



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 31, 2023 – 05:21 PM EDT

PDB ID : 3KQZ
Title : Structure of a protease 2
Authors : McGowan, S.; Whisstock, J.C.
Deposited on : 2009-11-17
Resolution : 2.39 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

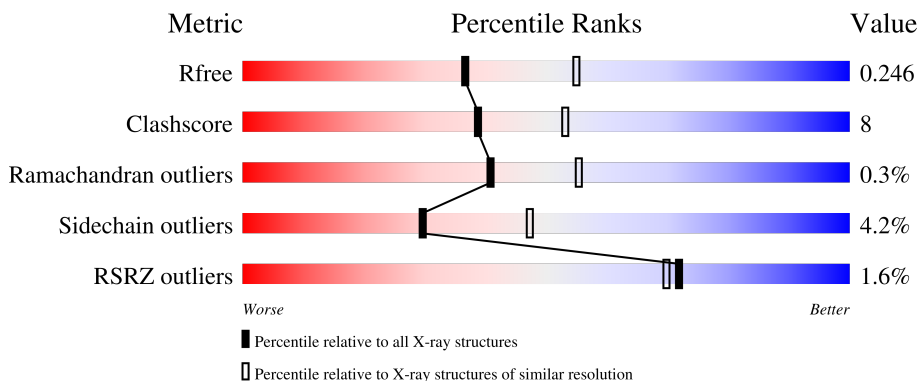
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	528	 81% 15% ..
1	B	528	 79% 17% ..
1	C	528	 83% 13% ..
1	D	528	 82% 15% ..
1	E	528	 79% 16% ..

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Mol	Chain	Length	Quality of chain
1	F	528	
1	G	528	
1	H	528	
1	I	528	
1	J	528	
1	K	528	
1	L	528	

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
4	SO4	K	18	-	-	X	-
5	1PE	L	25	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 50062 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 M17 leucyl aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	514	3941	2534	632	756	19	0	0	0
1	B	510	3867	2489	624	735	19	0	0	0
1	C	518	3952	2542	638	753	19	0	0	0
1	D	514	3931	2532	633	746	20	0	0	0
1	E	509	3888	2506	622	741	19	0	0	0
1	F	510	3798	2445	612	722	19	0	0	0
1	G	514	3945	2536	632	758	19	0	0	0
1	H	510	3866	2488	624	735	19	0	0	0
1	I	515	3930	2529	633	749	19	0	0	0
1	J	514	3931	2532	633	746	20	0	0	0
1	K	509	3891	2507	624	741	19	0	0	0
1	L	508	3809	2450	613	727	19	0	0	0

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	152	GLN	ASN	engineered mutation	UNP Q8IL11
A	515	GLN	ASN	engineered mutation	UNP Q8IL11
A	546	GLN	ASN	engineered mutation	UNP Q8IL11
A	606	HIS	-	expression tag	UNP Q8IL11
A	607	HIS	-	expression tag	UNP Q8IL11

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Chain	Residue	Modelled	Actual	Comment	Reference
A	608	HIS	-	expression tag	UNP Q8IL11
A	609	HIS	-	expression tag	UNP Q8IL11
A	610	HIS	-	expression tag	UNP Q8IL11
A	611	HIS	-	expression tag	UNP Q8IL11
B	152	GLN	ASN	engineered mutation	UNP Q8IL11
B	515	GLN	ASN	engineered mutation	UNP Q8IL11
B	546	GLN	ASN	engineered mutation	UNP Q8IL11
B	606	HIS	-	expression tag	UNP Q8IL11
B	607	HIS	-	expression tag	UNP Q8IL11
B	608	HIS	-	expression tag	UNP Q8IL11
B	609	HIS	-	expression tag	UNP Q8IL11
B	610	HIS	-	expression tag	UNP Q8IL11
B	611	HIS	-	expression tag	UNP Q8IL11
C	152	GLN	ASN	engineered mutation	UNP Q8IL11
C	515	GLN	ASN	engineered mutation	UNP Q8IL11
C	546	GLN	ASN	engineered mutation	UNP Q8IL11
C	606	HIS	-	expression tag	UNP Q8IL11
C	607	HIS	-	expression tag	UNP Q8IL11
C	608	HIS	-	expression tag	UNP Q8IL11
C	609	HIS	-	expression tag	UNP Q8IL11
C	610	HIS	-	expression tag	UNP Q8IL11
C	611	HIS	-	expression tag	UNP Q8IL11
D	152	GLN	ASN	engineered mutation	UNP Q8IL11
D	515	GLN	ASN	engineered mutation	UNP Q8IL11
D	546	GLN	ASN	engineered mutation	UNP Q8IL11
D	606	HIS	-	expression tag	UNP Q8IL11
D	607	HIS	-	expression tag	UNP Q8IL11
D	608	HIS	-	expression tag	UNP Q8IL11
D	609	HIS	-	expression tag	UNP Q8IL11
D	610	HIS	-	expression tag	UNP Q8IL11
D	611	HIS	-	expression tag	UNP Q8IL11
E	152	GLN	ASN	engineered mutation	UNP Q8IL11
E	515	GLN	ASN	engineered mutation	UNP Q8IL11
E	546	GLN	ASN	engineered mutation	UNP Q8IL11
E	606	HIS	-	expression tag	UNP Q8IL11
E	607	HIS	-	expression tag	UNP Q8IL11
E	608	HIS	-	expression tag	UNP Q8IL11
E	609	HIS	-	expression tag	UNP Q8IL11
E	610	HIS	-	expression tag	UNP Q8IL11
E	611	HIS	-	expression tag	UNP Q8IL11
F	152	GLN	ASN	engineered mutation	UNP Q8IL11
F	515	GLN	ASN	engineered mutation	UNP Q8IL11

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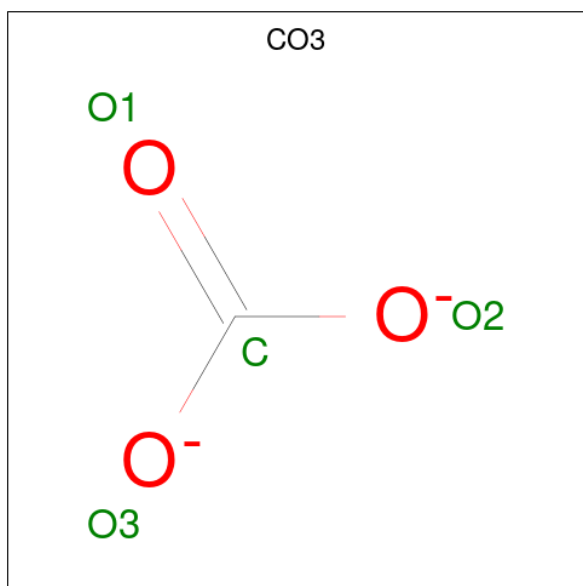
Chain	Residue	Modelled	Actual	Comment	Reference
F	546	GLN	ASN	engineered mutation	UNP Q8IL11
F	606	HIS	-	expression tag	UNP Q8IL11
F	607	HIS	-	expression tag	UNP Q8IL11
F	608	HIS	-	expression tag	UNP Q8IL11
F	609	HIS	-	expression tag	UNP Q8IL11
F	610	HIS	-	expression tag	UNP Q8IL11
F	611	HIS	-	expression tag	UNP Q8IL11
G	152	GLN	ASN	engineered mutation	UNP Q8IL11
G	515	GLN	ASN	engineered mutation	UNP Q8IL11
G	546	GLN	ASN	engineered mutation	UNP Q8IL11
G	606	HIS	-	expression tag	UNP Q8IL11
G	607	HIS	-	expression tag	UNP Q8IL11
G	608	HIS	-	expression tag	UNP Q8IL11
G	609	HIS	-	expression tag	UNP Q8IL11
G	610	HIS	-	expression tag	UNP Q8IL11
G	611	HIS	-	expression tag	UNP Q8IL11
H	152	GLN	ASN	engineered mutation	UNP Q8IL11
H	515	GLN	ASN	engineered mutation	UNP Q8IL11
H	546	GLN	ASN	engineered mutation	UNP Q8IL11
H	606	HIS	-	expression tag	UNP Q8IL11
H	607	HIS	-	expression tag	UNP Q8IL11
H	608	HIS	-	expression tag	UNP Q8IL11
H	609	HIS	-	expression tag	UNP Q8IL11
H	610	HIS	-	expression tag	UNP Q8IL11
H	611	HIS	-	expression tag	UNP Q8IL11
I	152	GLN	ASN	engineered mutation	UNP Q8IL11
I	515	GLN	ASN	engineered mutation	UNP Q8IL11
I	546	GLN	ASN	engineered mutation	UNP Q8IL11
I	606	HIS	-	expression tag	UNP Q8IL11
I	607	HIS	-	expression tag	UNP Q8IL11
I	608	HIS	-	expression tag	UNP Q8IL11
I	609	HIS	-	expression tag	UNP Q8IL11
I	610	HIS	-	expression tag	UNP Q8IL11
I	611	HIS	-	expression tag	UNP Q8IL11
J	152	GLN	ASN	engineered mutation	UNP Q8IL11
J	515	GLN	ASN	engineered mutation	UNP Q8IL11
J	546	GLN	ASN	engineered mutation	UNP Q8IL11
J	606	HIS	-	expression tag	UNP Q8IL11
J	607	HIS	-	expression tag	UNP Q8IL11
J	608	HIS	-	expression tag	UNP Q8IL11
J	609	HIS	-	expression tag	UNP Q8IL11
J	610	HIS	-	expression tag	UNP Q8IL11

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Chain	Residue	Modelled	Actual	Comment	Reference
J	611	HIS	-	expression tag	UNP Q8IL11
K	152	GLN	ASN	engineered mutation	UNP Q8IL11
K	515	GLN	ASN	engineered mutation	UNP Q8IL11
K	546	GLN	ASN	engineered mutation	UNP Q8IL11
K	606	HIS	-	expression tag	UNP Q8IL11
K	607	HIS	-	expression tag	UNP Q8IL11
K	608	HIS	-	expression tag	UNP Q8IL11
K	609	HIS	-	expression tag	UNP Q8IL11
K	610	HIS	-	expression tag	UNP Q8IL11
K	611	HIS	-	expression tag	UNP Q8IL11
L	152	GLN	ASN	engineered mutation	UNP Q8IL11
L	515	GLN	ASN	engineered mutation	UNP Q8IL11
L	546	GLN	ASN	engineered mutation	UNP Q8IL11
L	606	HIS	-	expression tag	UNP Q8IL11
L	607	HIS	-	expression tag	UNP Q8IL11
L	608	HIS	-	expression tag	UNP Q8IL11
L	609	HIS	-	expression tag	UNP Q8IL11
L	610	HIS	-	expression tag	UNP Q8IL11
L	611	HIS	-	expression tag	UNP Q8IL11

- Molecule 2 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	1	3		
2	B	1	Total	C	O	0	0
			4	1	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total C O 4 1 3	0	0
2	D	1	Total C O 4 1 3	0	0
2	E	1	Total C O 4 1 3	0	0
2	F	1	Total C O 4 1 3	0	0
2	G	1	Total C O 4 1 3	0	0
2	H	1	Total C O 4 1 3	0	0
2	I	1	Total C O 4 1 3	0	0
2	J	1	Total C O 4 1 3	0	0
2	K	1	Total C O 4 1 3	0	0
2	L	1	Total C O 4 1 3	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

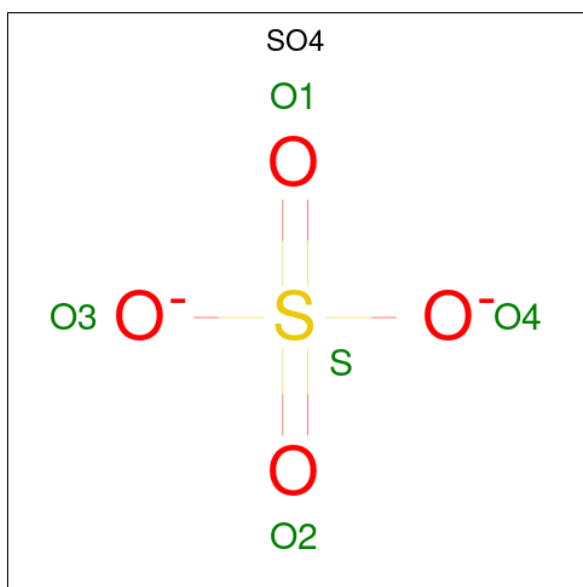
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Zn 2 2	0	0
3	B	2	Total Zn 2 2	0	0
3	C	2	Total Zn 2 2	0	0
3	D	2	Total Zn 2 2	0	0
3	E	2	Total Zn 2 2	0	0
3	F	2	Total Zn 2 2	0	0
3	G	2	Total Zn 2 2	0	0
3	H	2	Total Zn 2 2	0	0
3	I	2	Total Zn 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	2	Total	Zn	0	0
			2	2		
3	K	2	Total	Zn	0	0
			2	2		
3	L	2	Total	Zn	0	0
			2	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



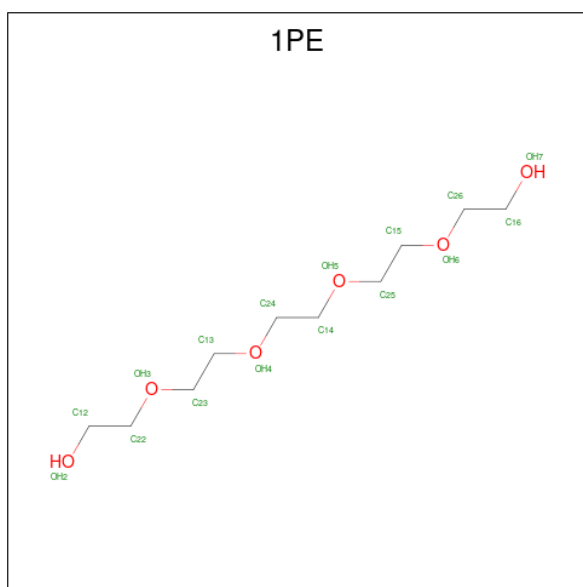
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	C	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	H	1	5	4	1	0	0
4	I	1	5	4	1	0	0
4	I	1	5	4	1	0	0
4	J	1	5	4	1	0	0
4	K	1	5	4	1	0	0
4	K	1	5	4	1	0	0
4	K	1	5	4	1	0	0
4	K	1	5	4	1	0	0
4	K	1	5	4	1	0	0

- Molecule 5 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			9	6	3		
5	A	1	Total	C	O	0	0
			12	8	4		
5	A	1	Total	C	O	0	0
			9	6	3		
5	A	1	Total	C	O	0	0
			6	4	2		
5	B	1	Total	C	O	0	0
			11	7	4		
5	C	1	Total	C	O	0	0
			13	9	4		
5	C	1	Total	C	O	0	0
			9	6	3		
5	C	1	Total	C	O	0	0
			8	5	3		
5	D	1	Total	C	O	0	0
			10	7	3		
5	D	1	Total	C	O	0	0
			9	6	3		
5	D	1	Total	C	O	0	0
			11	8	3		
5	D	1	Total	C	O	0	0
			10	6	4		
5	D	1	Total	C	O	0	0
			11	8	3		
5	D	1	Total	C	O	0	0
			5	3	2		

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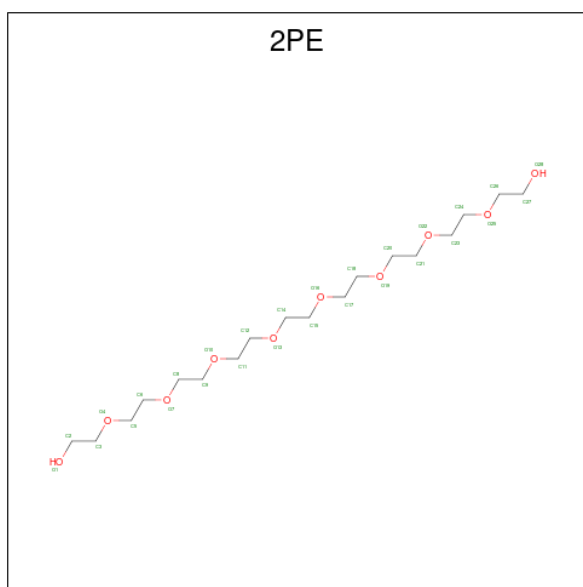
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	E	1	Total	C	O	0	0
			12	8	4		
5	E	1	Total	C	O	0	0
			12	8	4		
5	E	1	Total	C	O	0	0
			11	7	4		
5	E	1	Total	C	O	0	0
			10	6	4		
5	E	1	Total	C	O	0	0
			8	5	3		
5	E	1	Total	C	O	0	0
			9	6	3		
5	F	1	Total	C	O	0	0
			10	6	4		
5	F	1	Total	C	O	0	0
			10	6	4		
5	F	1	Total	C	O	0	0
			10	6	4		
5	F	1	Total	C	O	0	0
			12	8	4		
5	G	1	Total	C	O	0	0
			9	6	3		
5	G	1	Total	C	O	0	0
			10	6	4		
5	G	1	Total	C	O	0	0
			7	4	3		
5	G	1	Total	C	O	0	0
			6	4	2		
5	G	1	Total	C	O	0	0
			6	4	2		
5	G	1	Total	C	O	0	0
			15	10	5		
5	H	1	Total	C	O	0	0
			6	4	2		
5	I	1	Total	C	O	0	0
			15	10	5		
5	I	1	Total	C	O	0	0
			11	8	3		
5	I	1	Total	C	O	0	0
			9	6	3		
5	I	1	Total	C	O	0	0
			5	3	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	J	1	Total	C	O	0	0
			11	7	4		
5	J	1	Total	C	O	0	0
			10	6	4		
5	J	1	Total	C	O	0	0
			12	8	4		
5	J	1	Total	C	O	0	0
			11	8	3		
5	J	1	Total	C	O	0	0
			11	7	4		
5	J	1	Total	C	O	0	0
			9	6	3		
5	K	1	Total	C	O	0	0
			11	7	4		
5	K	1	Total	C	O	0	0
			12	8	4		
5	K	1	Total	C	O	0	0
			12	8	4		
5	K	1	Total	C	O	0	0
			11	7	4		
5	K	1	Total	C	O	0	0
			6	4	2		
5	K	1	Total	C	O	0	0
			11	7	4		
5	K	1	Total	C	O	0	0
			8	5	3		
5	L	1	Total	C	O	0	0
			10	6	4		
5	L	1	Total	C	O	0	0
			12	8	4		
5	L	1	Total	C	O	0	0
			10	6	4		
5	L	1	Total	C	O	0	0
			11	7	4		
5	L	1	Total	C	O	0	0
			12	8	4		

- Molecule 6 is NONAETHYLENE GLYCOL (three-letter code: 2PE) (formula: C₁₈H₃₈O₁₀).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 26 17 9	0	0
6	F	1	Total C O 6 4 2	0	0
6	H	1	Total C O 25 16 9	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	224	Total O 224 224	0	0
7	B	180	Total O 180 180	0	0
7	C	242	Total O 242 242	0	0
7	D	249	Total O 249 249	0	0
7	E	257	Total O 257 257	0	0
7	F	156	Total O 156 156	0	0
7	G	230	Total O 230 230	0	0
7	H	163	Total O 163 163	0	0
7	I	180	Total O 180 180	0	0

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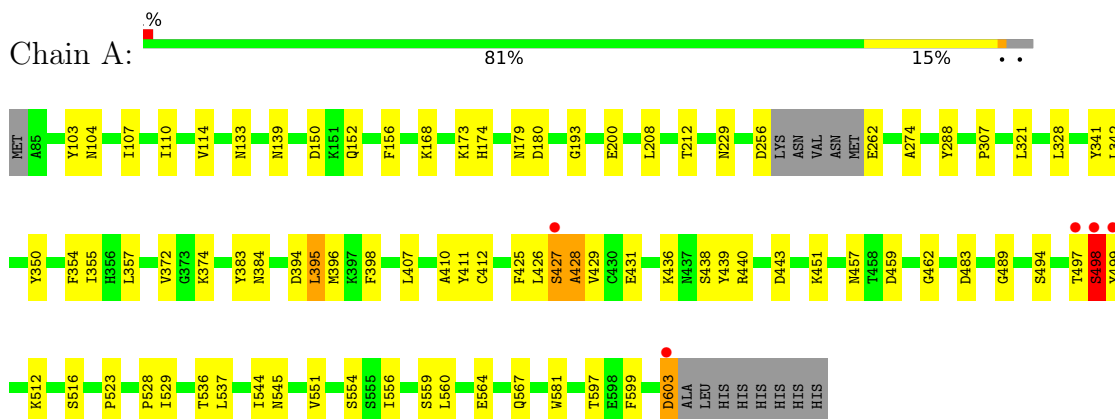
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	J	219	Total 219	O 219	0	0
7	K	237	Total 237	O 237	0	0
7	L	186	Total 186	O 186	0	0

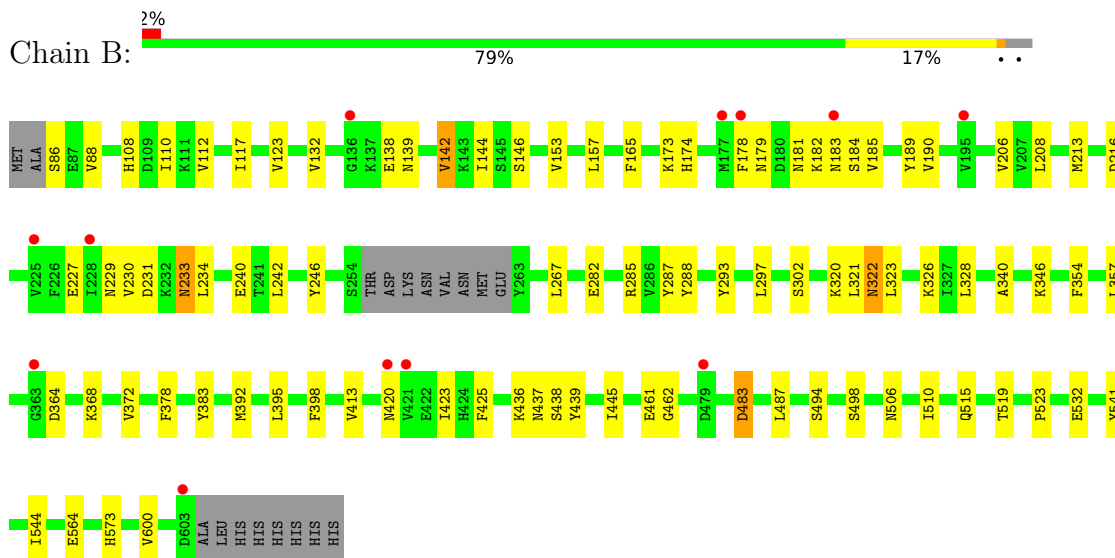
3 Residue-property plots [i](#)

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

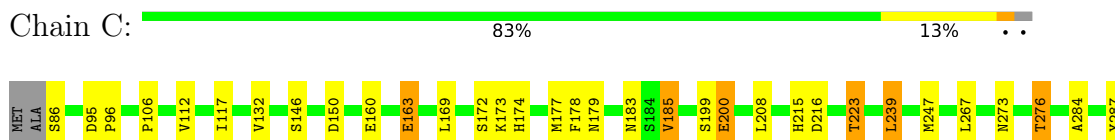
- Molecule 1: M17 leucyl aminopeptidase

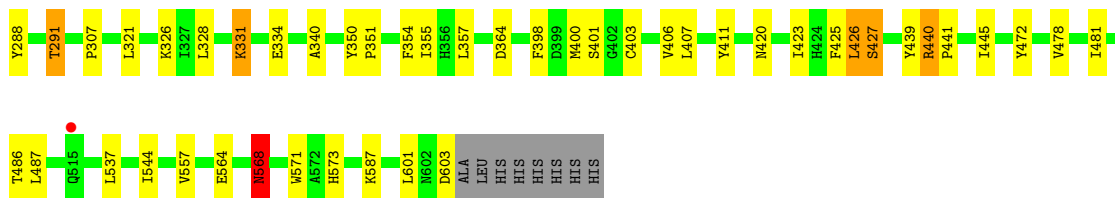


- Molecule 1: M17 leucyl aminopeptidase

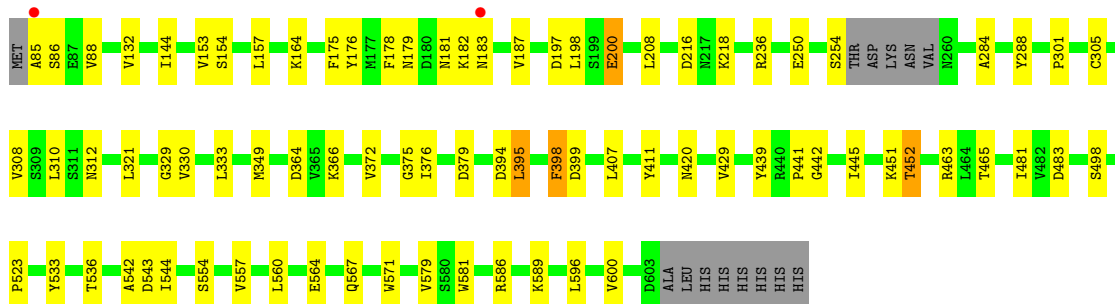
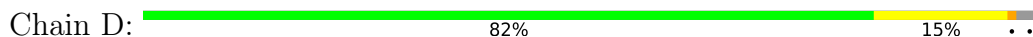


- Molecule 1: M17 leucyl aminopeptidase

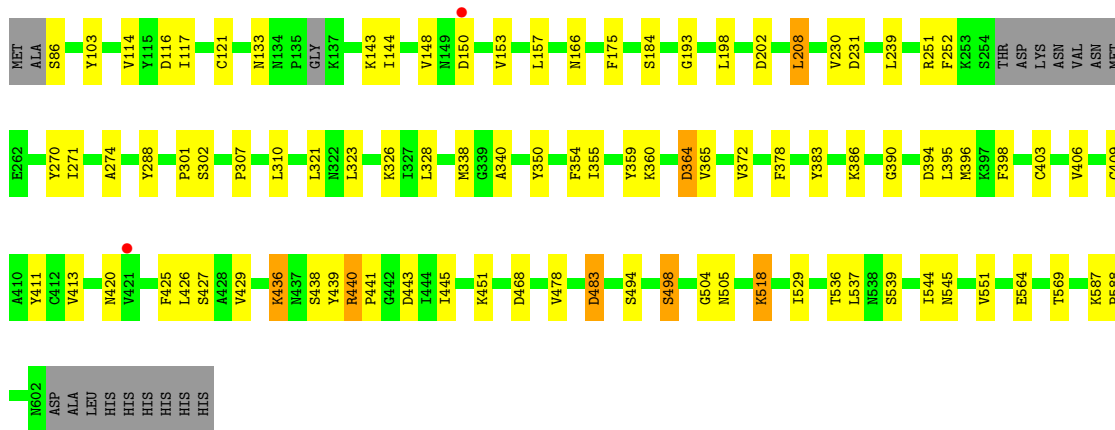
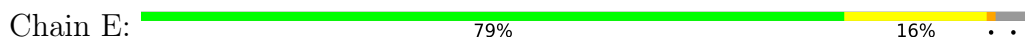




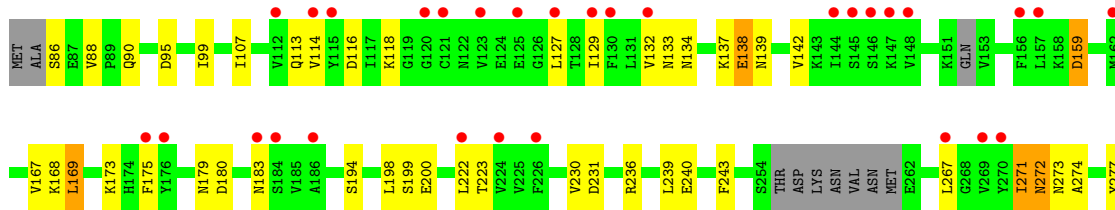
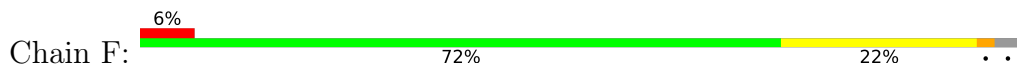
● Molecule 1: M17 leucyl aminopeptidase



● Molecule 1: M17 leucyl aminopeptidase



● Molecule 1: M17 leucyl aminopeptidase

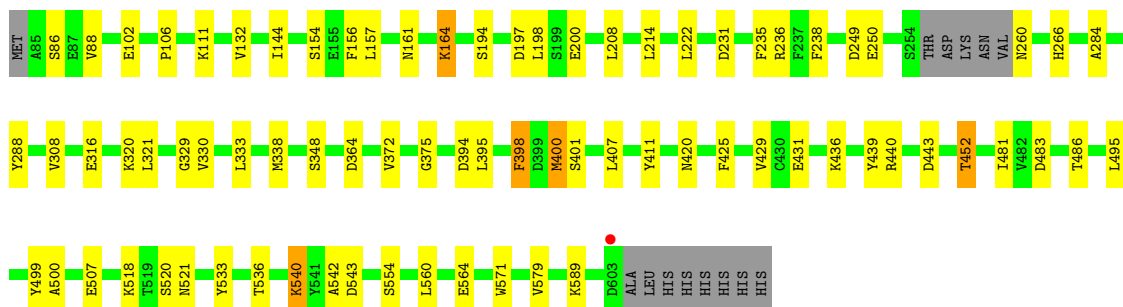
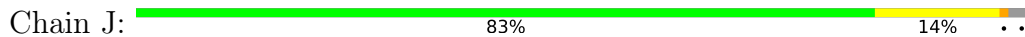


● Molecule 1: M17 leucyl aminopeptidase

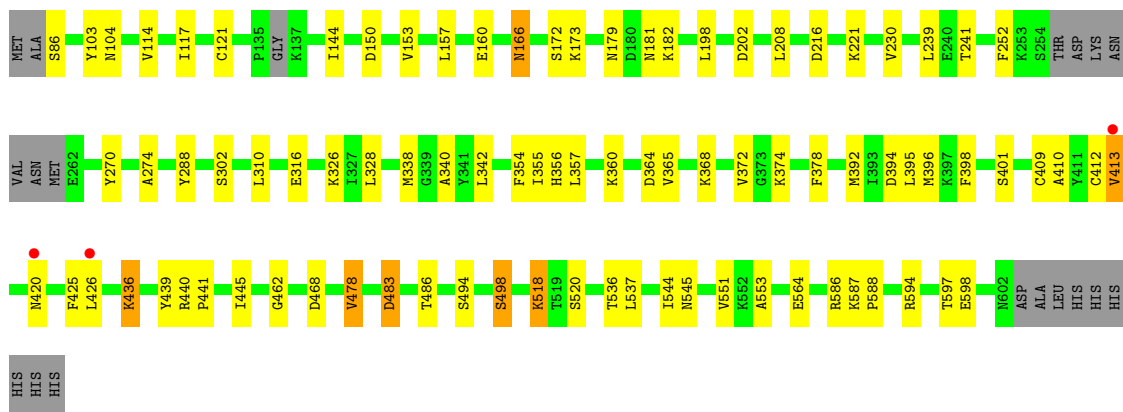




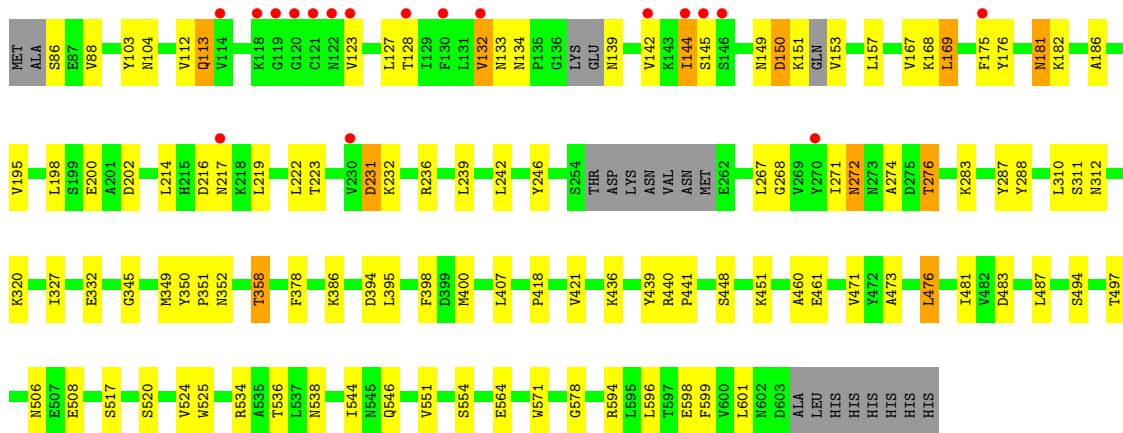
• Molecule 1: M17 leucyl aminopeptidase



• Molecule 1: M17 leucyl aminopeptidase



• Molecule 1: M17 leucyl aminopeptidase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	171.70Å 173.73Å 220.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.08 – 2.39 56.08 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.1 (56.08-2.39) 99.1 (56.08-2.39)	Depositor EDS
R_{merge}	0.37	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.40Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.176 , 0.242 0.182 , 0.246	Depositor DCC
R_{free} test set	12914 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	30.3	Xtrriage
Anisotropy	0.420	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	50062	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.05 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0488e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 1PE, 2PE, CO3, SO4

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	0.84	0/4017	0.81	2/5448 (0.0%)
1	B	0.78	0/3944	0.79	0/5357
1	C	0.85	0/4030	0.79	0/5469
1	D	0.87	0/4008	0.83	2/5435 (0.0%)
1	E	0.89	0/3964	0.83	1/5378 (0.0%)
1	F	0.82	0/3874	0.86	2/5273 (0.0%)
1	G	0.83	0/4022	0.79	2/5455 (0.0%)
1	H	0.76	0/3943	0.77	1/5356 (0.0%)
1	I	0.84	0/4007	0.81	0/5437
1	J	0.88	0/4008	0.82	1/5435 (0.0%)
1	K	0.89	1/3967 (0.0%)	0.81	1/5382 (0.0%)
1	L	0.87	1/3883 (0.0%)	0.87	0/5279
All	All	0.84	2/47667 (0.0%)	0.81	12/64704 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	461	GLU	CD-OE1	5.98	1.32	1.25
1	K	121	CYS	CB-SG	-5.31	1.73	1.81

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	594	ARG	NE-CZ-NH2	-5.93	117.34	120.30
1	D	463	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	D	586	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	H	399	ASP	CB-CG-OD2	5.77	123.49	118.30
1	F	169	LEU	CA-CB-CG	5.42	127.77	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3941	0	3868	73	0
1	B	3867	0	3762	61	1
1	C	3952	0	3877	52	0
1	D	3931	0	3866	56	1
1	E	3888	0	3810	65	0
1	F	3798	0	3614	95	0
1	G	3945	0	3873	48	0
1	H	3866	0	3760	53	1
1	I	3930	0	3855	39	0
1	J	3931	0	3866	57	0
1	K	3891	0	3816	74	0
1	L	3809	0	3651	79	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
2	E	4	0	0	0	0
2	F	4	0	0	0	0
2	G	4	0	0	0	0
2	H	4	0	0	0	0
2	I	4	0	0	0	0
2	J	4	0	0	0	0
2	K	4	0	0	0	0
2	L	4	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0
3	I	2	0	0	0	0
3	J	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	2	0	0	0	0
3	L	2	0	0	0	0
4	A	10	0	0	1	0
4	B	15	0	0	1	0
4	C	20	0	0	0	0
4	D	15	0	0	1	0
4	E	15	0	0	2	0
4	F	5	0	0	1	0
4	G	10	0	0	0	0
4	H	5	0	0	0	0
4	I	10	0	0	1	0
4	J	5	0	0	0	0
4	K	25	0	0	4	0
5	A	36	0	36	7	0
5	B	11	0	12	1	0
5	C	30	0	32	2	0
5	D	56	0	60	2	0
5	E	62	0	71	3	0
5	F	42	0	51	5	0
5	G	53	0	59	6	0
5	H	6	0	4	2	0
5	I	40	0	45	3	0
5	J	64	0	74	10	0
5	K	71	0	76	10	0
5	L	55	0	66	15	0
6	B	26	0	33	2	0
6	F	6	0	4	0	0
6	H	25	0	33	1	0
7	A	224	0	0	7	0
7	B	180	0	0	1	1
7	C	242	0	0	5	0
7	D	249	0	0	4	0
7	E	257	0	0	3	0
7	F	156	0	0	7	0
7	G	230	0	0	7	0
7	H	163	0	0	5	0
7	I	180	0	0	3	0
7	J	219	0	0	6	0
7	K	237	0	0	9	0
7	L	186	0	0	10	0
All	All	50062	0	46274	705	2

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 8.

The worst 5 of 705 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:K:395:LEU:HB2	5:K:55:1PE:OH6	1.26	1.31
1:B:216:ASP:CB	1:F:173:LYS:NZ	2.11	1.14
1:F:138:GLU:N	1:F:139:ASN:HA	1.50	1.14
1:J:452:THR:HG22	1:J:543:ASP:H	1.17	1.08
1:D:452:THR:HG22	1:D:543:ASP:H	1.18	1.08

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	Interatomic distance (Å)	Clash overlap (Å)
1:B:322:ASN:ND2	1:H:322:ASN:ND2[2_664]	1.92	0.28
1:D:366:LYS:CE	7:B:895:HOH:O[4_455]	2.06	0.14

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	510/528 (97%)	495 (97%)	12 (2%)	3 (1%)	25 36
1	B	506/528 (96%)	482 (95%)	24 (5%)	0	100 100
1	C	516/528 (98%)	496 (96%)	18 (4%)	2 (0%)	34 48
1	D	510/528 (97%)	491 (96%)	19 (4%)	0	100 100
1	E	503/528 (95%)	480 (95%)	23 (5%)	0	100 100
1	F	504/528 (96%)	473 (94%)	24 (5%)	7 (1%)	11 15
1	G	510/528 (97%)	497 (98%)	11 (2%)	2 (0%)	34 48
1	H	506/528 (96%)	485 (96%)	21 (4%)	0	100 100
1	I	511/528 (97%)	501 (98%)	10 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	510/528 (97%)	494 (97%)	16 (3%)	0	100	100
1	K	503/528 (95%)	487 (97%)	16 (3%)	0	100	100
1	L	500/528 (95%)	476 (95%)	19 (4%)	5 (1%)	15	23
All	All	6089/6336 (96%)	5857 (96%)	213 (4%)	19 (0%)	41	55

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	427	SER
1	F	272	ASN
1	G	427	SER
1	L	272	ASN
1	A	498	SER

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	420/455 (92%)	411 (98%)	9 (2%)	53	72
1	B	405/455 (89%)	393 (97%)	12 (3%)	41	61
1	C	419/455 (92%)	395 (94%)	24 (6%)	20	33
1	D	416/455 (91%)	398 (96%)	18 (4%)	29	46
1	E	412/455 (90%)	395 (96%)	17 (4%)	30	48
1	F	385/455 (85%)	360 (94%)	25 (6%)	17	27
1	G	421/455 (92%)	413 (98%)	8 (2%)	57	75
1	H	405/455 (89%)	392 (97%)	13 (3%)	39	59
1	I	417/455 (92%)	393 (94%)	24 (6%)	20	32
1	J	416/455 (91%)	399 (96%)	17 (4%)	30	48
1	K	413/455 (91%)	397 (96%)	16 (4%)	32	50
1	L	391/455 (86%)	365 (93%)	26 (7%)	16	26
All	All	4920/5460 (90%)	4711 (96%)	209 (4%)	30	47

5 of 209 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	142	VAL
1	I	407	LEU
1	L	358	THR
1	H	229	ASN
1	I	185	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	183	ASN
1	L	322	ASN
1	J	139	ASN
1	L	134	ASN
1	I	113	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 119 ligands modelled in this entry, 24 are monoatomic - leaving 95 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
5	1PE	A	24	-	8,8,15	0.68	0	7,7,14	0.99	0
5	1PE	H	51	-	5,5,15	0.86	0	4,4,14	0.69	0
4	SO4	E	28	-	4,4,4	0.36	0	6,6,6	0.35	0
5	1PE	E	612	-	10,10,15	0.52	0	9,9,14	0.31	0
5	1PE	E	43	-	7,7,15	0.58	0	6,6,14	0.39	0
5	1PE	G	58	-	14,14,15	0.65	0	13,13,14	0.62	0
4	SO4	K	30	-	4,4,4	0.17	0	6,6,6	0.53	0
5	1PE	L	59	-	11,11,15	0.81	0	10,10,14	0.84	0
4	SO4	J	32	-	4,4,4	0.20	0	6,6,6	0.45	0
4	SO4	B	12	-	4,4,4	0.28	0	6,6,6	0.26	0
2	CO3	B	1002	-	2,3,3	0.44	0	2,3,3	0.24	0
5	1PE	K	55	-	7,7,15	0.50	0	6,6,14	0.50	0
5	1PE	C	41	-	7,7,15	0.89	0	6,6,14	0.82	0
5	1PE	K	36	-	10,10,15	0.80	0	9,9,14	0.70	0
6	2PE	B	14	-	25,25,27	0.53	0	24,24,26	0.33	0
5	1PE	A	57	-	5,5,15	0.76	0	4,4,14	0.46	0
4	SO4	B	3	-	4,4,4	0.16	0	6,6,6	0.75	0
5	1PE	A	20	-	11,11,15	0.90	0	10,10,14	0.85	0
5	1PE	A	19	-	8,8,15	0.56	0	7,7,14	0.65	0
4	SO4	K	20	-	4,4,4	0.16	0	6,6,6	0.29	0
2	CO3	C	1002	-	2,3,3	0.35	0	2,3,3	0.77	0
5	1PE	B	40	-	10,10,15	0.56	0	9,9,14	0.95	0
5	1PE	G	16	-	9,9,15	0.66	0	8,8,14	0.83	0
5	1PE	C	18	-	8,8,15	0.69	0	7,7,14	0.72	0
5	1PE	K	4	-	11,11,15	0.74	0	10,10,14	0.86	0
2	CO3	D	1002	-	2,3,3	0.29	0	2,3,3	1.27	0
5	1PE	D	62	-	4,4,15	0.81	0	3,3,14	0.27	0
5	1PE	D	23	-	10,10,15	0.69	0	9,9,14	0.89	0
5	1PE	F	612	-	9,9,15	0.63	0	8,8,14	0.70	0
5	1PE	L	25	-	11,11,15	0.51	0	10,10,14	0.39	0
5	1PE	D	612	-	8,8,15	0.83	0	7,7,14	0.81	0
5	1PE	G	48	-	5,5,15	0.70	0	4,4,14	0.77	0
2	CO3	J	1002	-	2,3,3	0.37	0	2,3,3	2.12	1 (50%)
5	1PE	E	7	-	11,11,15	0.72	0	10,10,14	0.67	0
5	1PE	J	49	-	10,10,15	0.56	0	9,9,14	0.39	0
5	1PE	E	46	-	8,8,15	0.61	0	7,7,14	0.59	0
5	1PE	I	27	-	8,8,15	0.75	0	7,7,14	0.61	0
5	1PE	J	15	-	11,11,15	0.58	0	10,10,14	1.10	1 (10%)
2	CO3	I	1002	-	2,3,3	0.41	0	2,3,3	0.81	0
5	1PE	K	52	-	10,10,15	0.64	0	9,9,14	0.50	0
2	CO3	L	1002	-	2,3,3	0.63	0	2,3,3	1.41	0
4	SO4	D	10	-	4,4,4	0.15	0	6,6,6	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	E	11	-	4,4,4	0.12	0	6,6,6	0.22	0
5	1PE	D	9	-	9,9,15	0.61	0	8,8,14	0.52	0
5	1PE	L	56	-	10,10,15	0.67	0	9,9,14	0.37	0
5	1PE	E	35	-	9,9,15	0.54	0	8,8,14	0.23	0
4	SO4	A	2	-	4,4,4	0.07	0	6,6,6	0.42	0
5	1PE	G	12	-	8,8,15	0.70	0	7,7,14	0.62	0
5	1PE	D	44	-	10,10,15	0.72	0	9,9,14	0.66	0
5	1PE	K	5	-	11,11,15	0.60	0	10,10,14	0.37	0
5	1PE	I	21	-	14,14,15	0.66	0	13,13,14	0.57	0
4	SO4	D	5	-	4,4,4	0.10	0	6,6,6	0.55	0
2	CO3	H	1002	-	2,3,3	0.45	0	2,3,3	0.24	0
4	SO4	D	7	-	4,4,4	0.36	0	6,6,6	0.18	0
4	SO4	G	23	-	4,4,4	0.17	0	6,6,6	0.38	0
5	1PE	G	30	-	6,6,15	0.40	0	5,5,14	0.65	0
4	SO4	K	18	-	4,4,4	0.44	0	6,6,6	0.45	0
5	1PE	F	32	-	9,9,15	0.63	0	8,8,14	0.31	0
4	SO4	I	34	-	4,4,4	0.36	0	6,6,6	0.64	0
2	CO3	F	1002	-	2,3,3	0.66	0	2,3,3	1.73	1 (50%)
5	1PE	J	2	-	10,10,15	0.63	0	9,9,14	0.57	0
4	SO4	I	17	-	4,4,4	0.34	0	6,6,6	0.56	0
4	SO4	B	29	-	4,4,4	0.22	0	6,6,6	0.48	0
4	SO4	G	27	-	4,4,4	0.13	0	6,6,6	0.75	0
4	SO4	E	25	-	4,4,4	0.22	0	6,6,6	0.39	0
4	SO4	K	19	-	4,4,4	0.24	0	6,6,6	0.32	0
2	CO3	E	1002	-	2,3,3	0.70	0	2,3,3	1.24	0
4	SO4	C	24	-	4,4,4	0.14	0	6,6,6	0.31	0
5	1PE	J	60	-	8,8,15	0.73	0	7,7,14	0.59	0
4	SO4	K	31	-	4,4,4	0.19	0	6,6,6	0.28	0
5	1PE	F	31	-	9,9,15	0.61	0	8,8,14	0.59	0
4	SO4	C	15	-	4,4,4	0.13	0	6,6,6	0.37	0
4	SO4	C	16	-	4,4,4	0.14	0	6,6,6	0.43	0
4	SO4	F	33	-	4,4,4	0.40	0	6,6,6	0.34	0
5	1PE	L	29	-	9,9,15	0.42	0	8,8,14	0.50	0
5	1PE	E	8	-	11,11,15	0.64	0	10,10,14	0.49	0
6	2PE	H	6	-	24,24,27	0.47	0	23,23,26	0.44	0
4	SO4	A	1	-	4,4,4	0.15	0	6,6,6	0.43	0
5	1PE	L	1	-	9,9,15	0.54	0	8,8,14	0.47	0
5	1PE	I	22	-	10,10,15	0.76	0	9,9,14	0.60	0
5	1PE	D	34	-	9,9,15	0.52	0	8,8,14	0.58	0
5	1PE	G	47	-	5,5,15	0.52	0	4,4,14	0.31	0
5	1PE	I	61	-	4,4,15	0.53	0	3,3,14	0.46	0
5	1PE	K	42	-	10,10,15	0.62	0	9,9,14	0.37	0
2	CO3	A	1002	-	2,3,3	0.59	0	2,3,3	1.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	1PE	J	3	-	9,9,15	0.65	0	8,8,14	0.56	0
5	1PE	C	17	-	12,12,15	0.71	0	11,11,14	0.50	0
2	CO3	G	1002	-	2,3,3	0.52	0	2,3,3	1.67	1 (50%)
5	1PE	F	53	-	11,11,15	0.74	0	10,10,14	0.43	0
4	SO4	H	26	-	4,4,4	0.18	0	6,6,6	0.49	0
6	2PE	F	63	-	5,5,27	1.03	0	4,4,26	1.07	0
4	SO4	C	6	-	4,4,4	0.33	0	6,6,6	0.27	0
5	1PE	K	50	-	5,5,15	0.55	0	4,4,14	0.25	0
2	CO3	K	1002	-	2,3,3	0.41	0	2,3,3	2.22	2 (100%)
5	1PE	J	45	-	10,10,15	0.65	0	9,9,14	0.47	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	1PE	D	44	-	-	1/8/8/13	-
5	1PE	K	4	-	-	4/9/9/13	-
5	1PE	A	24	-	-	5/6/6/13	-
5	1PE	D	62	-	-	2/2/2/13	-
5	1PE	D	23	-	-	2/8/8/13	-
5	1PE	H	51	-	-	1/3/3/13	-
5	1PE	F	31	-	-	5/7/7/13	-
5	1PE	K	5	-	-	1/9/9/13	-
5	1PE	F	612	-	-	6/7/7/13	-
5	1PE	E	612	-	-	4/8/8/13	-
5	1PE	I	21	-	-	6/12/12/13	-
5	1PE	L	25	-	-	4/9/9/13	-
5	1PE	D	612	-	-	6/6/6/13	-
5	1PE	E	43	-	-	1/5/5/13	-
5	1PE	L	29	-	-	4/7/7/13	-
5	1PE	G	48	-	-	2/3/3/13	-
5	1PE	E	8	-	-	2/9/9/13	-
5	1PE	G	58	-	-	3/12/12/13	-
5	1PE	E	7	-	-	2/9/9/13	-
5	1PE	L	59	-	-	5/9/9/13	-
6	2PE	H	6	-	-	13/22/22/25	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	1PE	J	45	-	-	6/8/8/13	-
5	1PE	J	49	-	-	4/8/8/13	-
5	1PE	E	46	-	-	2/6/6/13	-
5	1PE	G	30	-	-	3/4/4/13	-
5	1PE	I	27	-	-	1/6/6/13	-
5	1PE	J	15	-	-	3/9/9/13	-
5	1PE	F	32	-	-	2/7/7/13	-
5	1PE	L	1	-	-	3/7/7/13	-
5	1PE	I	22	-	-	3/8/8/13	-
5	1PE	D	34	-	-	2/7/7/13	-
5	1PE	G	47	-	-	2/3/3/13	-
5	1PE	I	61	-	-	1/2/2/13	-
5	1PE	K	42	-	-	2/8/8/13	-
5	1PE	K	52	-	-	6/8/8/13	-
5	1PE	K	55	-	-	4/5/5/13	-
5	1PE	J	2	-	-	4/8/8/13	-
5	1PE	C	41	-	-	1/5/5/13	-
5	1PE	K	36	-	-	5/8/8/13	-
5	1PE	J	3	-	-	4/7/7/13	-
5	1PE	C	17	-	-	5/10/10/13	-
5	1PE	D	9	-	-	6/7/7/13	-
5	1PE	A	57	-	-	3/3/3/13	-
5	1PE	A	20	-	-	4/9/9/13	-
5	1PE	A	19	-	-	2/6/6/13	-
5	1PE	F	53	-	-	8/9/9/13	-
6	2PE	B	14	-	-	9/23/23/25	-
5	1PE	C	18	-	-	4/6/6/13	-
5	1PE	L	56	-	-	2/8/8/13	-
6	2PE	F	63	-	-	2/3/3/25	-
5	1PE	B	40	-	-	4/8/8/13	-
5	1PE	K	50	-	-	3/3/3/13	-
5	1PE	G	16	-	-	3/7/7/13	-
5	1PE	E	35	-	-	4/7/7/13	-
5	1PE	J	60	-	-	5/6/6/13	-
5	1PE	G	12	-	-	6/6/6/13	-

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	1002	CO3	O3-C-O1	2.76	126.70	119.55
5	J	15	1PE	OH4-C13-C23	-2.30	100.00	110.39
2	K	1002	CO3	O2-C-O1	-2.30	113.58	119.55
2	F	1002	CO3	O3-C-O1	2.29	125.50	119.55
2	G	1002	CO3	O2-C-O1	2.25	125.39	119.55

There are no chirality outliers.

5 of 207 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	59	1PE	C13-C23-OH3-C22
5	L	59	1PE	C15-C25-OH5-C14
5	K	52	1PE	C24-C14-OH5-C25
5	A	19	1PE	OH4-C13-C23-OH3
5	J	15	1PE	OH4-C13-C23-OH3

There are no ring outliers.

44 monomers are involved in 80 short contacts:

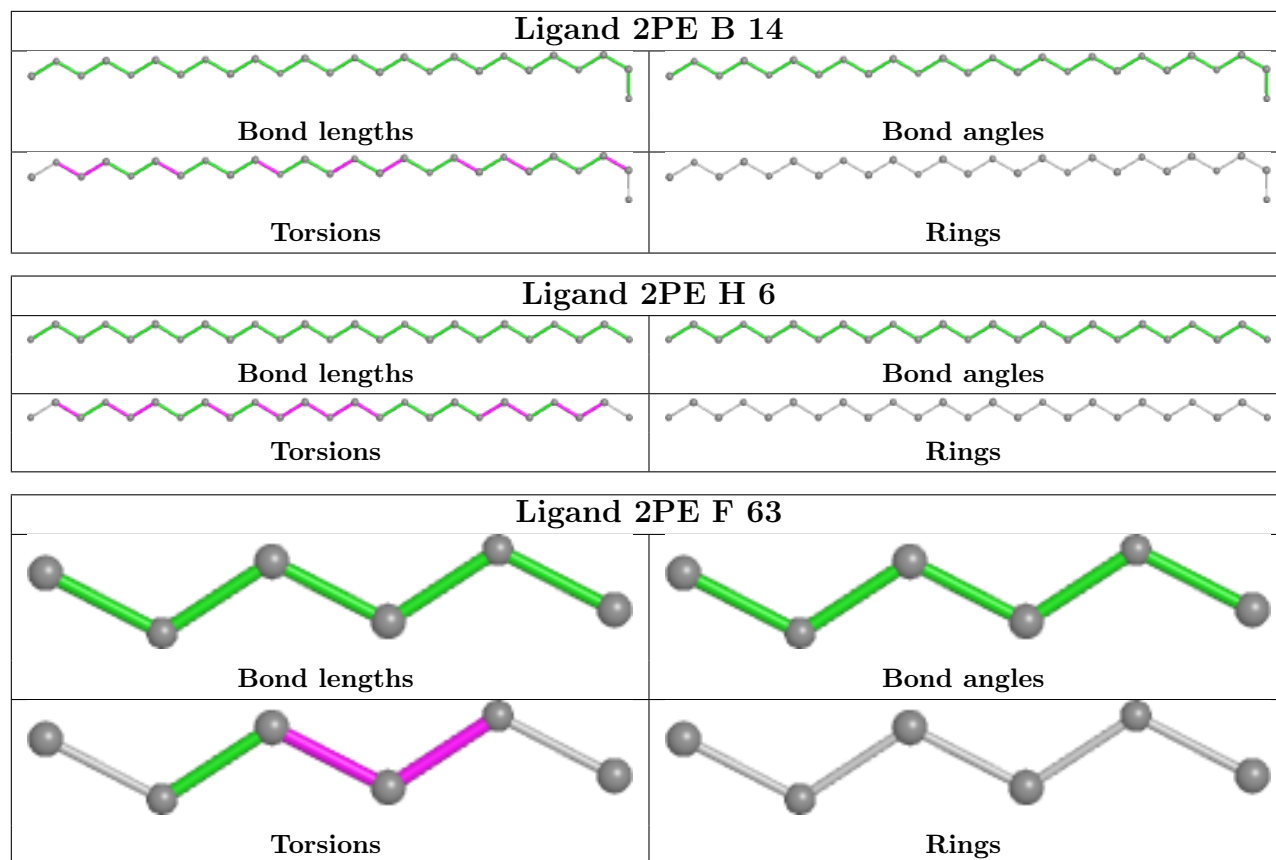
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	24	1PE	4	0
5	H	51	1PE	2	0
4	E	28	SO4	1	0
5	E	612	1PE	1	0
5	G	58	1PE	2	0
5	K	55	1PE	4	0
5	K	36	1PE	1	0
6	B	14	2PE	2	0
5	A	57	1PE	2	0
4	B	3	SO4	1	0
5	A	20	1PE	1	0
4	K	20	SO4	1	0
5	B	40	1PE	1	0
5	G	16	1PE	1	0
5	C	18	1PE	2	0
5	K	4	1PE	1	0
5	F	612	1PE	4	0
5	L	25	1PE	10	0
5	G	48	1PE	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	K	52	1PE	3	0
5	L	56	1PE	2	0
5	E	35	1PE	2	0
5	G	12	1PE	1	0
5	D	44	1PE	1	0
5	I	21	1PE	2	0
4	D	7	SO4	1	0
4	K	18	SO4	2	0
5	J	2	1PE	2	0
4	I	17	SO4	1	0
4	E	25	SO4	1	0
4	K	19	SO4	1	0
5	J	60	1PE	2	0
4	F	33	SO4	1	0
5	L	29	1PE	1	0
6	H	6	2PE	1	0
4	A	1	SO4	1	0
5	L	1	1PE	2	0
5	D	34	1PE	1	0
5	G	47	1PE	1	0
5	I	61	1PE	1	0
5	J	3	1PE	4	0
5	F	53	1PE	1	0
5	K	50	1PE	1	0
5	J	45	1PE	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	514/528 (97%)	-0.17	5 (0%) 82 80	20, 30, 52, 74	0
1	B	510/528 (96%)	0.04	12 (2%) 59 57	20, 35, 79, 99	1 (0%)
1	C	518/528 (98%)	-0.10	1 (0%) 95 94	19, 30, 58, 68	0
1	D	514/528 (97%)	-0.20	2 (0%) 92 91	19, 30, 50, 67	0
1	E	509/528 (96%)	-0.22	2 (0%) 92 91	19, 28, 44, 61	0
1	F	510/528 (96%)	0.10	31 (6%) 21 20	20, 36, 73, 82	0
1	G	514/528 (97%)	-0.15	3 (0%) 89 88	20, 29, 51, 72	0
1	H	510/528 (96%)	0.03	12 (2%) 59 57	21, 36, 80, 102	1 (0%)
1	I	515/528 (97%)	0.04	11 (2%) 63 61	19, 32, 63, 76	0
1	J	514/528 (97%)	-0.23	1 (0%) 95 94	19, 29, 51, 68	0
1	K	509/528 (96%)	-0.20	3 (0%) 89 88	19, 29, 48, 68	0
1	L	508/528 (96%)	0.02	18 (3%) 44 43	18, 31, 64, 80	0
All	All	6145/6336 (96%)	-0.09	101 (1%) 72 70	18, 31, 64, 102	2 (0%)

The worst 5 of 101 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	128	THR	5.0
1	F	156	PHE	4.9
1	F	123	VAL	4.8
1	F	114	VAL	4.6
1	L	119	GLY	4.6

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	C	16	5/5	0.71	0.36	94,103,106,110	0
4	SO4	E	11	5/5	0.74	0.24	105,107,109,112	0
5	1PE	F	53	12/16	0.80	0.17	64,70,81,85	0
6	2PE	F	63	6/28	0.80	0.34	31,41,53,57	0
5	1PE	I	27	9/16	0.81	0.31	38,42,50,52	0
5	1PE	D	612	9/16	0.82	0.19	46,54,69,75	0
5	1PE	K	55	8/16	0.83	0.26	46,68,77,84	0
5	1PE	A	57	6/16	0.83	0.20	31,44,52,54	0
5	1PE	K	52	11/16	0.84	0.19	57,63,73,74	0
5	1PE	A	20	12/16	0.85	0.17	32,50,57,57	0
5	1PE	H	51	6/16	0.86	0.26	29,45,54,56	0
5	1PE	J	3	10/16	0.87	0.17	43,49,52,52	0
5	1PE	D	62	5/16	0.87	0.25	35,41,56,66	0
5	1PE	J	45	11/16	0.88	0.22	40,56,73,77	0
5	1PE	L	59	12/16	0.88	0.26	34,50,60,60	0
5	1PE	D	44	11/16	0.88	0.24	38,56,64,65	0
5	1PE	E	46	9/16	0.89	0.21	30,43,55,56	0
5	1PE	F	31	10/16	0.89	0.16	35,44,53,55	0
5	1PE	J	60	9/16	0.89	0.17	38,48,56,58	0
5	1PE	K	4	12/16	0.89	0.16	33,46,57,60	0
5	1PE	F	32	10/16	0.89	0.17	44,63,69,73	0
5	1PE	D	34	10/16	0.89	0.16	45,56,64,64	0
5	1PE	B	40	11/16	0.89	0.24	35,50,57,58	0
5	1PE	A	24	9/16	0.89	0.29	29,41,53,61	0
5	1PE	G	16	10/16	0.90	0.26	29,40,63,63	0
5	1PE	G	58	15/16	0.90	0.16	39,49,60,63	0
4	SO4	B	12	5/5	0.90	0.23	75,79,85,86	0
5	1PE	C	41	8/16	0.90	0.23	23,43,46,48	0
5	1PE	F	612	10/16	0.91	0.18	31,44,57,61	0
5	1PE	J	49	11/16	0.91	0.26	43,74,78,80	0
5	1PE	J	15	12/16	0.92	0.31	24,36,58,61	0
5	1PE	I	22	11/16	0.92	0.17	33,46,57,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	1PE	E	7	12/16	0.92	0.18	40,49,56,57	0
5	1PE	G	48	6/16	0.92	0.12	30,35,38,48	0
6	2PE	B	14	26/28	0.92	0.15	36,57,77,82	0
5	1PE	K	36	11/16	0.92	0.22	33,42,55,56	0
5	1PE	E	8	12/16	0.93	0.15	33,41,51,51	0
5	1PE	L	56	11/16	0.93	0.17	44,58,76,77	0
5	1PE	E	35	10/16	0.93	0.15	48,59,65,66	0
5	1PE	K	50	6/16	0.93	0.13	53,55,56,58	0
5	1PE	C	17	13/16	0.93	0.17	33,47,60,60	0
5	1PE	G	47	6/16	0.94	0.16	39,47,50,61	0
5	1PE	A	19	9/16	0.94	0.13	17,39,41,52	0
4	SO4	D	5	5/5	0.94	0.14	60,60,65,67	0
5	1PE	L	29	10/16	0.94	0.14	44,56,65,68	0
5	1PE	G	12	9/16	0.94	0.16	23,31,44,46	0
5	1PE	I	21	15/16	0.94	0.20	30,51,64,69	0
5	1PE	D	23	11/16	0.94	0.25	18,35,45,47	0
5	1PE	G	30	7/16	0.94	0.30	45,56,62,66	0
6	2PE	H	6	25/28	0.94	0.14	33,62,78,83	0
5	1PE	J	2	11/16	0.95	0.21	29,44,63,75	0
5	1PE	L	1	10/16	0.95	0.16	19,38,54,60	0
5	1PE	L	25	12/16	0.95	0.14	32,43,49,52	0
5	1PE	C	18	9/16	0.95	0.11	28,34,47,48	0
4	SO4	C	15	5/5	0.95	0.12	73,74,78,79	0
5	1PE	K	5	12/16	0.95	0.17	23,35,58,59	0
5	1PE	K	42	11/16	0.95	0.17	39,42,58,63	0
4	SO4	K	30	5/5	0.95	0.10	63,67,74,75	0
5	1PE	E	612	11/16	0.95	0.17	31,38,55,55	0
5	1PE	D	9	10/16	0.96	0.14	30,44,52,54	0
4	SO4	E	28	5/5	0.96	0.15	54,56,64,72	0
5	1PE	E	43	8/16	0.96	0.15	42,50,55,58	0
4	SO4	K	31	5/5	0.97	0.12	48,60,63,64	0
2	CO3	F	1002	4/4	0.97	0.13	24,25,26,29	0
4	SO4	D	10	5/5	0.97	0.13	52,58,67,71	0
4	SO4	B	29	5/5	0.97	0.13	52,62,71,72	0
2	CO3	H	1002	4/4	0.97	0.12	25,26,26,26	0
4	SO4	K	20	5/5	0.97	0.13	56,65,70,76	0
2	CO3	J	1002	4/4	0.97	0.14	19,21,22,23	0
2	CO3	A	1002	4/4	0.98	0.12	29,30,30,31	0
2	CO3	G	1002	4/4	0.98	0.15	26,28,29,32	0
2	CO3	B	1002	4/4	0.98	0.19	25,25,26,28	0
4	SO4	C	24	5/5	0.98	0.16	54,62,62,64	0
2	CO3	C	1002	4/4	0.98	0.14	27,29,30,32	0

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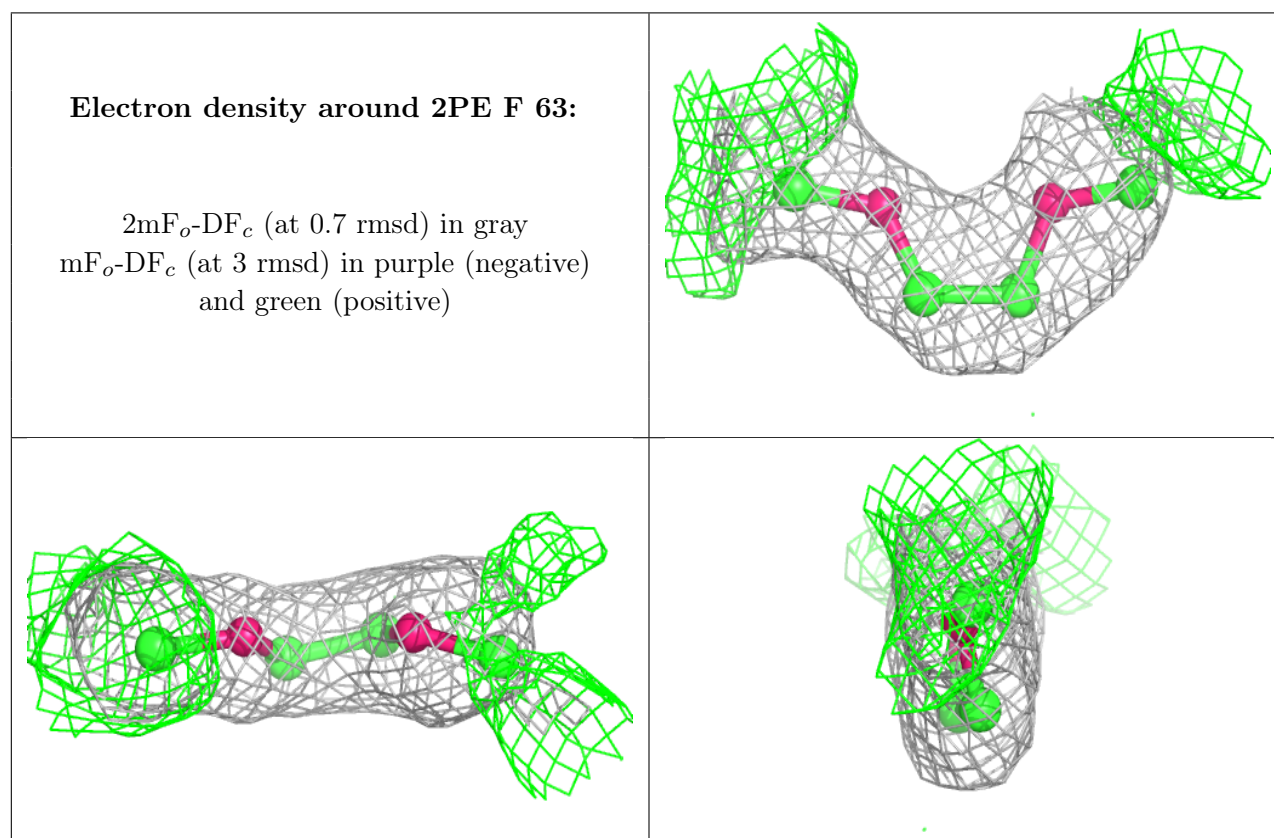
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CO3	K	1002	4/4	0.98	0.13	22,23,24,27	0
2	CO3	L	1002	4/4	0.98	0.12	18,21,23,26	0
4	SO4	E	25	5/5	0.98	0.13	46,50,53,56	0
3	ZN	J	1004	1/1	0.98	0.13	32,32,32,32	0
4	SO4	F	33	5/5	0.98	0.10	50,53,57,64	0
4	SO4	G	23	5/5	0.98	0.13	49,60,70,72	0
4	SO4	H	26	5/5	0.98	0.11	46,50,60,61	0
4	SO4	I	34	5/5	0.98	0.18	42,48,51,52	0
4	SO4	J	32	5/5	0.98	0.25	53,55,61,69	0
4	SO4	K	19	5/5	0.98	0.10	47,54,56,62	0
3	ZN	K	1004	1/1	0.98	0.12	36,36,36,36	0
5	1PE	I	61	5/16	0.98	0.12	26,27,38,40	0
4	SO4	A	2	5/5	0.98	0.12	49,58,59,64	0
2	CO3	E	1002	4/4	0.98	0.13	27,28,31,32	0
3	ZN	D	1001	1/1	0.99	0.12	28,28,28,28	0
3	ZN	D	1004	1/1	0.99	0.12	29,29,29,29	0
3	ZN	E	1001	1/1	0.99	0.14	27,27,27,27	0
3	ZN	E	1004	1/1	0.99	0.12	31,31,31,31	0
3	ZN	F	1004	1/1	0.99	0.11	26,26,26,26	0
3	ZN	G	1001	1/1	0.99	0.14	32,32,32,32	0
3	ZN	G	1004	1/1	0.99	0.10	29,29,29,29	0
3	ZN	H	1001	1/1	0.99	0.12	37,37,37,37	0
4	SO4	G	27	5/5	0.99	0.10	43,46,48,57	0
3	ZN	H	1004	1/1	0.99	0.12	33,33,33,33	0
3	ZN	I	1001	1/1	0.99	0.11	27,27,27,27	0
3	ZN	J	1001	1/1	0.99	0.13	28,28,28,28	0
2	CO3	I	1002	4/4	0.99	0.14	23,24,24,28	0
3	ZN	K	1001	1/1	0.99	0.14	32,32,32,32	0
2	CO3	D	1002	4/4	0.99	0.13	23,25,26,27	0
3	ZN	L	1001	1/1	0.99	0.10	30,30,30,30	0
4	SO4	A	1	5/5	0.99	0.11	47,47,58,59	0
3	ZN	A	1004	1/1	0.99	0.12	27,27,27,27	0
4	SO4	B	3	5/5	0.99	0.12	20,23,25,27	0
3	ZN	A	1001	1/1	0.99	0.13	29,29,29,29	0
3	ZN	B	1004	1/1	0.99	0.12	26,26,26,26	0
4	SO4	C	6	5/5	0.99	0.10	32,40,47,56	0
3	ZN	B	1001	1/1	0.99	0.14	27,27,27,27	0
3	ZN	C	1004	1/1	0.99	0.12	25,25,25,25	0
3	ZN	C	1001	1/1	1.00	0.11	23,23,23,23	0
4	SO4	D	7	5/5	1.00	0.09	23,23,24,32	0
4	SO4	K	18	5/5	1.00	0.15	25,28,32,33	0
3	ZN	I	1004	1/1	1.00	0.12	29,29,29,29	0

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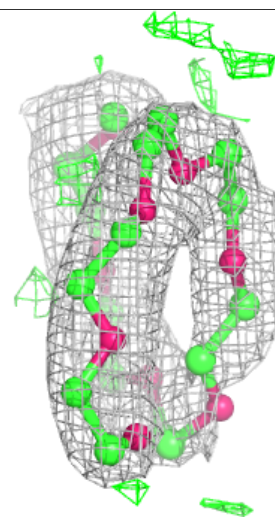
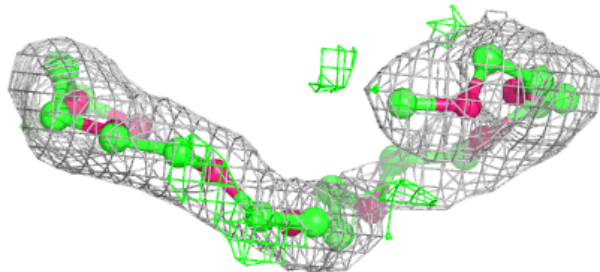
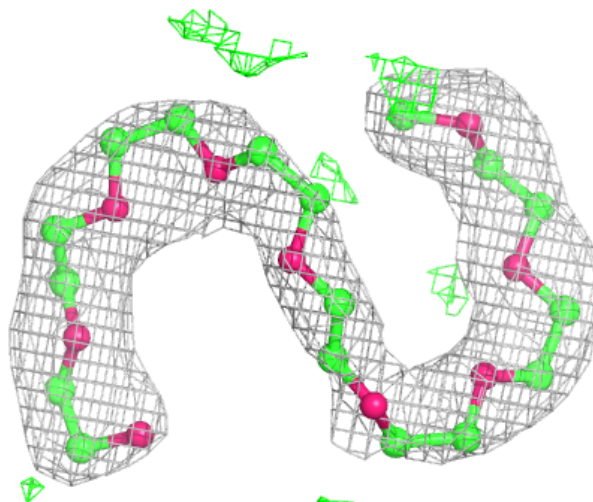
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ZN	L	1004	1/1	1.00	0.12	26,26,26,26	0
3	ZN	F	1001	1/1	1.00	0.14	26,26,26,26	0
4	SO4	I	17	5/5	1.00	0.13	25,26,28,28	0

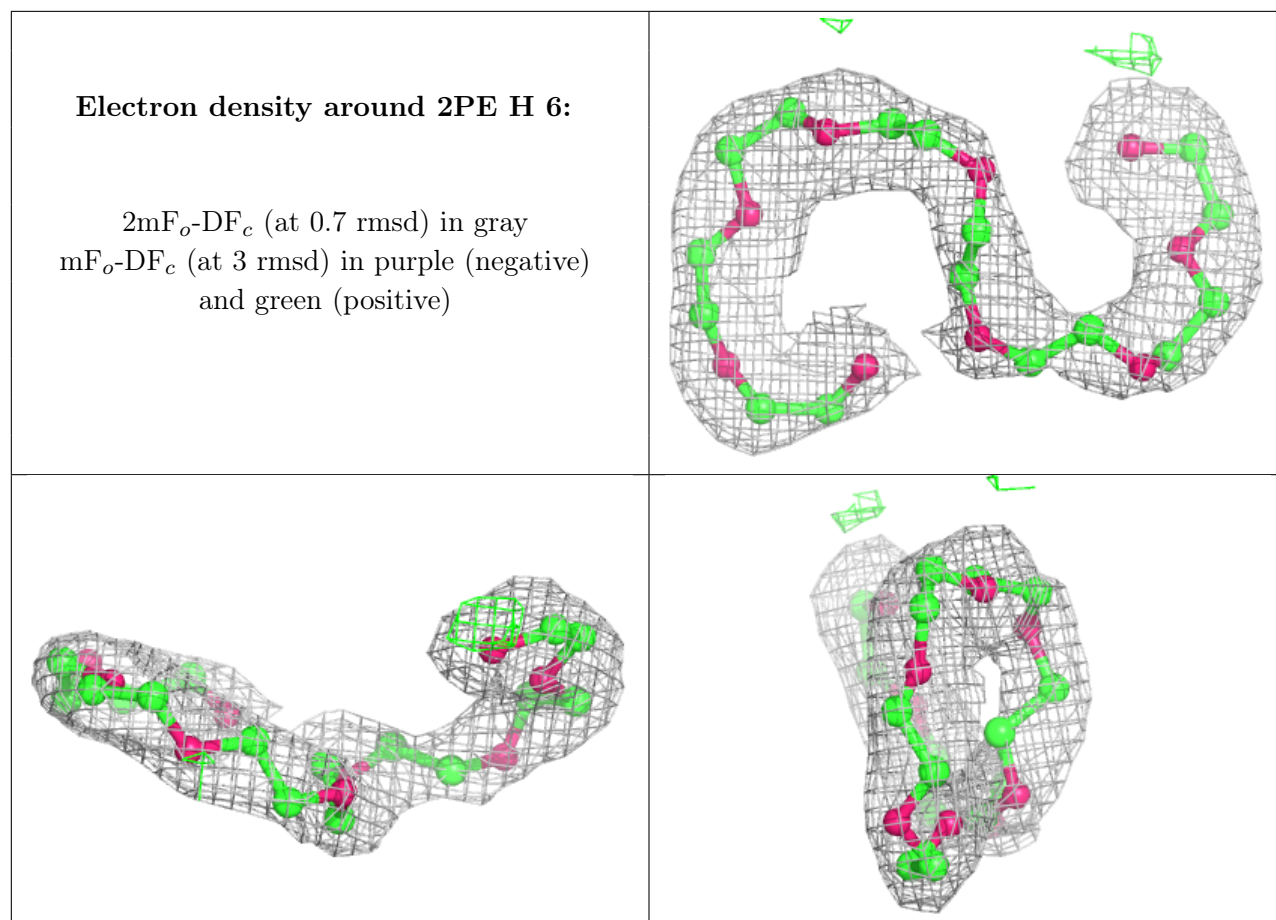
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around 2PE B 14:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.