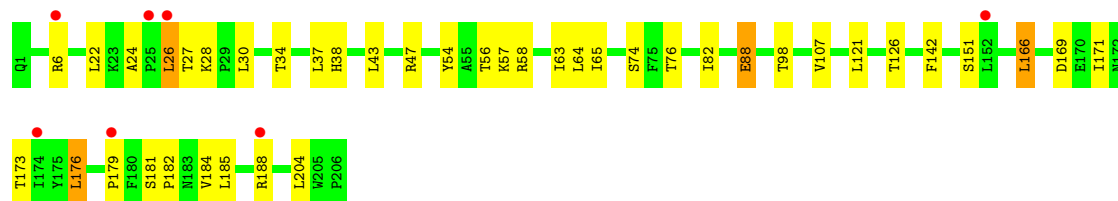
- Molecule 1: C-reactive protein

Chain H:



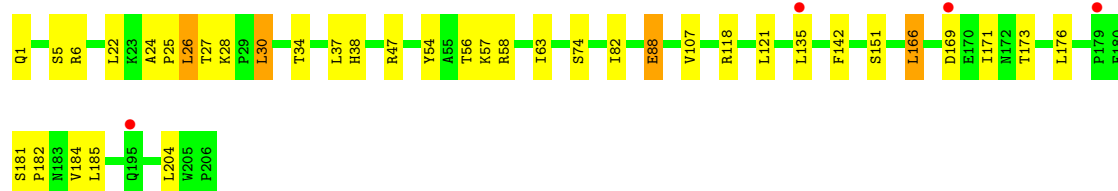
- Molecule 1: C-reactive protein

Chain I:



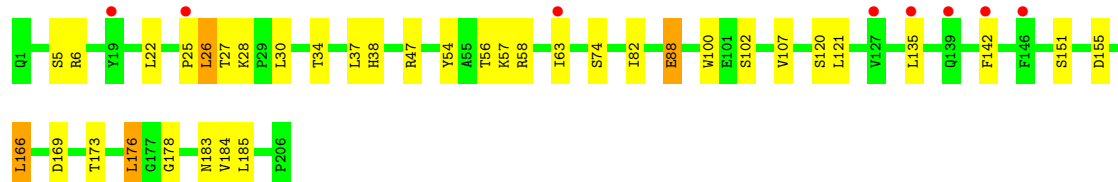
- Molecule 1: C-reactive protein

Chain J: 



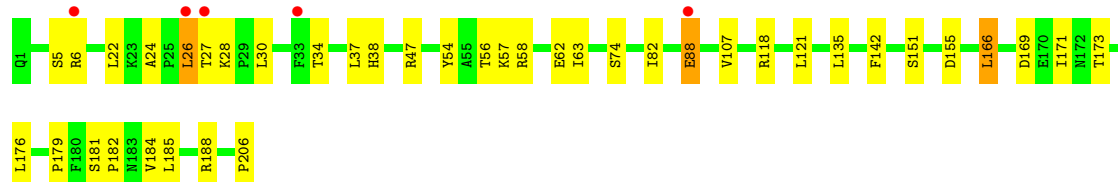
- Molecule 1: C-reactive protein

Chain K: 



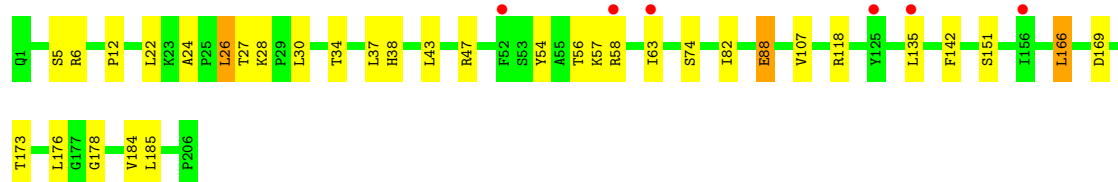
- Molecule 1: C-reactive protein

Chain L: 



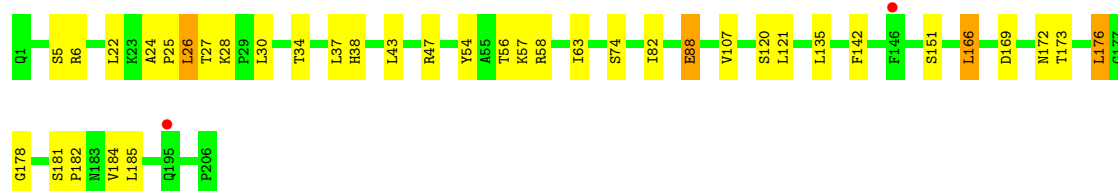
- Molecule 1: C-reactive protein

Chain M: 



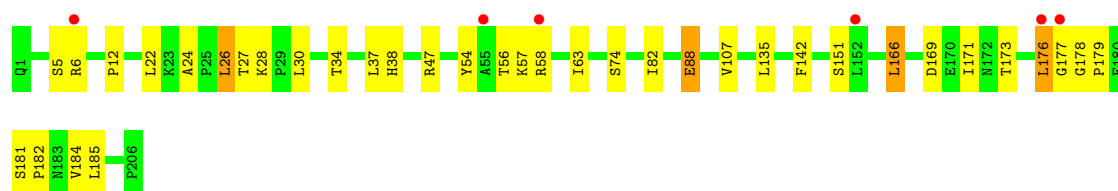
- Molecule 1: C-reactive protein

Chain N: 



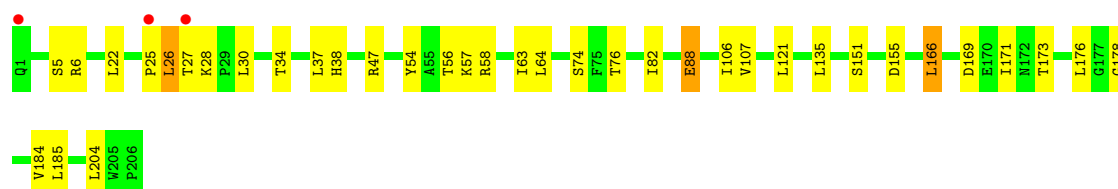
- Molecule 1: C-reactive protein

Chain O: 



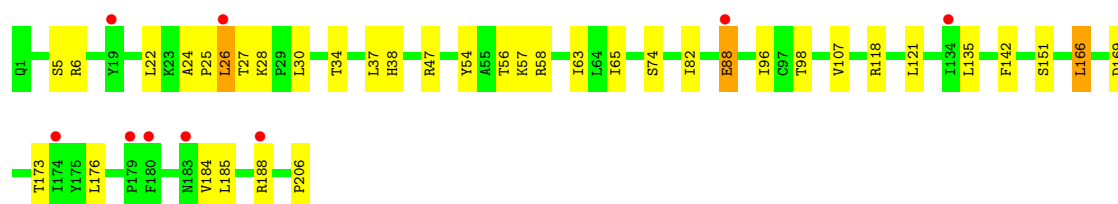
- Molecule 1: C-reactive protein

Chain P:



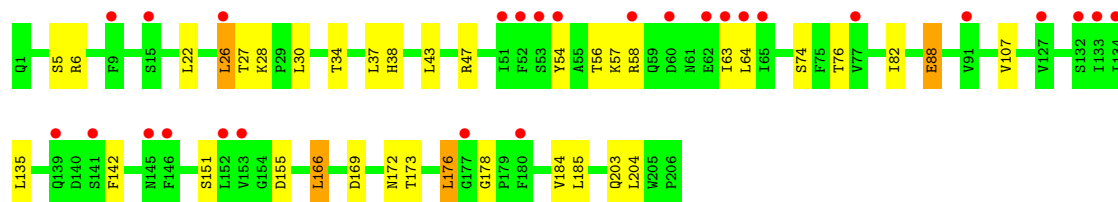
- Molecule 1: C-reactive protein

Chain Q:



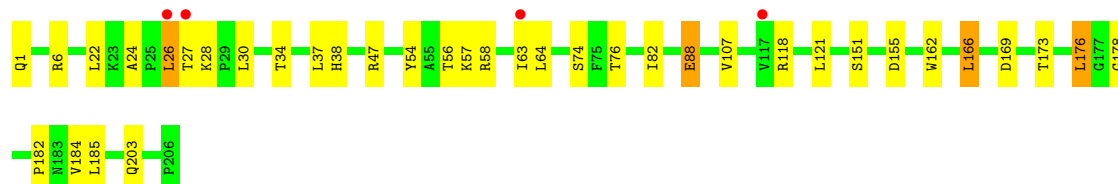
- Molecule 1: C-reactive protein

Chain R:



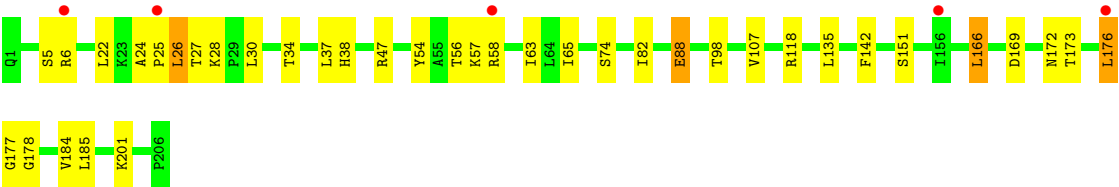
- Molecule 1: C-reactive protein

Chain S:



- Molecule 1: C-reactive protein

Chain T:



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	278.45Å 278.45Å 92.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	124.53 – 2.70 124.53 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (124.53-2.70) 99.3 (124.53-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.224 , 0.246 0.216 , 0.238	Depositor DCC
R_{free} test set	9713 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	60.3	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.7	EDS
Estimated twinning fraction	0.016 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 192826 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	32993	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.88% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.44	0/1678	0.56	0/2279
1	B	0.46	0/1678	0.56	0/2279
1	C	0.43	0/1678	0.57	0/2279
1	D	0.42	0/1678	0.55	0/2279
1	E	0.44	0/1678	0.56	0/2279
1	F	0.46	0/1678	0.55	0/2279
1	G	0.45	0/1678	0.56	0/2279
1	H	0.42	0/1678	0.55	0/2279
1	I	0.44	0/1678	0.57	0/2279
1	J	0.44	0/1678	0.56	0/2279
1	K	0.43	0/1678	0.55	0/2279
1	L	0.46	0/1678	0.58	0/2279
1	M	0.41	0/1678	0.56	0/2279
1	N	0.43	0/1678	0.56	0/2279
1	O	0.43	0/1678	0.58	0/2279
1	P	0.45	0/1678	0.56	0/2279
1	Q	0.46	0/1678	0.56	0/2279
1	R	0.51	0/1678	0.58	0/2279
1	S	0.46	0/1678	0.57	0/2279
1	T	0.44	0/1678	0.57	0/2279
All	All	0.44	0/33560	0.56	0/45580

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1632	0	1593	32	0
1	B	1632	0	1593	31	2
1	C	1632	0	1593	30	0
1	D	1632	0	1593	26	0
1	E	1632	0	1593	31	2
1	F	1632	0	1593	25	0
1	G	1632	0	1593	26	0
1	H	1632	0	1593	37	0
1	I	1632	0	1593	59	0
1	J	1632	0	1593	28	0
1	K	1632	0	1593	29	0
1	L	1632	0	1593	35	0
1	M	1632	0	1593	24	0
1	N	1632	0	1593	25	0
1	O	1632	0	1593	30	0
1	P	1632	0	1593	28	0
1	Q	1632	0	1593	51	0
1	R	1632	0	1593	26	0
1	S	1632	0	1593	29	0
1	T	1632	0	1593	28	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
2	O	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	P	2	0	0	0	0
2	Q	2	0	0	0	0
2	R	2	0	0	0	0
2	S	2	0	0	0	0
2	T	2	0	0	0	0
3	A	8	0	6	0	0
3	B	8	0	6	0	0
3	C	8	0	6	0	0
3	D	8	0	6	0	0
3	E	8	0	6	0	0
3	F	8	0	6	0	0
3	G	8	0	6	0	0
3	H	8	0	6	0	0
3	I	8	0	6	0	0
3	J	8	0	6	0	0
3	K	8	0	6	0	0
3	L	8	0	6	0	0
3	M	8	0	6	0	0
3	N	8	0	6	0	0
3	O	8	0	6	0	0
3	P	8	0	6	0	0
3	Q	8	0	6	0	0
3	R	8	0	6	0	0
3	S	8	0	6	0	0
3	T	8	0	6	0	0
4	A	11	0	0	2	0
4	B	13	0	0	0	0
4	C	12	0	0	0	0
4	D	8	0	0	2	0
4	E	12	0	0	1	0
4	F	2	0	0	1	0
4	G	7	0	0	0	0
4	H	12	0	0	4	0
4	I	7	0	0	0	0
4	J	7	0	0	0	0
4	K	7	0	0	0	0
4	L	2	0	0	0	0
4	M	6	0	0	0	0
4	N	6	0	0	0	0
4	O	7	0	0	1	0
4	P	10	0	0	0	0
4	Q	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	R	3	0	0	0	0
4	S	4	0	0	0	0
4	T	15	0	0	0	0
All	All	32993	0	31980	552	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (552) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:188:ARG:NH2	1:Q:6:ARG:NH1	1.88	1.21
1:S:56:THR:HG22	1:S:58:ARG:H	1.14	1.08
1:H:56:THR:HG22	1:H:58:ARG:H	1.18	1.07
1:P:56:THR:HG22	1:P:58:ARG:H	1.18	1.07
1:L:56:THR:HG22	1:L:58:ARG:H	1.16	1.07
1:I:188:ARG:HH21	1:Q:6:ARG:NH1	1.48	1.05
1:B:56:THR:HG22	1:B:58:ARG:H	1.16	1.05
1:C:56:THR:HG22	1:C:58:ARG:H	1.19	1.05
1:Q:56:THR:HG22	1:Q:58:ARG:H	1.21	1.05
1:N:56:THR:HG22	1:N:58:ARG:H	1.16	1.05
1:J:56:THR:HG22	1:J:58:ARG:H	1.17	1.04
1:I:6:ARG:HH12	1:Q:188:ARG:NH2	1.54	1.04
1:I:188:ARG:NH2	1:Q:6:ARG:HH12	1.51	1.04
1:O:56:THR:HG22	1:O:58:ARG:H	1.24	1.02
1:E:56:THR:HG22	1:E:58:ARG:H	1.16	1.02
1:I:56:THR:HG22	1:I:58:ARG:H	1.21	1.02
1:D:56:THR:HG22	1:D:58:ARG:H	1.20	1.02
1:A:56:THR:HG22	1:A:58:ARG:H	1.23	1.01
1:M:56:THR:HG22	1:M:58:ARG:H	1.24	1.01
1:G:56:THR:HG22	1:G:58:ARG:H	1.24	1.01
1:R:56:THR:HG22	1:R:58:ARG:H	1.22	1.01
1:I:188:ARG:HH21	1:Q:6:ARG:HH11	1.06	1.01
1:T:56:THR:HG22	1:T:58:ARG:H	1.23	1.00
1:K:56:THR:HG22	1:K:58:ARG:H	1.23	1.00
1:F:56:THR:HG22	1:F:58:ARG:H	1.22	0.98
1:I:6:ARG:NH1	1:Q:188:ARG:HH21	1.60	0.98
1:H:173:THR:HG22	1:P:173:THR:HG22	1.46	0.97
1:I:188:ARG:CZ	1:Q:6:ARG:NH1	2.29	0.95
1:C:169:ASP:OD1	1:L:188:ARG:NH2	2.04	0.91
1:I:6:ARG:HH12	1:Q:188:ARG:HH21	0.93	0.90
1:H:27:THR:HG22	4:H:212:HOH:O	1.71	0.90
1:I:179:PRO:CB	1:Q:206:PRO:HB3	2.05	0.85

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:188:ARG:CZ	1:Q:6:ARG:HH12	1.89	0.81
1:B:188:ARG:NH2	1:M:169:ASP:OD1	2.15	0.80
1:F:82:ILE:HD11	1:F:107:VAL:HG21	1.65	0.78
1:S:56:THR:HG22	1:S:58:ARG:N	1.97	0.78
1:N:56:THR:HG22	1:N:58:ARG:N	1.97	0.78
1:I:179:PRO:CG	1:Q:206:PRO:CB	2.62	0.78
1:O:26:LEU:HD21	1:O:30:LEU:HD11	1.66	0.78
1:L:26:LEU:HD21	1:L:30:LEU:HD11	1.64	0.78
1:H:26:LEU:HD21	1:H:30:LEU:HD11	1.65	0.77
1:E:56:THR:HG22	1:E:58:ARG:N	1.96	0.77
1:I:26:LEU:HD21	1:I:30:LEU:HD11	1.65	0.77
1:G:26:LEU:HD21	1:G:30:LEU:HD11	1.67	0.77
1:A:26:LEU:HD21	1:A:30:LEU:HD11	1.67	0.77
1:R:26:LEU:HD21	1:R:30:LEU:HD11	1.67	0.77
1:K:26:LEU:HD21	1:K:30:LEU:HD11	1.65	0.77
1:G:82:ILE:HD11	1:G:107:VAL:HG21	1.65	0.77
1:C:26:LEU:HD21	1:C:30:LEU:HD11	1.65	0.76
1:B:56:THR:HG22	1:B:58:ARG:N	1.98	0.76
1:J:56:THR:HG22	1:J:58:ARG:N	1.98	0.76
1:J:82:ILE:HD11	1:J:107:VAL:HG21	1.67	0.76
1:I:179:PRO:CG	1:Q:206:PRO:HB3	2.16	0.76
1:I:82:ILE:HD11	1:I:107:VAL:HG21	1.67	0.76
1:S:26:LEU:HD21	1:S:30:LEU:HD11	1.68	0.75
1:S:82:ILE:HD11	1:S:107:VAL:HG21	1.68	0.75
1:C:56:THR:HG22	1:C:58:ARG:N	2.00	0.75
1:Q:56:THR:HG22	1:Q:58:ARG:N	2.01	0.75
1:P:82:ILE:HD11	1:P:107:VAL:HG21	1.69	0.75
1:J:26:LEU:HD21	1:J:30:LEU:HD11	1.68	0.75
1:D:26:LEU:HD21	1:D:30:LEU:HD11	1.69	0.75
1:H:173:THR:CG2	1:P:173:THR:HG22	2.16	0.74
1:D:82:ILE:HD11	1:D:107:VAL:HG21	1.69	0.74
1:M:82:ILE:HD11	1:M:107:VAL:HG21	1.69	0.74
1:N:82:ILE:HD11	1:N:107:VAL:HG21	1.69	0.74
1:M:26:LEU:HD21	1:M:30:LEU:HD11	1.66	0.74
1:H:6:ARG:NH1	4:H:210:HOH:O	2.15	0.74
1:Q:26:LEU:HD21	1:Q:30:LEU:HD11	1.69	0.74
1:R:56:THR:HG22	1:R:58:ARG:N	2.01	0.74
1:N:26:LEU:HD21	1:N:30:LEU:HD11	1.70	0.74
1:R:82:ILE:HD11	1:R:107:VAL:HG21	1.70	0.74
1:F:26:LEU:HD21	1:F:30:LEU:HD11	1.69	0.74
1:A:82:ILE:HD11	1:A:107:VAL:HG21	1.70	0.73
1:I:179:PRO:HG2	1:Q:206:PRO:CB	2.17	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:56:THR:HG22	1:H:58:ARG:N	2.00	0.73
1:I:188:ARG:NE	1:Q:6:ARG:NH1	2.35	0.73
1:D:56:THR:HG22	1:D:58:ARG:N	2.00	0.73
1:F:56:THR:HG22	1:F:58:ARG:N	2.01	0.73
1:D:126:THR:H	1:H:145:ASN:HD21	1.35	0.73
1:O:82:ILE:HD11	1:O:107:VAL:HG21	1.71	0.73
1:T:82:ILE:HD11	1:T:107:VAL:HG21	1.70	0.73
1:C:145:ASN:HD21	1:I:126:THR:H	1.37	0.73
1:A:56:THR:HG22	1:A:58:ARG:N	2.02	0.73
1:L:82:ILE:HD11	1:L:107:VAL:HG21	1.69	0.73
1:P:56:THR:HG22	1:P:58:ARG:N	2.00	0.73
1:Q:82:ILE:HD11	1:Q:107:VAL:HG21	1.71	0.73
1:P:26:LEU:HD21	1:P:30:LEU:HD11	1.71	0.72
1:T:26:LEU:HD21	1:T:30:LEU:HD11	1.71	0.72
1:K:82:ILE:HD11	1:K:107:VAL:HG21	1.72	0.72
1:C:82:ILE:HD11	1:C:107:VAL:HG21	1.72	0.72
1:A:25:PRO:HD2	1:O:179:PRO:HG2	1.70	0.72
1:A:88:GLU:HG3	1:A:88:GLU:O	1.90	0.72
1:L:56:THR:HG22	1:L:58:ARG:N	1.98	0.71
1:O:56:THR:HG22	1:O:58:ARG:N	2.02	0.71
1:H:82:ILE:HD11	1:H:107:VAL:HG21	1.71	0.71
1:E:82:ILE:HD11	1:E:107:VAL:HG21	1.72	0.71
1:G:56:THR:HG22	1:G:58:ARG:N	2.04	0.71
1:D:88:GLU:O	1:D:88:GLU:HG3	1.91	0.71
1:T:56:THR:HG22	1:T:58:ARG:N	2.04	0.71
1:E:26:LEU:HD21	1:E:30:LEU:HD11	1.71	0.70
1:R:88:GLU:O	1:R:88:GLU:HG3	1.89	0.70
1:I:6:ARG:NH1	1:Q:188:ARG:HE	1.90	0.70
1:K:56:THR:HG22	1:K:58:ARG:N	2.03	0.70
1:B:34:THR:HG21	1:B:166:LEU:HD22	1.74	0.70
1:I:56:THR:HG22	1:I:58:ARG:N	2.02	0.70
1:B:26:LEU:HD21	1:B:30:LEU:HD11	1.73	0.70
1:R:34:THR:HG21	1:R:166:LEU:HD22	1.74	0.70
1:F:88:GLU:HG3	1:F:88:GLU:O	1.91	0.69
1:J:88:GLU:HG3	1:J:88:GLU:O	1.92	0.69
1:M:88:GLU:HG3	1:M:88:GLU:O	1.93	0.69
1:E:88:GLU:O	1:E:88:GLU:HG3	1.92	0.69
1:H:88:GLU:O	1:H:88:GLU:HG3	1.91	0.69
1:E:179:PRO:HG2	1:K:25:PRO:HD2	1.75	0.68
1:J:34:THR:HG21	1:J:166:LEU:HD22	1.75	0.68
1:B:88:GLU:HG3	1:B:88:GLU:O	1.92	0.68
1:Q:88:GLU:O	1:Q:88:GLU:HG3	1.91	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:P:34:THR:HG21	1:P:166:LEU:HD22	1.76	0.67
1:T:88:GLU:O	1:T:88:GLU:HG3	1.93	0.67
1:I:179:PRO:HG2	1:Q:206:PRO:HB3	1.75	0.67
1:B:82:ILE:HD11	1:B:107:VAL:HG21	1.75	0.67
1:I:88:GLU:O	1:I:88:GLU:HG3	1.94	0.67
1:R:169:ASP:O	1:R:173:THR:HG23	1.95	0.66
1:P:88:GLU:O	1:P:88:GLU:HG3	1.93	0.66
1:S:88:GLU:O	1:S:88:GLU:HG3	1.93	0.66
1:G:88:GLU:O	1:G:88:GLU:HG3	1.96	0.66
1:K:88:GLU:O	1:K:88:GLU:HG3	1.93	0.66
1:L:88:GLU:O	1:L:88:GLU:HG3	1.94	0.66
1:N:88:GLU:HG3	1:N:88:GLU:O	1.94	0.66
1:O:88:GLU:O	1:O:88:GLU:HG3	1.94	0.66
1:E:168:PRO:HD3	4:E:207:HOH:O	1.96	0.65
1:B:206:PRO:HB3	1:L:179:PRO:CG	2.26	0.65
1:A:173:THR:HG22	1:K:173:THR:HG22	1.78	0.65
1:I:179:PRO:CG	1:Q:206:PRO:HB2	2.27	0.65
1:C:88:GLU:HG3	1:C:88:GLU:O	1.94	0.65
1:M:56:THR:HG22	1:M:58:ARG:N	2.04	0.64
1:F:184:VAL:HG12	1:F:185:LEU:HD13	1.78	0.64
1:H:34:THR:HG21	1:H:166:LEU:HD22	1.79	0.64
1:I:34:THR:HG21	1:I:166:LEU:HD22	1.80	0.64
1:A:184:VAL:HA	1:O:179:PRO:HG3	1.79	0.64
1:F:34:THR:HG21	1:F:166:LEU:HD22	1.80	0.64
1:E:34:THR:HG21	1:E:166:LEU:HD22	1.80	0.63
1:H:189:ALA:HB2	1:T:176:LEU:HG	1.81	0.63
1:B:206:PRO:HB3	1:L:179:PRO:HG3	1.80	0.63
1:C:34:THR:HG21	1:C:166:LEU:HD22	1.81	0.63
1:M:34:THR:HG21	1:M:166:LEU:HD22	1.80	0.63
1:O:34:THR:HG21	1:O:166:LEU:HD22	1.81	0.62
1:C:145:ASN:ND2	1:I:126:THR:H	1.96	0.62
1:O:184:VAL:HG12	1:O:185:LEU:HD13	1.82	0.62
1:D:184:VAL:HG12	1:D:185:LEU:HD13	1.80	0.62
1:I:179:PRO:HB2	1:Q:206:PRO:HB3	1.81	0.61
1:P:169:ASP:O	1:P:173:THR:HG23	1.99	0.61
1:Q:34:THR:HG21	1:Q:166:LEU:HD22	1.82	0.61
1:L:34:THR:HG21	1:L:166:LEU:HD22	1.81	0.61
1:I:179:PRO:HG2	1:Q:206:PRO:HB2	1.80	0.61
1:R:155:ASP:OD2	1:S:118:ARG:NH1	2.32	0.61
1:L:26:LEU:HD12	1:L:27:THR:H	1.66	0.61
1:S:34:THR:HG21	1:S:166:LEU:HD22	1.83	0.61
1:N:184:VAL:HG12	1:N:185:LEU:HD13	1.82	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:126:THR:H	1:H:145:ASN:ND2	1.98	0.60
1:A:26:LEU:HD12	1:A:27:THR:H	1.66	0.60
1:Q:184:VAL:HG12	1:Q:185:LEU:HD13	1.82	0.60
1:K:34:THR:HG21	1:K:166:LEU:HD22	1.82	0.60
1:G:184:VAL:HG12	1:G:185:LEU:HD13	1.83	0.60
1:I:179:PRO:CB	1:Q:206:PRO:CB	2.78	0.60
1:K:26:LEU:HD12	1:K:27:THR:H	1.66	0.60
1:C:26:LEU:HD12	1:C:27:THR:H	1.65	0.60
1:J:184:VAL:HG12	1:J:185:LEU:HD13	1.84	0.60
1:B:184:VAL:HG12	1:B:185:LEU:HD13	1.84	0.59
1:B:26:LEU:HD12	1:B:27:THR:H	1.67	0.59
1:N:34:THR:HG21	1:N:166:LEU:HD22	1.84	0.59
1:E:184:VAL:HG12	1:E:185:LEU:HD13	1.84	0.59
1:I:6:ARG:HH12	1:Q:188:ARG:CZ	2.13	0.59
1:G:34:THR:HG21	1:G:166:LEU:HD22	1.83	0.59
1:H:27:THR:CG2	4:H:212:HOH:O	2.41	0.59
1:N:169:ASP:O	1:N:173:THR:HG23	2.03	0.58
1:F:25:PRO:HG3	4:F:207:HOH:O	2.03	0.58
1:T:34:THR:HG21	1:T:166:LEU:HD22	1.84	0.58
1:P:26:LEU:HD12	1:P:27:THR:H	1.68	0.58
1:D:34:THR:HG21	1:D:166:LEU:HD22	1.85	0.58
1:A:169:ASP:O	1:A:173:THR:HG23	2.03	0.58
1:B:6:ARG:NH1	1:L:188:ARG:HE	2.02	0.58
1:F:47:ARG:NH2	1:F:151:SER:O	2.37	0.58
1:I:26:LEU:HD12	1:I:27:THR:H	1.68	0.58
1:S:184:VAL:HG12	1:S:185:LEU:HD13	1.85	0.58
1:D:26:LEU:HD12	1:D:27:THR:H	1.69	0.57
1:I:188:ARG:NH2	1:R:169:ASP:OD1	2.36	0.57
1:J:47:ARG:NH2	1:J:151:SER:O	2.37	0.57
1:M:184:VAL:HG12	1:M:185:LEU:HD13	1.86	0.57
1:F:169:ASP:O	1:F:173:THR:HG23	2.04	0.57
1:O:26:LEU:HD12	1:O:27:THR:H	1.70	0.57
1:J:26:LEU:HD12	1:J:27:THR:H	1.69	0.57
1:K:169:ASP:O	1:K:173:THR:HG23	2.04	0.57
1:M:26:LEU:HD12	1:M:27:THR:H	1.69	0.57
1:F:26:LEU:HD12	1:F:27:THR:H	1.70	0.57
1:N:47:ARG:NH2	1:N:151:SER:O	2.38	0.57
1:L:184:VAL:HG12	1:L:185:LEU:HD13	1.87	0.57
1:I:188:ARG:HE	1:Q:6:ARG:NH1	2.02	0.57
1:R:26:LEU:HD12	1:R:27:THR:H	1.70	0.57
1:B:179:PRO:HG3	1:L:206:PRO:HB3	1.87	0.56
1:Q:47:ARG:NH2	1:Q:151:SER:O	2.37	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:T:184:VAL:HG12	1:T:185:LEU:HD13	1.87	0.56
1:S:169:ASP:O	1:S:173:THR:HG23	2.05	0.56
1:A:34:THR:HG21	1:A:166:LEU:HD22	1.87	0.56
1:H:183:ASN:HA	1:T:177:GLY:O	2.04	0.56
1:C:184:VAL:HG12	1:C:185:LEU:HD13	1.87	0.56
1:R:184:VAL:HG12	1:R:185:LEU:HD13	1.86	0.56
1:N:26:LEU:HD12	1:N:27:THR:H	1.70	0.56
1:C:169:ASP:O	1:C:173:THR:HG23	2.05	0.56
1:O:47:ARG:NH2	1:O:151:SER:O	2.39	0.56
1:I:184:VAL:HG12	1:I:185:LEU:HD13	1.87	0.56
1:H:26:LEU:HD12	1:H:27:THR:H	1.72	0.55
1:S:26:LEU:HD12	1:S:27:THR:H	1.71	0.55
1:P:184:VAL:HG12	1:P:185:LEU:HD13	1.87	0.55
1:E:179:PRO:HG3	1:K:184:VAL:HA	1.88	0.55
1:L:169:ASP:O	1:L:173:THR:HG23	2.06	0.55
1:G:47:ARG:NH2	1:G:151:SER:O	2.40	0.55
1:B:47:ARG:NH2	1:B:151:SER:O	2.40	0.55
1:E:26:LEU:HD12	1:E:27:THR:H	1.73	0.54
1:K:184:VAL:HG12	1:K:185:LEU:HD13	1.90	0.54
1:R:88:GLU:CG	1:R:88:GLU:O	2.55	0.54
1:H:169:ASP:O	1:H:173:THR:HG23	2.08	0.54
1:D:169:ASP:O	1:D:173:THR:HG23	2.08	0.54
1:M:169:ASP:O	1:M:173:THR:HG23	2.07	0.54
1:H:88:GLU:O	1:H:88:GLU:CG	2.56	0.54
1:T:169:ASP:O	1:T:173:THR:HG23	2.08	0.53
1:G:26:LEU:HD12	1:G:27:THR:H	1.73	0.53
1:O:169:ASP:O	1:O:173:THR:HG23	2.08	0.53
1:E:177:GLY:O	1:K:183:ASN:HA	2.09	0.53
1:I:6:ARG:NH1	1:Q:188:ARG:NE	2.56	0.53
1:Q:26:LEU:HD12	1:Q:27:THR:H	1.74	0.53
1:O:27:THR:HG23	1:O:28:LYS:H	1.73	0.53
1:A:184:VAL:HG12	1:A:185:LEU:HD13	1.90	0.53
1:T:27:THR:HG23	1:T:28:LYS:H	1.74	0.53
1:T:26:LEU:HD12	1:T:27:THR:H	1.73	0.53
1:J:169:ASP:O	1:J:173:THR:HG23	2.09	0.53
1:Q:37:LEU:C	1:Q:37:LEU:HD12	2.30	0.52
1:S:37:LEU:C	1:S:37:LEU:HD12	2.29	0.52
1:S:88:GLU:CG	1:S:88:GLU:O	2.58	0.52
1:S:47:ARG:NH2	1:S:151:SER:O	2.42	0.52
1:B:88:GLU:CG	1:B:88:GLU:O	2.58	0.52
1:K:88:GLU:O	1:K:88:GLU:CG	2.57	0.52
1:M:47:ARG:NH2	1:M:151:SER:O	2.42	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:47:ARG:NH2	1:I:151:SER:O	2.41	0.52
1:F:88:GLU:CG	1:F:88:GLU:O	2.57	0.52
1:P:204:LEU:HD11	1:Q:118:ARG:HG3	1.92	0.52
1:T:37:LEU:HD12	1:T:37:LEU:C	2.29	0.52
1:A:17:THR:HG22	4:A:213:HOH:O	2.09	0.52
1:D:88:GLU:O	1:D:88:GLU:CG	2.57	0.52
1:D:27:THR:HG23	1:D:28:LYS:H	1.74	0.52
1:I:88:GLU:O	1:I:88:GLU:CG	2.58	0.52
1:P:27:THR:HG23	1:P:28:LYS:H	1.75	0.52
1:D:47:ARG:NH2	1:D:151:SER:O	2.43	0.52
1:E:47:ARG:NH2	1:E:151:SER:O	2.43	0.52
1:B:169:ASP:O	1:B:173:THR:HG23	2.10	0.51
1:E:169:ASP:O	1:E:173:THR:HG23	2.08	0.51
1:F:37:LEU:HD12	1:F:37:LEU:C	2.30	0.51
1:K:27:THR:HG23	1:K:28:LYS:H	1.76	0.51
1:E:88:GLU:CG	1:E:88:GLU:O	2.57	0.51
1:Q:88:GLU:O	1:Q:88:GLU:CG	2.57	0.51
1:P:47:ARG:NH2	1:P:151:SER:O	2.44	0.51
1:I:37:LEU:HD12	1:I:37:LEU:C	2.31	0.51
1:T:88:GLU:O	1:T:88:GLU:CG	2.58	0.51
1:P:88:GLU:O	1:P:88:GLU:CG	2.58	0.51
1:O:88:GLU:O	1:O:88:GLU:CG	2.59	0.51
1:G:12:PRO:HB2	1:H:120:SER:HB2	1.91	0.51
1:F:184:VAL:HG12	1:F:185:LEU:CD1	2.41	0.50
1:E:27:THR:HG23	1:E:28:LYS:H	1.75	0.50
1:R:27:THR:HG23	1:R:28:LYS:H	1.76	0.50
1:A:88:GLU:O	1:A:88:GLU:CG	2.56	0.50
1:A:183:ASN:HA	1:O:177:GLY:O	2.11	0.50
1:T:47:ARG:NH2	1:T:151:SER:O	2.45	0.50
1:A:37:LEU:HD12	1:A:37:LEU:C	2.32	0.50
1:A:27:THR:HG23	1:A:28:LYS:H	1.76	0.50
1:G:27:THR:HG23	1:G:28:LYS:H	1.77	0.50
1:G:169:ASP:O	1:G:173:THR:HG23	2.11	0.50
1:M:27:THR:HG23	1:M:28:LYS:H	1.76	0.49
1:J:88:GLU:CG	1:J:88:GLU:O	2.57	0.49
1:H:115:PRO:HD2	4:H:207:HOH:O	2.11	0.49
1:L:37:LEU:C	1:L:37:LEU:HD12	2.32	0.49
1:E:179:PRO:HD2	1:K:25:PRO:HG2	1.94	0.49
1:G:88:GLU:O	1:G:88:GLU:CG	2.60	0.49
1:B:37:LEU:HD12	1:B:37:LEU:C	2.32	0.49
1:I:27:THR:HG23	1:I:28:LYS:H	1.77	0.49
1:C:54:TYR:HB3	1:C:63:ILE:HB	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:Q:184:VAL:HG12	1:Q:185:LEU:CD1	2.43	0.49
1:Q:169:ASP:O	1:Q:173:THR:HG23	2.11	0.49
1:D:37:LEU:HD12	1:D:37:LEU:C	2.33	0.49
1:K:47:ARG:NH2	1:K:151:SER:O	2.45	0.49
1:K:26:LEU:HD12	1:K:27:THR:N	2.27	0.49
1:F:27:THR:HG23	1:F:28:LYS:H	1.77	0.49
1:M:88:GLU:CG	1:M:88:GLU:O	2.58	0.49
4:D:208:HOH:O	1:E:117:VAL:CG2	2.60	0.49
1:O:37:LEU:HD12	1:O:37:LEU:C	2.32	0.49
1:N:88:GLU:CG	1:N:88:GLU:O	2.58	0.49
1:I:169:ASP:O	1:I:173:THR:HG23	2.13	0.49
1:Q:27:THR:HG23	1:Q:28:LYS:H	1.78	0.48
1:L:88:GLU:O	1:L:88:GLU:CG	2.58	0.48
1:E:37:LEU:C	1:E:37:LEU:HD12	2.33	0.48
1:A:47:ARG:NH2	1:A:151:SER:O	2.46	0.48
1:S:27:THR:HG23	1:S:28:LYS:H	1.77	0.48
1:R:47:ARG:NH2	1:R:151:SER:O	2.45	0.48
1:R:37:LEU:C	1:R:37:LEU:HD12	2.34	0.48
1:G:184:VAL:HG12	1:G:185:LEU:CD1	2.44	0.48
1:K:37:LEU:HD12	1:K:37:LEU:C	2.34	0.48
1:E:56:THR:CG2	1:E:57:LYS:N	2.77	0.48
1:N:56:THR:CG2	1:N:57:LYS:N	2.76	0.48
1:J:27:THR:HG23	1:J:28:LYS:H	1.79	0.48
1:L:47:ARG:NH2	1:L:151:SER:O	2.47	0.48
1:C:60:ASP:CG	1:I:58:ARG:NH2	2.67	0.48
1:G:37:LEU:C	1:G:37:LEU:HD12	2.34	0.48
1:J:56:THR:CG2	1:J:57:LYS:N	2.77	0.47
1:L:26:LEU:HD12	1:L:27:THR:N	2.29	0.47
1:B:206:PRO:CB	1:L:179:PRO:HG3	2.44	0.47
1:H:184:VAL:HG12	1:H:185:LEU:HD13	1.94	0.47
1:P:37:LEU:C	1:P:37:LEU:HD12	2.34	0.47
1:S:56:THR:CG2	1:S:57:LYS:N	2.77	0.47
1:H:37:LEU:C	1:H:37:LEU:HD12	2.34	0.47
1:B:6:ARG:HH12	1:L:188:ARG:HE	1.60	0.47
1:D:24:ALA:HB2	1:D:185:LEU:HD11	1.95	0.47
1:F:24:ALA:HA	1:F:25:PRO:HD3	1.74	0.47
1:N:184:VAL:HG12	1:N:185:LEU:CD1	2.45	0.47
1:A:65:ILE:HD11	1:A:98:THR:HG21	1.96	0.47
1:P:5:SER:O	1:P:6:ARG:HB3	2.15	0.47
1:H:24:ALA:HA	1:H:25:PRO:HD3	1.71	0.47
1:G:179:PRO:HG2	1:P:25:PRO:HD2	1.95	0.47
1:O:54:TYR:HB3	1:O:63:ILE:HB	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:26:LEU:HD12	1:A:27:THR:N	2.29	0.47
1:H:5:SER:O	1:H:6:ARG:HB3	2.15	0.47
1:C:47:ARG:NH2	1:C:151:SER:O	2.47	0.47
1:O:56:THR:CG2	1:O:57:LYS:N	2.78	0.47
1:H:27:THR:HG23	1:H:28:LYS:H	1.80	0.47
1:N:24:ALA:HA	1:N:25:PRO:HD3	1.73	0.47
1:C:26:LEU:HD12	1:C:27:THR:N	2.30	0.47
4:D:208:HOH:O	1:E:117:VAL:HG23	2.15	0.47
1:A:120:SER:HB2	1:E:12:PRO:HB2	1.96	0.47
1:F:54:TYR:HB3	1:F:63:ILE:HB	1.97	0.47
1:R:184:VAL:HG12	1:R:185:LEU:CD1	2.44	0.46
1:D:56:THR:CG2	1:D:57:LYS:N	2.78	0.46
1:S:54:TYR:HB3	1:S:63:ILE:HB	1.97	0.46
1:K:155:ASP:OD2	1:L:118:ARG:NH1	2.44	0.46
1:M:37:LEU:HD12	1:M:37:LEU:C	2.35	0.46
1:S:155:ASP:OD2	1:T:118:ARG:NH1	2.46	0.46
1:B:184:VAL:HG12	1:B:185:LEU:CD1	2.46	0.46
1:L:184:VAL:HG12	1:L:185:LEU:CD1	2.45	0.46
1:E:54:TYR:HB3	1:E:63:ILE:HB	1.96	0.46
1:J:54:TYR:HB3	1:J:63:ILE:HB	1.96	0.46
1:P:56:THR:CG2	1:P:57:LYS:N	2.78	0.46
1:J:37:LEU:HD12	1:J:37:LEU:C	2.35	0.46
1:I:204:LEU:HD11	1:J:118:ARG:HG3	1.97	0.46
1:A:27:THR:HG23	1:A:28:LYS:N	2.31	0.46
1:Q:24:ALA:HB2	1:Q:185:LEU:HD11	1.98	0.46
1:B:179:PRO:CG	1:L:206:PRO:HB3	2.46	0.46
1:J:181:SER:HA	1:J:182:PRO:HD3	1.82	0.46
1:P:27:THR:HG23	1:P:28:LYS:N	2.31	0.46
1:J:24:ALA:HA	1:J:25:PRO:HD3	1.71	0.46
1:B:56:THR:CG2	1:B:57:LYS:N	2.78	0.46
1:A:56:THR:CG2	1:A:57:LYS:N	2.79	0.46
1:O:184:VAL:HG12	1:O:185:LEU:CD1	2.46	0.46
1:R:64:LEU:HB3	1:R:76:THR:HB	1.96	0.45
1:B:54:TYR:HB3	1:B:63:ILE:HB	1.97	0.45
1:T:54:TYR:HB3	1:T:63:ILE:HB	1.98	0.45
1:R:54:TYR:HB3	1:R:63:ILE:HB	1.98	0.45
1:C:37:LEU:HD12	1:C:37:LEU:C	2.36	0.45
1:H:56:THR:CG2	1:H:57:LYS:N	2.78	0.45
1:Q:56:THR:CG2	1:Q:57:LYS:N	2.79	0.45
1:H:47:ARG:NH2	1:H:151:SER:O	2.49	0.45
1:M:184:VAL:HG12	1:M:185:LEU:CD1	2.46	0.45
1:D:64:LEU:HB3	1:D:76:THR:HB	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:J:5:SER:O	1:J:6:ARG:HB3	2.17	0.45
1:K:56:THR:CG2	1:K:57:LYS:N	2.79	0.45
1:S:82:ILE:HG23	1:S:121:LEU:HD13	1.99	0.45
1:P:26:LEU:HD12	1:P:27:THR:N	2.30	0.45
1:C:60:ASP:OD1	1:I:58:ARG:NH2	2.50	0.45
1:E:184:VAL:HG12	1:E:185:LEU:CD1	2.47	0.45
1:A:155:ASP:OD2	1:B:118:ARG:NH1	2.44	0.45
1:P:106:ILE:HD12	1:T:201:LYS:HE3	1.99	0.45
1:S:184:VAL:HG12	1:S:185:LEU:CD1	2.47	0.45
1:N:54:TYR:HB3	1:N:63:ILE:HB	1.98	0.45
1:I:24:ALA:C	1:I:26:LEU:H	2.21	0.44
1:S:24:ALA:HB2	1:S:185:LEU:HD11	2.00	0.44
1:D:125:TYR:CD1	1:H:145:ASN:ND2	2.81	0.44
1:B:26:LEU:HD12	1:B:27:THR:N	2.31	0.44
1:A:5:SER:O	1:A:6:ARG:HB3	2.18	0.44
1:J:26:LEU:HD12	1:J:27:THR:N	2.31	0.44
1:B:27:THR:HG23	1:B:28:LYS:H	1.82	0.44
1:J:184:VAL:HG12	1:J:185:LEU:CD1	2.46	0.44
1:N:37:LEU:HD12	1:N:37:LEU:C	2.38	0.44
1:G:54:TYR:HB3	1:G:63:ILE:HB	1.99	0.44
1:K:54:TYR:HB3	1:K:63:ILE:HB	1.98	0.44
1:A:25:PRO:HG2	1:O:179:PRO:HD2	2.00	0.44
1:H:82:ILE:HG23	1:H:121:LEU:HD13	2.00	0.44
1:E:24:ALA:HA	1:E:25:PRO:HD3	1.72	0.44
1:O:26:LEU:HD12	1:O:27:THR:N	2.33	0.44
1:D:26:LEU:HD12	1:D:27:THR:N	2.32	0.44
1:A:64:LEU:HB3	1:A:76:THR:HB	1.99	0.44
1:O:27:THR:HG23	1:O:28:LYS:N	2.32	0.44
1:Q:54:TYR:HB3	1:Q:63:ILE:HB	2.00	0.44
1:D:54:TYR:HB3	1:D:63:ILE:HB	2.00	0.44
1:F:26:LEU:HD12	1:F:27:THR:N	2.33	0.44
1:P:64:LEU:HB3	1:P:76:THR:HB	2.00	0.44
1:I:56:THR:CG2	1:I:57:LYS:N	2.81	0.44
1:G:56:THR:CG2	1:G:57:LYS:N	2.80	0.44
1:I:26:LEU:HD12	1:I:27:THR:N	2.31	0.44
1:N:27:THR:HG23	1:N:28:LYS:H	1.82	0.44
1:I:64:LEU:HB3	1:I:76:THR:HB	2.00	0.44
1:R:172:ASN:OD1	1:R:176:LEU:HD23	2.18	0.44
1:I:6:ARG:NH1	1:Q:188:ARG:NH2	2.33	0.43
1:M:24:ALA:HB2	1:M:185:LEU:HD11	2.00	0.43
1:S:162:TRP:CD1	1:S:182:PRO:HA	2.53	0.43
1:D:184:VAL:HG12	1:D:185:LEU:CD1	2.46	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:M:27:THR:HG23	1:M:28:LYS:N	2.33	0.43
1:C:88:GLU:CG	1:C:88:GLU:O	2.59	0.43
1:C:184:VAL:HG12	1:C:185:LEU:CD1	2.48	0.43
1:E:5:SER:O	1:E:6:ARG:HB3	2.18	0.43
1:O:176:LEU:HA	1:O:176:LEU:HD13	1.82	0.43
1:P:82:ILE:HG23	1:P:121:LEU:HD13	2.00	0.43
1:G:172:ASN:OD1	1:G:176:LEU:HD23	2.17	0.43
1:A:54:TYR:HB3	1:A:63:ILE:HB	2.01	0.43
1:I:54:TYR:HB3	1:I:63:ILE:HB	2.01	0.43
1:C:60:ASP:CG	1:I:58:ARG:HH22	2.22	0.43
1:N:5:SER:O	1:N:6:ARG:HB3	2.17	0.43
1:S:27:THR:HG23	1:S:28:LYS:N	2.34	0.43
1:F:27:THR:HG23	1:F:28:LYS:N	2.34	0.43
1:T:24:ALA:C	1:T:26:LEU:H	2.22	0.43
1:I:6:ARG:CZ	1:Q:188:ARG:HE	2.31	0.43
1:M:54:TYR:HB3	1:M:63:ILE:HB	2.00	0.43
1:K:176:LEU:HA	1:K:176:LEU:HD13	1.89	0.43
1:G:204:LEU:HD11	1:H:118:ARG:HG3	2.01	0.43
1:O:24:ALA:HB2	1:O:185:LEU:HD11	2.00	0.43
1:S:26:LEU:HD12	1:S:27:THR:N	2.33	0.43
1:L:5:SER:O	1:L:6:ARG:HB3	2.19	0.43
1:M:12:PRO:HB2	1:N:120:SER:HB2	2.01	0.43
1:L:56:THR:CG2	1:L:57:LYS:N	2.82	0.43
1:S:24:ALA:C	1:S:26:LEU:H	2.22	0.43
1:H:166:LEU:HB3	1:H:171:ILE:HG13	2.00	0.43
1:P:54:TYR:HB3	1:P:63:ILE:HB	2.00	0.43
1:F:56:THR:CG2	1:F:57:LYS:N	2.82	0.43
1:M:24:ALA:C	1:M:26:LEU:H	2.23	0.43
1:C:56:THR:CG2	1:C:57:LYS:N	2.81	0.42
1:C:60:ASP:OD2	1:I:58:ARG:NH2	2.51	0.42
1:J:82:ILE:HG23	1:J:121:LEU:HD13	2.01	0.42
1:T:24:ALA:HA	1:T:25:PRO:HD3	1.72	0.42
1:S:64:LEU:HB3	1:S:76:THR:HB	2.01	0.42
1:G:26:LEU:HD12	1:G:27:THR:N	2.34	0.42
1:I:181:SER:OG	1:R:172:ASN:OD1	2.37	0.42
1:O:5:SER:O	1:O:6:ARG:HB3	2.19	0.42
1:F:118:ARG:HG3	1:J:204:LEU:HD11	2.00	0.42
1:M:26:LEU:HD12	1:M:27:THR:N	2.34	0.42
1:E:27:THR:HG23	1:E:28:LYS:N	2.35	0.42
1:I:65:ILE:HD11	1:I:98:THR:HG21	2.01	0.42
1:R:27:THR:HG23	1:R:28:LYS:N	2.34	0.42
1:R:56:THR:CG2	1:R:57:LYS:N	2.82	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:J:27:THR:HG23	1:J:28:LYS:N	2.35	0.42
1:K:82:ILE:HG23	1:K:121:LEU:HD13	2.00	0.42
1:K:120:SER:HB2	1:O:12:PRO:HB2	2.01	0.42
1:I:24:ALA:HB2	1:I:185:LEU:HD11	2.00	0.42
1:R:26:LEU:HD12	1:R:27:THR:N	2.33	0.42
1:N:82:ILE:HG23	1:N:121:LEU:HD13	2.01	0.42
1:N:26:LEU:HD12	1:N:27:THR:N	2.33	0.42
1:T:5:SER:O	1:T:6:ARG:HB3	2.19	0.42
1:H:54:TYR:HB3	1:H:63:ILE:HB	2.01	0.42
1:K:27:THR:HG23	1:K:28:LYS:N	2.33	0.42
1:T:27:THR:HG23	1:T:28:LYS:N	2.34	0.42
1:C:24:ALA:HB2	1:C:185:LEU:HD11	2.02	0.42
1:M:56:THR:CG2	1:M:57:LYS:N	2.83	0.42
1:H:26:LEU:HD12	1:H:27:THR:N	2.33	0.42
1:E:82:ILE:HG23	1:E:121:LEU:HD13	2.00	0.42
1:B:24:ALA:C	1:B:26:LEU:H	2.23	0.42
1:C:24:ALA:HA	1:C:25:PRO:HD3	1.72	0.42
1:Q:5:SER:O	1:Q:6:ARG:HB3	2.20	0.42
1:Q:27:THR:HG23	1:Q:28:LYS:N	2.35	0.42
1:Q:82:ILE:HG23	1:Q:121:LEU:HD13	2.02	0.42
1:R:204:LEU:HD11	1:S:118:ARG:HG3	2.01	0.42
1:C:5:SER:O	1:C:6:ARG:HB3	2.20	0.42
1:K:5:SER:O	1:K:6:ARG:HB3	2.20	0.42
1:L:27:THR:HG23	1:L:28:LYS:H	1.85	0.42
1:F:24:ALA:HB2	1:F:185:LEU:HD11	2.02	0.42
1:I:166:LEU:HB3	1:I:171:ILE:HG13	2.02	0.42
1:K:100:TRP:CH2	1:K:102:SER:HB2	2.55	0.42
1:L:155:ASP:OD2	1:M:118:ARG:NH1	2.49	0.42
1:J:166:LEU:HB3	1:J:171:ILE:HG13	2.01	0.41
1:C:204:LEU:HD11	1:D:118:ARG:HG3	2.01	0.41
1:A:184:VAL:HG12	1:A:185:LEU:CD1	2.50	0.41
1:L:54:TYR:HB3	1:L:63:ILE:HB	2.01	0.41
1:T:56:THR:CG2	1:T:57:LYS:N	2.83	0.41
1:O:24:ALA:C	1:O:26:LEU:H	2.24	0.41
1:T:24:ALA:HB2	1:T:185:LEU:HD11	2.02	0.41
1:P:166:LEU:HB3	1:P:171:ILE:HG13	2.02	0.41
1:N:24:ALA:HB2	1:N:185:LEU:HD11	2.02	0.41
1:L:62:GLU:OE1	1:L:62:GLU:HA	2.21	0.41
1:T:65:ILE:HD11	1:T:98:THR:HG21	2.02	0.41
1:H:27:THR:HG23	1:H:28:LYS:N	2.35	0.41
1:D:27:THR:HG23	1:D:28:LYS:N	2.33	0.41
1:Q:184:VAL:O	1:Q:185:LEU:HD12	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:82:ILE:HG23	1:L:121:LEU:HD13	2.02	0.41
1:C:64:LEU:HB3	1:C:76:THR:HB	2.03	0.41
1:D:24:ALA:C	1:D:26:LEU:H	2.23	0.41
1:D:24:ALA:HA	1:D:25:PRO:HD3	1.70	0.41
1:T:172:ASN:OD1	1:T:176:LEU:HD23	2.21	0.41
1:O:181:SER:HA	1:O:182:PRO:HD3	1.85	0.41
1:G:27:THR:HG23	1:G:28:LYS:N	2.35	0.41
1:I:82:ILE:HG23	1:I:121:LEU:HD13	2.02	0.41
1:C:166:LEU:HB3	1:C:171:ILE:HG13	2.02	0.41
1:N:181:SER:HA	1:N:182:PRO:HD3	1.80	0.41
1:M:5:SER:O	1:M:6:ARG:HB3	2.21	0.41
1:N:56:THR:HG22	1:N:57:LYS:N	2.36	0.41
1:L:166:LEU:HB3	1:L:171:ILE:HG13	2.03	0.41
1:E:24:ALA:HB2	1:E:185:LEU:HD11	2.03	0.41
1:A:195:GLN:HG3	4:A:213:HOH:O	2.20	0.41
1:Q:96:ILE:HG21	1:Q:96:ILE:HD13	1.78	0.41
1:Q:24:ALA:HA	1:Q:25:PRO:HD3	1.71	0.41
1:A:82:ILE:HG23	1:A:121:LEU:HD13	2.02	0.41
1:T:26:LEU:HD12	1:T:27:THR:N	2.35	0.41
1:G:24:ALA:HB2	1:G:185:LEU:HD11	2.03	0.41
1:H:24:ALA:HB2	1:H:185:LEU:HD11	2.03	0.41
1:A:204:LEU:HD11	1:B:118:ARG:HG3	2.02	0.41
1:G:176:LEU:HA	1:G:176:LEU:HD13	1.87	0.41
1:H:176:LEU:HA	1:H:176:LEU:HD13	1.88	0.41
1:F:82:ILE:HG23	1:F:121:LEU:HD13	2.02	0.41
1:O:166:LEU:HB3	1:O:171:ILE:HG13	2.03	0.41
1:P:184:VAL:HG12	1:P:185:LEU:CD1	2.50	0.41
1:C:172:ASN:OD1	1:C:176:LEU:HD23	2.21	0.41
1:S:176:LEU:HA	1:S:176:LEU:HD13	1.86	0.41
1:L:181:SER:HA	1:L:182:PRO:HD3	1.83	0.41
1:B:6:ARG:HH12	1:L:188:ARG:NE	2.18	0.40
1:F:82:ILE:CD1	1:F:107:VAL:HG21	2.45	0.40
1:L:24:ALA:C	1:L:26:LEU:H	2.24	0.40
1:B:24:ALA:HB2	1:B:185:LEU:HD11	2.03	0.40
1:G:5:SER:O	1:G:6:ARG:HB3	2.21	0.40
1:J:82:ILE:CD1	1:J:107:VAL:HG21	2.44	0.40
1:K:184:VAL:HG12	1:K:185:LEU:CD1	2.51	0.40
1:B:206:PRO:HB3	1:L:179:PRO:CB	2.50	0.40
1:I:181:SER:HA	1:I:182:PRO:HD3	1.82	0.40
1:E:65:ILE:HD11	1:E:98:THR:HG21	2.03	0.40
1:S:1:GLN:N	1:S:1:GLN:OE1	2.52	0.40
1:I:27:THR:HG23	1:I:28:LYS:N	2.36	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:P:82:ILE:CD1	1:P:107:VAL:HG21	2.47	0.40
1:Q:24:ALA:C	1:Q:26:LEU:H	2.24	0.40
1:J:24:ALA:HB2	1:J:185:LEU:HD11	2.03	0.40
1:O:12:PRO:HD2	4:O:207:HOH:O	2.21	0.40
1:J:1:GLN:OE1	1:J:1:GLN:N	2.50	0.40
1:I:176:LEU:HD13	1:I:176:LEU:HA	1.81	0.40
1:T:184:VAL:HG12	1:T:185:LEU:CD1	2.49	0.40
1:E:166:LEU:HB3	1:E:171:ILE:HG13	2.02	0.40
1:R:6:ARG:HD3	1:R:203:GLN:HG2	2.04	0.40
1:R:5:SER:O	1:R:6:ARG:HB3	2.22	0.40
1:G:62:GLU:OE1	1:G:62:GLU:HA	2.21	0.40
1:H:64:LEU:HB3	1:H:76:THR:HB	2.04	0.40
1:F:24:ALA:C	1:F:26:LEU:H	2.24	0.40
1:Q:65:ILE:HD11	1:Q:98:THR:HG21	2.03	0.40
1:N:172:ASN:OD1	1:N:176:LEU:HD23	2.21	0.40
1:S:6:ARG:HD3	1:S:203:GLN:HG2	2.04	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:147:GLU:OE2	1:E:28:LYS:NZ[1_556]	1.91	0.29
1:B:140:ASP:OD2	1:E:28:LYS:CE[1_556]	2.18	0.02

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	38	70
1	B	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51
1	C	204/206 (99%)	195 (96%)	7 (3%)	2 (1%)	22	51
1	D	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51
1	E	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51
1	G	204/206 (99%)	195 (96%)	7 (3%)	2 (1%)	22	51
1	H	204/206 (99%)	195 (96%)	8 (4%)	1 (0%)	38	70
1	I	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	38	70
1	J	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	38	70
1	K	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51
1	L	204/206 (99%)	195 (96%)	8 (4%)	1 (0%)	38	70
1	M	204/206 (99%)	195 (96%)	7 (3%)	2 (1%)	22	51
1	N	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51
1	O	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51
1	P	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	38	70
1	Q	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	38	70
1	R	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51
1	S	204/206 (99%)	196 (96%)	7 (3%)	1 (0%)	38	70
1	T	204/206 (99%)	196 (96%)	6 (3%)	2 (1%)	22	51
All	All	4080/4120 (99%)	3915 (96%)	133 (3%)	32 (1%)	27	58

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	178	GLY
1	G	178	GLY
1	M	178	GLY
1	O	178	GLY
1	T	178	GLY
1	D	178	GLY
1	E	142	PHE
1	F	142	PHE
1	H	142	PHE
1	J	142	PHE
1	L	142	PHE
1	R	142	PHE
1	R	178	GLY
1	T	142	PHE
1	B	142	PHE
1	C	142	PHE
1	D	142	PHE

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Mol	Chain	Res	Type
1	G	142	PHE
1	I	142	PHE
1	K	142	PHE
1	K	178	GLY
1	M	142	PHE
1	O	142	PHE
1	Q	142	PHE
1	A	178	GLY
1	F	178	GLY
1	N	142	PHE
1	S	178	GLY
1	B	178	GLY
1	N	178	GLY
1	P	178	GLY
1	C	178	GLY

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	180/180 (100%)	172 (96%)	8 (4%)	39	71
1	B	180/180 (100%)	172 (96%)	8 (4%)	39	71
1	C	180/180 (100%)	173 (96%)	7 (4%)	43	76
1	D	180/180 (100%)	172 (96%)	8 (4%)	39	71
1	E	180/180 (100%)	171 (95%)	9 (5%)	34	66
1	F	180/180 (100%)	171 (95%)	9 (5%)	34	66
1	G	180/180 (100%)	171 (95%)	9 (5%)	34	66
1	H	180/180 (100%)	171 (95%)	9 (5%)	34	66
1	I	180/180 (100%)	172 (96%)	8 (4%)	39	71
1	J	180/180 (100%)	171 (95%)	9 (5%)	34	66
1	K	180/180 (100%)	172 (96%)	8 (4%)	39	71
1	L	180/180 (100%)	172 (96%)	8 (4%)	39	71
1	M	180/180 (100%)	171 (95%)	9 (5%)	34	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	N	180/180 (100%)	171 (95%)	9 (5%)	34	66
1	O	180/180 (100%)	172 (96%)	8 (4%)	39	71
1	P	180/180 (100%)	171 (95%)	9 (5%)	34	66
1	Q	180/180 (100%)	172 (96%)	8 (4%)	39	71
1	R	180/180 (100%)	171 (95%)	9 (5%)	34	66
1	S	180/180 (100%)	173 (96%)	7 (4%)	43	76
1	T	180/180 (100%)	172 (96%)	8 (4%)	39	71
All	All	3600/3600 (100%)	3433 (95%)	167 (5%)	37	70

All (167) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LEU
1	A	26	LEU
1	A	38	HIS
1	A	74	SER
1	A	88	GLU
1	A	135	LEU
1	A	166	LEU
1	A	176	LEU
1	B	22	LEU
1	B	26	LEU
1	B	38	HIS
1	B	74	SER
1	B	88	GLU
1	B	135	LEU
1	B	166	LEU
1	B	176	LEU
1	C	22	LEU
1	C	26	LEU
1	C	38	HIS
1	C	74	SER
1	C	88	GLU
1	C	166	LEU
1	C	176	LEU
1	D	22	LEU
1	D	26	LEU
1	D	38	HIS
1	D	74	SER
1	D	88	GLU

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Mol	Chain	Res	Type
1	D	135	LEU
1	D	166	LEU
1	D	176	LEU
1	E	22	LEU
1	E	26	LEU
1	E	38	HIS
1	E	43	LEU
1	E	74	SER
1	E	88	GLU
1	E	135	LEU
1	E	166	LEU
1	E	176	LEU
1	F	22	LEU
1	F	26	LEU
1	F	38	HIS
1	F	43	LEU
1	F	74	SER
1	F	88	GLU
1	F	135	LEU
1	F	166	LEU
1	F	176	LEU
1	G	22	LEU
1	G	26	LEU
1	G	38	HIS
1	G	43	LEU
1	G	74	SER
1	G	88	GLU
1	G	135	LEU
1	G	166	LEU
1	G	176	LEU
1	H	22	LEU
1	H	26	LEU
1	H	38	HIS
1	H	43	LEU
1	H	74	SER
1	H	88	GLU
1	H	135	LEU
1	H	166	LEU
1	H	176	LEU
1	I	22	LEU
1	I	26	LEU
1	I	38	HIS

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Mol	Chain	Res	Type
1	I	43	LEU
1	I	74	SER
1	I	88	GLU
1	I	166	LEU
1	I	176	LEU
1	J	22	LEU
1	J	26	LEU
1	J	30	LEU
1	J	38	HIS
1	J	74	SER
1	J	88	GLU
1	J	135	LEU
1	J	166	LEU
1	J	176	LEU
1	K	22	LEU
1	K	26	LEU
1	K	38	HIS
1	K	74	SER
1	K	88	GLU
1	K	135	LEU
1	K	166	LEU
1	K	176	LEU
1	L	22	LEU
1	L	26	LEU
1	L	38	HIS
1	L	74	SER
1	L	88	GLU
1	L	135	LEU
1	L	166	LEU
1	L	176	LEU
1	M	22	LEU
1	M	26	LEU
1	M	38	HIS
1	M	43	LEU
1	M	74	SER
1	M	88	GLU
1	M	135	LEU
1	M	166	LEU
1	M	176	LEU
1	N	22	LEU
1	N	26	LEU
1	N	38	HIS

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Mol	Chain	Res	Type
1	N	43	LEU
1	N	74	SER
1	N	88	GLU
1	N	135	LEU
1	N	166	LEU
1	N	176	LEU
1	O	22	LEU
1	O	26	LEU
1	O	38	HIS
1	O	74	SER
1	O	88	GLU
1	O	135	LEU
1	O	166	LEU
1	O	176	LEU
1	P	22	LEU
1	P	26	LEU
1	P	38	HIS
1	P	74	SER
1	P	88	GLU
1	P	135	LEU
1	P	155	ASP
1	P	166	LEU
1	P	176	LEU
1	Q	22	LEU
1	Q	26	LEU
1	Q	38	HIS
1	Q	74	SER
1	Q	88	GLU
1	Q	135	LEU
1	Q	166	LEU
1	Q	176	LEU
1	R	22	LEU
1	R	26	LEU
1	R	38	HIS
1	R	43	LEU
1	R	74	SER
1	R	88	GLU
1	R	135	LEU
1	R	166	LEU
1	R	176	LEU
1	S	22	LEU
1	S	26	LEU

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Mol	Chain	Res	Type
1	S	38	HIS
1	S	74	SER
1	S	88	GLU
1	S	166	LEU
1	S	176	LEU
1	T	22	LEU
1	T	26	LEU
1	T	38	HIS
1	T	74	SER
1	T	88	GLU
1	T	135	LEU
1	T	166	LEU
1	T	176	LEU

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

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 60 ligands modelled in this entry, 40 are monoatomic - leaving 20 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
3	OPE	A	550	2	7,7,7	0.98	0	9,9,9	1.20	2 (22%)
3	OPE	B	950	2	7,7,7	1.02	0	9,9,9	0.94	0
3	OPE	C	650	2	7,7,7	0.96	0	9,9,9	1.18	1 (11%)
3	OPE	D	450	2	7,7,7	0.93	0	9,9,9	0.94	1 (11%)
3	OPE	E	350	2	7,7,7	0.91	0	9,9,9	1.09	0
3	OPE	F	7700	2	7,7,7	0.72	0	9,9,9	1.51	3 (33%)
3	OPE	G	8700	2	7,7,7	0.77	0	9,9,9	1.13	1 (11%)
3	OPE	H	5700	2	7,7,7	1.01	0	9,9,9	1.24	2 (22%)
3	OPE	I	800	2	7,7,7	0.79	0	9,9,9	1.17	1 (11%)
3	OPE	J	6700	2	7,7,7	0.79	0	9,9,9	1.11	1 (11%)
3	OPE	K	500	2	7,7,7	0.86	0	9,9,9	1.19	2 (22%)
3	OPE	L	300	2	7,7,7	1.00	0	9,9,9	1.25	2 (22%)
3	OPE	M	400	2	7,7,7	0.94	0	9,9,9	0.86	0
3	OPE	N	900	2	7,7,7	1.01	0	9,9,9	0.89	0
3	OPE	O	600	2	7,7,7	0.66	0	9,9,9	1.16	2 (22%)
3	OPE	P	700	2	7,7,7	1.00	1 (14%)	9,9,9	1.15	1 (11%)
3	OPE	Q	1700	2	7,7,7	0.86	0	9,9,9	1.51	2 (22%)
3	OPE	R	3700	2	7,7,7	0.73	0	9,9,9	1.09	1 (11%)
3	OPE	S	4700	2	7,7,7	0.79	0	9,9,9	1.09	2 (22%)
3	OPE	T	2700	2	7,7,7	0.86	0	9,9,9	1.21	1 (11%)

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
3	OPE	A	550	2	-	0/5/5/5	0/0/0/0
3	OPE	B	950	2	-	0/5/5/5	0/0/0/0
3	OPE	C	650	2	-	0/5/5/5	0/0/0/0
3	OPE	D	450	2	-	0/5/5/5	0/0/0/0
3	OPE	E	350	2	-	0/5/5/5	0/0/0/0
3	OPE	F	7700	2	-	0/5/5/5	0/0/0/0
3	OPE	G	8700	2	-	0/5/5/5	0/0/0/0
3	OPE	H	5700	2	-	0/5/5/5	0/0/0/0
3	OPE	I	800	2	-	0/5/5/5	0/0/0/0
3	OPE	J	6700	2	-	0/5/5/5	0/0/0/0
3	OPE	K	500	2	-	0/5/5/5	0/0/0/0
3	OPE	L	300	2	-	0/5/5/5	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OPE	M	400	2	-	0/5/5/5	0/0/0/0
3	OPE	N	900	2	-	0/5/5/5	0/0/0/0
3	OPE	O	600	2	-	0/5/5/5	0/0/0/0
3	OPE	P	700	2	-	0/5/5/5	0/0/0/0
3	OPE	Q	1700	2	-	0/5/5/5	0/0/0/0
3	OPE	R	3700	2	-	0/5/5/5	0/0/0/0
3	OPE	S	4700	2	-	0/5/5/5	0/0/0/0
3	OPE	T	2700	2	-	0/5/5/5	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	700	OPE	P-O3	-2.10	1.44	1.51

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	1700	OPE	O4-P-O3	2.87	115.13	106.71
3	P	700	OPE	O4-CA-CB	2.81	120.32	108.95
3	G	8700	OPE	O4-CA-CB	2.77	120.16	108.95
3	J	6700	OPE	O4-CA-CB	2.56	119.31	108.95
3	Q	1700	OPE	O4-CA-CB	2.55	119.25	108.95
3	I	800	OPE	O4-CA-CB	2.48	119.00	108.95
3	F	7700	OPE	O4-P-O3	2.47	113.95	106.71
3	T	2700	OPE	P-O4-CA	2.45	125.28	118.19
3	A	550	OPE	O4-CA-CB	2.45	118.85	108.95
3	A	550	OPE	O4-P-O3	2.37	113.67	106.71
3	L	300	OPE	P-O4-CA	2.37	125.06	118.19
3	L	300	OPE	O4-P-O3	2.37	113.65	106.71
3	D	450	OPE	O4-CA-CB	2.32	118.31	108.95
3	H	5700	OPE	O4-CA-CB	2.31	118.30	108.95
3	R	3700	OPE	O4-CA-CB	2.25	118.06	108.95
3	K	500	OPE	O4-CA-CB	2.24	118.02	108.95
3	F	7700	OPE	O4-CA-CB	2.23	117.96	108.95
3	O	600	OPE	O4-CA-CB	2.16	117.67	108.95
3	H	5700	OPE	O4-P-O3	2.14	112.98	106.71
3	S	4700	OPE	O4-CA-CB	2.13	117.55	108.95
3	F	7700	OPE	O2-P-O4	-2.12	100.80	106.65
3	O	600	OPE	O4-P-O3	2.10	112.85	106.71
3	S	4700	OPE	O4-P-O3	2.08	112.81	106.71
3	C	650	OPE	O4-CA-CB	2.07	117.31	108.95
3	K	500	OPE	O4-P-O3	2.04	112.69	106.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 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	206/206 (100%)	0.35	3 (1%) 70 75	34, 48, 83, 131	0
1	B	206/206 (100%)	0.44	5 (2%) 56 62	36, 48, 83, 133	0
1	C	206/206 (100%)	0.35	3 (1%) 70 75	35, 48, 80, 132	0
1	D	206/206 (100%)	0.35	3 (1%) 70 75	38, 49, 82, 133	0
1	E	206/206 (100%)	0.45	6 (2%) 49 55	34, 49, 83, 132	0
1	F	206/206 (100%)	0.41	10 (4%) 28 31	40, 54, 86, 132	0
1	G	206/206 (100%)	0.48	10 (4%) 28 31	38, 53, 86, 135	0
1	H	206/206 (100%)	0.36	2 (0%) 79 83	36, 48, 82, 131	0
1	I	206/206 (100%)	0.40	7 (3%) 43 48	36, 48, 81, 132	0
1	J	206/206 (100%)	0.39	4 (1%) 64 70	36, 49, 84, 133	0
1	K	206/206 (100%)	0.47	8 (3%) 37 42	40, 53, 84, 133	0
1	L	206/206 (100%)	0.38	5 (2%) 56 62	37, 51, 84, 133	0
1	M	206/206 (100%)	0.35	6 (2%) 49 55	38, 50, 83, 133	0
1	N	206/206 (100%)	0.34	2 (0%) 79 83	38, 50, 85, 133	0
1	O	206/206 (100%)	0.43	6 (2%) 49 55	37, 50, 83, 134	0
1	P	206/206 (100%)	0.37	3 (1%) 70 75	35, 47, 84, 133	0
1	Q	206/206 (100%)	0.59	9 (4%) 33 37	38, 52, 85, 135	0
1	R	206/206 (100%)	0.75	27 (13%) 4 4	42, 56, 88, 132	0
1	S	206/206 (100%)	0.26	4 (1%) 64 70	41, 53, 86, 133	0
1	T	206/206 (100%)	0.45	5 (2%) 56 62	35, 47, 80, 133	0
All	All	4120/4120 (100%)	0.42	128 (3%) 47 52	34, 50, 86, 135	0

All (128) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	54	TYR	5.5
1	Q	174	ILE	4.8
1	E	28	LYS	4.8
1	R	63	ILE	4.5
1	G	6	ARG	4.3
1	T	176	LEU	3.9
1	C	27	THR	3.6
1	R	64	LEU	3.4
1	G	127	VAL	3.4
1	B	27	THR	3.4
1	R	9	PHE	3.4
1	F	135	LEU	3.4
1	F	152	LEU	3.3
1	R	51	ILE	3.3
1	E	25	PRO	3.2
1	K	146	PHE	3.2
1	H	25	PRO	3.2
1	I	6	ARG	3.2
1	G	53	SER	3.1
1	C	88	GLU	3.1
1	R	77	VAL	3.1
1	Q	88	GLU	3.0
1	K	19	TYR	3.0
1	B	26	LEU	3.0
1	R	134	ILE	3.0
1	G	177	GLY	2.9
1	R	133	ILE	2.9
1	F	142	PHE	2.9
1	Q	26	LEU	2.9
1	E	6	ARG	2.8
1	O	152	LEU	2.8
1	F	58	ARG	2.8
1	O	177	GLY	2.8
1	G	55	ALA	2.8
1	S	27	THR	2.8
1	B	179	PRO	2.7
1	T	6	ARG	2.7
1	R	127	VAL	2.7
1	I	25	PRO	2.7
1	A	25	PRO	2.7
1	I	179	PRO	2.7
1	F	134	ILE	2.7
1	K	25	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	R	52	PHE	2.7
1	I	174	ILE	2.7
1	F	54	TYR	2.7
1	R	26	LEU	2.6
1	O	6	ARG	2.6
1	A	152	LEU	2.6
1	T	58	ARG	2.6
1	S	63	ILE	2.6
1	G	30	LEU	2.6
1	J	169	ASP	2.6
1	M	52	PHE	2.6
1	L	26	LEU	2.6
1	B	180	PHE	2.6
1	B	174	ILE	2.6
1	S	117	VAL	2.6
1	R	177	GLY	2.5
1	Q	134	ILE	2.5
1	R	65	ILE	2.5
1	M	63	ILE	2.5
1	O	55	ALA	2.5
1	P	25	PRO	2.5
1	F	156	ILE	2.5
1	Q	188	ARG	2.4
1	R	15	SER	2.4
1	K	63	ILE	2.4
1	E	176	LEU	2.4
1	R	91	VAL	2.4
1	R	62	GLU	2.4
1	R	60	ASP	2.4
1	K	135	LEU	2.4
1	F	9	PHE	2.4
1	M	156	ILE	2.4
1	R	53	SER	2.4
1	P	27	THR	2.4
1	R	141	SER	2.4
1	Q	19	TYR	2.4
1	O	58	ARG	2.3
1	H	152	LEU	2.3
1	O	176	LEU	2.3
1	F	55	ALA	2.3
1	T	156	ILE	2.3
1	T	25	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	26	LEU	2.3
1	Q	179	PRO	2.3
1	N	146	PHE	2.3
1	R	145	ASN	2.3
1	R	146	PHE	2.3
1	K	139	GLN	2.3
1	R	139	GLN	2.3
1	R	180	PHE	2.3
1	A	1	GLN	2.2
1	P	1	GLN	2.2
1	R	58	ARG	2.2
1	L	88	GLU	2.2
1	F	26	LEU	2.2
1	G	176	LEU	2.2
1	K	142	PHE	2.2
1	S	26	LEU	2.2
1	G	149	SER	2.2
1	E	27	THR	2.2
1	M	58	ARG	2.2
1	R	153	VAL	2.1
1	L	6	ARG	2.1
1	L	33	PHE	2.1
1	R	152	LEU	2.1
1	J	195	GLN	2.1
1	R	132	SER	2.1
1	G	64	LEU	2.1
1	I	26	LEU	2.1
1	L	27	THR	2.1
1	K	127	VAL	2.1
1	D	174	ILE	2.1
1	D	28	LYS	2.1
1	I	152	LEU	2.1
1	Q	180	PHE	2.1
1	G	134	ILE	2.1
1	E	26	LEU	2.1
1	D	25	PRO	2.0
1	M	125	TYR	2.0
1	J	179	PRO	2.0
1	J	135	LEU	2.0
1	Q	183	ASN	2.0
1	N	195	GLN	2.0
1	M	135	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	I	188	ARG	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	OPE	F	7700	8/8	0.26	1.10	62,72,85,100	0
3	OPE	C	650	8/8	0.23	0.55	36,42,65,65	0
3	OPE	I	800	8/8	0.21	0.51	37,47,59,61	0
2	CA	T	302	1/1	0.19	0.50	47,47,47,47	0
3	OPE	O	600	8/8	0.20	0.46	28,61,81,83	0
2	CA	A	301	1/1	0.18	0.31	47,47,47,47	0
3	OPE	T	2700	8/8	0.19	0.29	37,43,66,77	0
3	OPE	H	5700	8/8	0.20	0.10	37,44,55,91	0
2	CA	O	301	1/1	0.17	0.04	49,49,49,49	0
3	OPE	S	4700	8/8	0.22	0.03	27,61,65,92	0
3	OPE	M	400	8/8	0.18	0.00	42,46,56,62	0
3	OPE	Q	1700	8/8	0.20	-0.10	44,66,83,85	0
2	CA	T	301	1/1	0.18	-0.14	43,43,43,43	0
3	OPE	D	450	8/8	0.20	-0.15	33,40,55,60	0
3	OPE	G	8700	8/8	0.21	-0.17	53,59,85,89	0
3	OPE	N	900	8/8	0.17	-0.42	37,52,63,73	0
2	CA	O	302	1/1	0.15	-0.42	59,59,59,59	0
2	CA	Q	302	1/1	0.18	-0.48	66,66,66,66	0
3	OPE	A	550	8/8	0.17	-0.49	28,42,51,54	0
3	OPE	P	700	8/8	0.19	-0.50	22,36,55,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	OPE	B	950	8/8	0.18	-0.57	30,37,50,50	0
2	CA	J	302	1/1	0.17	-0.58	54,54,54,54	0
2	CA	A	302	1/1	0.17	-0.63	53,53,53,53	0
2	CA	D	301	1/1	0.16	-0.73	48,48,48,48	0
3	OPE	E	350	8/8	0.17	-0.74	37,55,75,76	0
2	CA	J	301	1/1	0.17	-0.83	52,52,52,52	0
2	CA	D	302	1/1	0.15	-0.86	46,46,46,46	0
3	OPE	J	6700	8/8	0.17	-0.91	31,51,59,59	0
2	CA	F	301	1/1	0.15	-1.04	67,67,67,67	0
3	OPE	L	300	8/8	0.18	-1.07	38,60,80,85	0
2	CA	E	302	1/1	0.15	-1.08	46,46,46,46	0
2	CA	B	302	1/1	0.12	-1.09	39,39,39,39	0
3	OPE	K	500	8/8	0.15	-1.19	46,67,81,92	0
2	CA	H	301	1/1	0.15	-1.20	46,46,46,46	0
2	CA	N	302	1/1	0.15	-1.22	44,44,44,44	0
2	CA	H	302	1/1	0.15	-1.28	47,47,47,47	0
2	CA	C	301	1/1	0.16	-1.35	42,42,42,42	0
2	CA	P	301	1/1	0.15	-1.46	39,39,39,39	0
2	CA	S	301	1/1	0.12	-1.52	50,50,50,50	0
2	CA	I	301	1/1	0.14	-1.52	44,44,44,44	0
2	CA	G	301	1/1	0.13	-1.53	56,56,56,56	0
2	CA	M	302	1/1	0.17	-1.66	53,53,53,53	0
2	CA	Q	301	1/1	0.15	-1.66	49,49,49,49	0
2	CA	L	301	1/1	0.12	-1.74	50,50,50,50	0
2	CA	I	302	1/1	0.13	-1.89	54,54,54,54	0
3	OPE	R	3700	8/8	0.14	-1.94	61,84,119,122	0
2	CA	N	301	1/1	0.15	-1.97	43,43,43,43	0
2	CA	K	301	1/1	0.09	-2.21	69,69,69,69	0
2	CA	P	302	1/1	0.15	-2.32	41,41,41,41	0
2	CA	C	302	1/1	0.18	-2.44	43,43,43,43	0
2	CA	S	302	1/1	0.14	-2.44	57,57,57,57	0
2	CA	K	302	1/1	0.09	-2.56	72,72,72,72	0
2	CA	M	301	1/1	0.16	-2.73	49,49,49,49	0
2	CA	G	302	1/1	0.10	-3.04	71,71,71,71	0
2	CA	R	302	1/1	0.10	-3.18	80,80,80,80	0
2	CA	F	302	1/1	0.14	-3.61	86,86,86,86	0
2	CA	R	301	1/1	0.06	-3.63	87,87,87,87	0
2	CA	E	301	1/1	0.14	-4.47	47,47,47,47	0
2	CA	L	302	1/1	0.14	-5.72	53,53,53,53	0
2	CA	B	301	1/1	0.12	-5.76	41,41,41,41	0

6.5 Other polymers ⓘ

There are no such residues in this entry.