



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:31 PM UTC

PDB ID : 4ORY / pdb_00004ory
Title : Three-dimensional structure of the C65A-K59A double mutant of Human lipocalin-type Prostaglandin D Synthase holo, second crystal form
Authors : Perduca, M.; Bovi, M.; Bertinelli, M.; Bertini, E.; Destefanis, L.; Carrizo, M.E.; Capaldi, S.; Monaco, H.L.
Deposited on : 2014-02-12
Resolution : 1.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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:

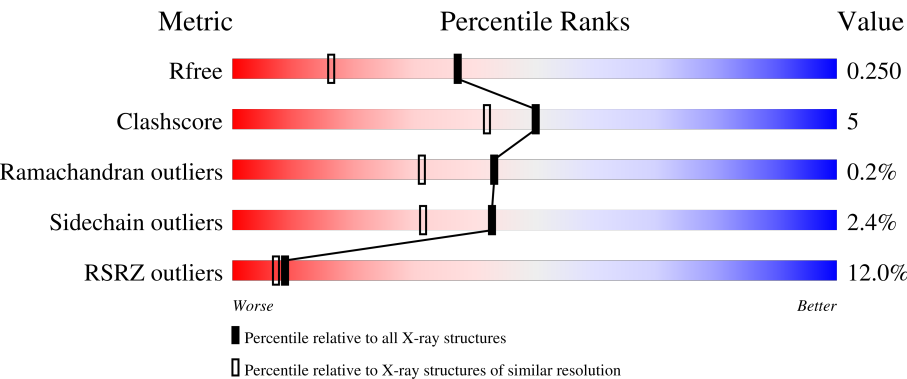
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	190	2% 75% 8% 16%
1	B	190	26% 64% 19% • 15%
1	C	190	8% 71% 13% • 16%
1	D	190	33% 64% 17% • 17%

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Mol	Chain	Length	Quality of chain
1	E	190	5% 75% 9% 16%
1	F	190	2% 81% 7% 12%
1	G	190	2% 77% 9% • 13%
1	H	190	4% 80% • 17%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10337 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 Prostaglandin-H2 D-isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	159	Total	C	N	O	S	0	0	0
			1241	783	211	240	7			
1	B	161	Total	C	N	O	S	0	0	0
			1257	792	213	245	7			
1	C	160	Total	C	N	O	S	0	0	0
			1248	787	212	242	7			
1	D	157	Total	C	N	O	S	0	0	0
			1227	775	209	237	6			
1	E	160	Total	C	N	O	S	0	0	0
			1248	787	212	242	7			
1	F	167	Total	C	N	O	S	0	0	0
			1299	818	220	254	7			
1	G	166	Total	C	N	O	S	0	0	0
			1290	813	219	251	7			
1	H	158	Total	C	N	O	S	0	0	0
			1233	778	210	239	6			

There are 16 discrepancies between the modelled and reference sequences:

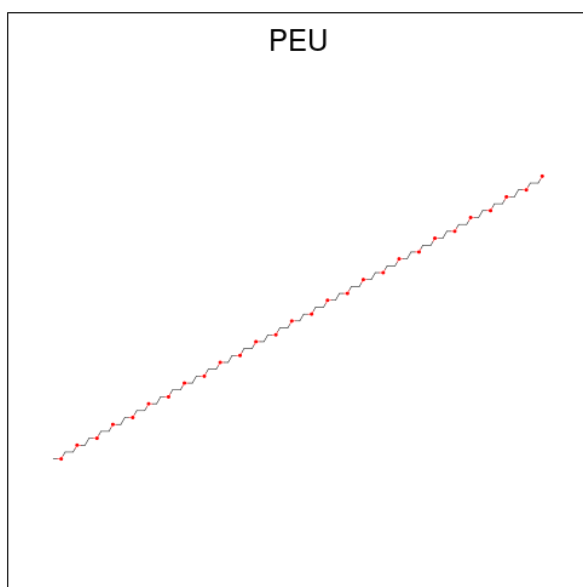
Chain	Residue	Modelled	Actual	Comment	Reference
A	59	ALA	LYS	engineered mutation	UNP P41222
A	65	ALA	CYS	engineered mutation	UNP P41222
B	59	ALA	LYS	engineered mutation	UNP P41222
B	65	ALA	CYS	engineered mutation	UNP P41222
C	59	ALA	LYS	engineered mutation	UNP P41222
C	65	ALA	CYS	engineered mutation	UNP P41222
D	59	ALA	LYS	engineered mutation	UNP P41222
D	65	ALA	CYS	engineered mutation	UNP P41222
E	59	ALA	LYS	engineered mutation	UNP P41222
E	65	ALA	CYS	engineered mutation	UNP P41222
F	59	ALA	LYS	engineered mutation	UNP P41222
F	65	ALA	CYS	engineered mutation	UNP P41222
G	59	ALA	LYS	engineered mutation	UNP P41222

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Chain	Residue	Modelled	Actual	Comment	Reference
G	65	ALA	CYS	engineered mutation	UNP P41222
H	59	ALA	LYS	engineered mutation	UNP P41222
H	65	ALA	CYS	engineered mutation	UNP P41222

- Molecule 2 is 2,5,8,11,14,17,20,23,26,29,32,35,38,41,44,47,50,53,56,59,62,65,68,71,74,77,80-H EPTACOSAOXADOCTACONTAN-82-OL (CCD ID: PEU) (formula: $C_{55}H_{112}O_{28}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	E	1	Total	C	O	0	0
			76	50	26		
2	G	1	Total	C	O	0	0
			76	50	26		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	25	Total	O	0	0
			25	25		
3	C	7	Total	O	0	0
			7	7		
3	D	2	Total	O	0	0
			2	2		
3	E	31	Total	O	0	0
			31	31		
3	F	32	Total	O	0	0
			32	32		

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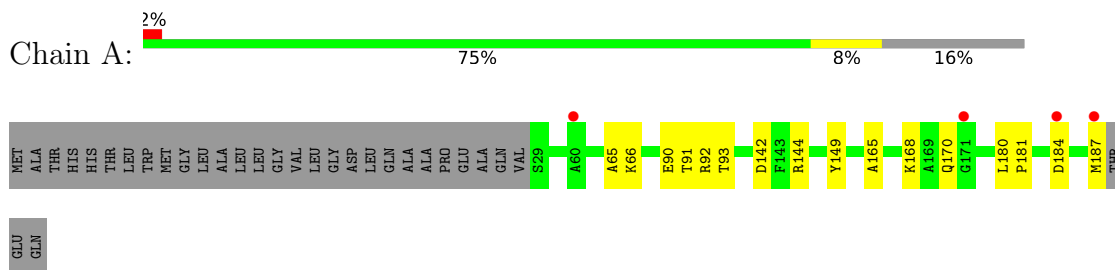
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	26	Total	O	0	0
			26	26		
3	H	19	Total	O	0	0
			19	19		

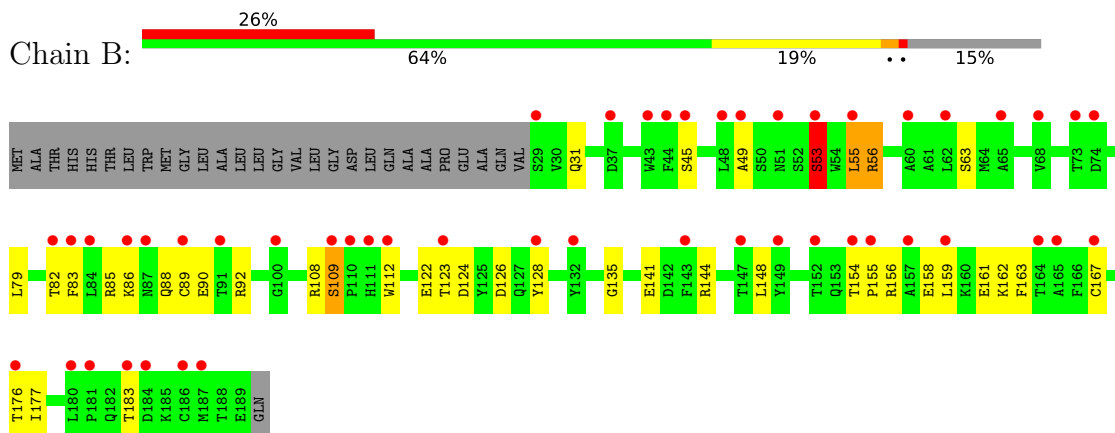
3 Residue-property plots [i](#)

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.

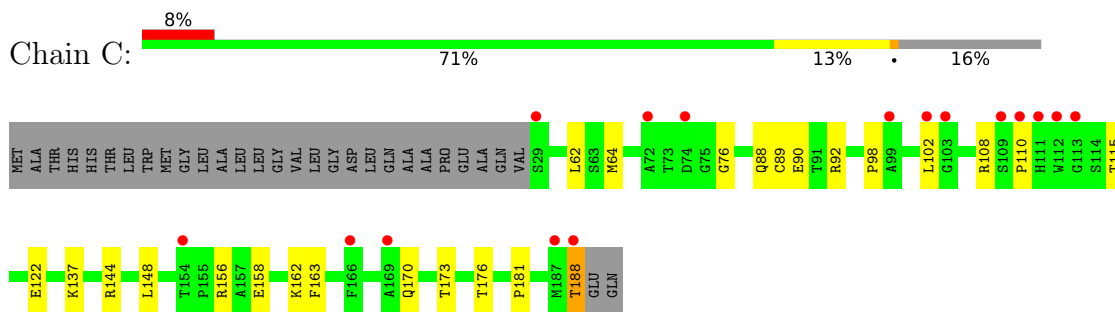
- Molecule 1: Prostaglandin-H2 D-isomerase



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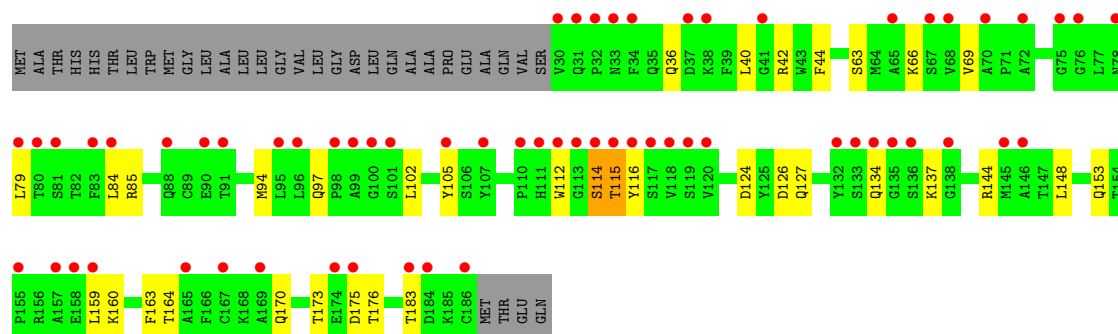


- Molecule 1: Prostaglandin-H2 D-isomerase

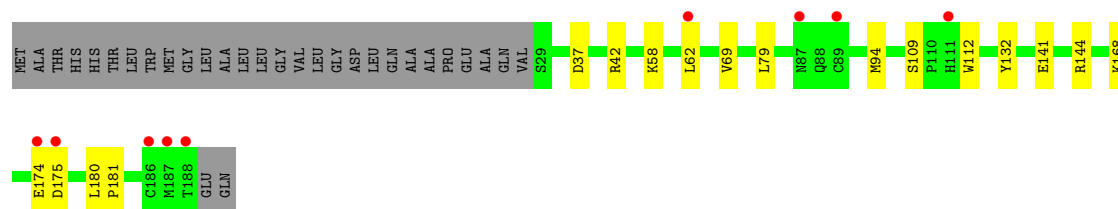
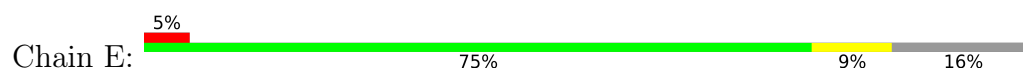


- Molecule 1: Prostaglandin-H2 D-isomerase

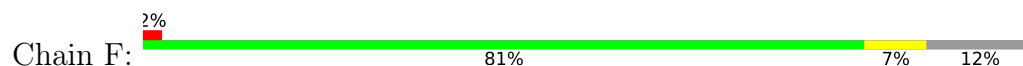




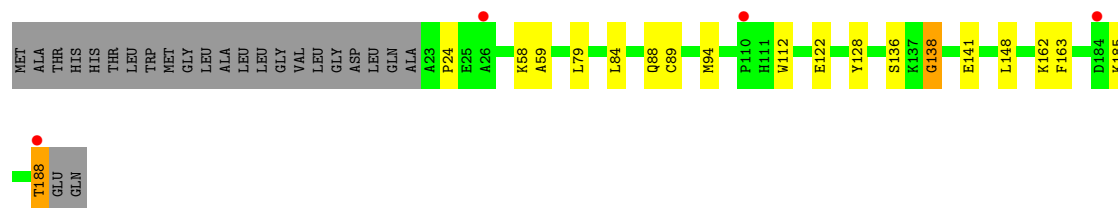
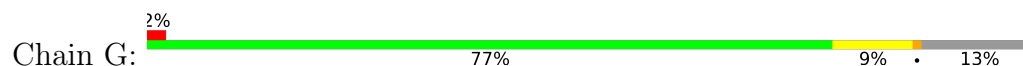
• Molecule 1: Prostaglandin-H2 D-isomerase



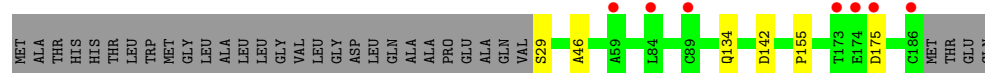
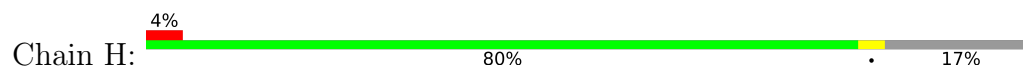
• Molecule 1: Prostaglandin-H2 D-isomerase



• Molecule 1: Prostaglandin-H2 D-isomerase



• Molecule 1: Prostaglandin-H2 D-isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	67.38Å 67.38Å 287.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.17 – 1.80 49.17 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.17-1.80) 99.6 (49.17-1.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 1.79Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.208 , 0.249 0.209 , 0.250	Depositor DCC
R_{free} test set	5884 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.074 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10337	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

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

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: PEU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.37	0/1270	0.73	0/1718
1	B	0.37	0/1286	0.86	4/1740 (0.2%)
1	C	0.33	0/1277	0.71	0/1728
1	D	0.33	0/1256	0.75	0/1700
1	E	0.40	0/1277	0.78	1/1728 (0.1%)
1	F	0.40	0/1329	0.76	0/1800
1	G	0.38	0/1320	0.78	2/1788 (0.1%)
1	H	0.36	0/1262	0.73	0/1708
All	All	0.37	0/10277	0.76	7/13910 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	55	LEU	N-CA-C	-7.35	100.13	110.50
1	B	154	THR	CA-C-N	6.13	126.15	119.90
1	B	154	THR	C-N-CA	6.13	126.15	119.90
1	G	138	GLY	CA-C-N	6.03	126.47	119.47
1	G	138	GLY	C-N-CA	6.03	126.47	119.47
1	B	53	SER	N-CA-C	-5.62	105.54	112.90
1	E	141	GLU	N-CA-C	5.38	117.84	111.33

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	1241	0	1203	8	1
1	B	1257	0	1216	24	0
1	C	1248	0	1210	18	0
1	D	1227	0	1189	21	0
1	E	1248	0	1210	10	1
1	F	1299	0	1256	8	1
1	G	1290	0	1250	15	0
1	H	1233	0	1194	3	0
2	E	76	0	100	9	0
2	G	76	0	100	6	0
3	A	25	0	0	0	0
3	C	7	0	0	1	0
3	D	2	0	0	1	0
3	E	31	0	0	0	1
3	F	32	0	0	1	2
3	G	26	0	0	0	0
3	H	19	0	0	2	0
All	All	10337	0	9928	107	3

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 5.

All (107) 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:D:144:ARG:NH2	1:D:170:GLN:O	2.10	0.84
1:D:115:THR:HG22	1:D:137:LYS:HB2	1.60	0.83
1:B:155:PRO:HB3	1:B:159:LEU:HD23	1.67	0.77
1:A:144:ARG:NH2	1:A:170:GLN:O	2.19	0.76
1:D:127:GLN:HE21	1:D:159:LEU:HD11	1.49	0.75
1:C:144:ARG:NH2	1:C:170:GLN:O	2.18	0.75
1:C:122:GLU:OE2	1:C:162:LYS:NZ	2.22	0.70
1:G:94:MET:HE1	2:G:201:PEU:HCl1	1.74	0.70
1:B:63:SER:HB3	1:B:183:THR:HB	1.74	0.69
1:A:66:LYS:H	1:A:187:MET:HE1	1.58	0.68
1:A:91:THR:O	1:A:92:ARG:NH1	2.26	0.68
1:C:92:ARG:NH2	1:G:188:THR:HG21	2.09	0.68
1:D:153:GLN:NE2	3:D:201:HOH:O	2.26	0.68
1:E:109:SER:HG	1:E:112:TRP:HD1	1.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:ARG:NH2	1:C:158:GLU:OE1	2.26	0.66
1:B:31:GLN:OE1	1:B:123:THR:N	2.28	0.65
1:E:37:ASP:OD2	1:G:185:LYS:NZ	2.30	0.65
1:D:112:TRP:CD1	1:D:114:SER:HB2	2.31	0.64
1:C:90:GLU:OE2	1:C:92:ARG:NH2	2.31	0.63
1:C:88:GLN:NE2	1:G:89:CYS:H	1.97	0.63
1:B:49:ALA:HB2	1:B:177:ILE:HD13	1.81	0.61
1:E:168:LYS:HZ1	1:E:174:GLU:HA	1.64	0.61
1:B:55:LEU:O	1:B:56:ARG:HB3	2.02	0.60
1:C:92:ARG:HH22	1:G:188:THR:HG21	1.65	0.59
1:D:127:GLN:NE2	1:D:159:LEU:HD11	2.17	0.59
1:B:167:CYS:SG	1:B:177:ILE:HD11	2.43	0.58
1:E:109:SER:HG	1:E:112:TRP:CD1	2.20	0.58
2:E:201:PEU:HAV1	1:F:94:MET:HE1	1.87	0.57
1:A:90:GLU:OE1	1:A:92:ARG:NH2	2.39	0.56
1:F:135:GLY:HA3	1:F:141:GLU:HA	1.87	0.55
1:F:174:GLU:H	1:F:174:GLU:CD	2.14	0.55
1:F:122:GLU:OE1	1:F:128:TYR:OH	2.24	0.55
1:C:88:GLN:NE2	1:G:88:GLN:OE1	2.40	0.55
1:B:45:SER:O	1:B:45:SER:OG	2.27	0.53
1:B:56:ARG:HH11	1:B:176:THR:HA	1.74	0.53
1:D:153:GLN:H	1:D:153:GLN:CD	2.16	0.53
1:G:59:ALA:HB2	2:G:201:PEU:HCT1	1.91	0.53
1:B:124:ASP:C	1:B:126:ASP:H	2.17	0.52
1:D:173:THR:O	1:D:176:THR:OG1	2.26	0.52
1:B:86:LYS:NZ	1:B:88:GLN:OE1	2.43	0.52
1:B:128:TYR:CZ	1:B:162:LYS:HE2	2.45	0.52
1:E:109:SER:OG	1:E:112:TRP:HD1	1.93	0.51
1:B:122:GLU:OE2	1:B:162:LYS:NZ	2.28	0.51
1:E:94:MET:HE1	2:E:201:PEU:HCI2	1.93	0.51
1:C:108:ARG:HG2	1:C:115:THR:HG22	1.92	0.51
1:B:49:ALA:HA	1:B:176:THR:O	2.11	0.50
2:E:201:PEU:HCA2	1:F:52:SER:HB2	1.93	0.50
1:A:165:ALA:HA	1:A:168:LYS:HE2	1.93	0.50
2:G:201:PEU:HCD1	3:H:215:HOH:O	2.11	0.50
1:C:115:THR:OG1	1:C:137:LYS:HG2	2.12	0.48
1:B:135:GLY:HA3	1:B:141:GLU:HA	1.94	0.48
1:D:63:SER:HB3	1:D:183:THR:HB	1.96	0.48
1:C:188:THR:O	1:C:188:THR:OG1	2.19	0.48
1:G:122:GLU:OE2	1:G:162:LYS:NZ	2.46	0.48
1:G:84:LEU:HD11	1:G:185:LYS:HD3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:148:LEU:HB2	1:D:163:PHE:CD1	2.50	0.47
1:B:83:PHE:CE2	1:B:92:ARG:HG3	2.50	0.47
1:E:132:TYR:OH	1:E:144:ARG:HD2	2.15	0.47
1:C:62:LEU:O	1:C:181:PRO:HG2	2.16	0.46
1:C:173:THR:O	1:C:176:THR:OG1	2.31	0.46
1:D:124:ASP:O	1:D:126:ASP:N	2.42	0.46
2:E:201:PEU:HCD2	1:F:143:PHE:CD1	2.51	0.45
1:C:64:MET:HE3	3:C:204:HOH:O	2.16	0.45
1:D:112:TRP:NE1	1:D:116:TYR:OH	2.49	0.45
2:E:201:PEU:HCD1	3:F:208:HOH:O	2.16	0.45
1:D:36:GLN:OE1	1:D:105:TYR:OH	2.21	0.44
1:D:160:LYS:O	1:D:164:THR:HG23	2.18	0.44
1:C:76:GLY:HA2	1:C:98:PRO:HD3	1.99	0.44
1:D:44:PHE:CZ	1:D:153:GLN:HG3	2.52	0.44
1:D:40:LEU:HD23	1:D:69:VAL:HG12	2.00	0.44
1:D:42:ARG:HG3	1:D:66:LYS:HE3	2.00	0.44
1:G:138:GLY:O	1:G:141:GLU:HB2	2.16	0.44
1:B:148:LEU:HB2	1:B:163:PHE:CD1	2.52	0.44
2:G:201:PEU:HBR1	2:G:201:PEU:HBU1	1.82	0.43
1:B:109:SER:HB2	1:B:112:TRP:HB2	2.01	0.43
1:B:167:CYS:CB	1:B:177:ILE:HD11	2.49	0.43
1:A:65:ALA:HB1	1:A:187:MET:HE1	2.01	0.42
1:C:148:LEU:HB2	1:C:163:PHE:CD1	2.54	0.42
1:D:175:ASP:OD1	1:D:176:THR:HG23	2.20	0.42
2:E:201:PEU:HAC2	1:F:94:MET:HE1	2.01	0.42
1:G:148:LEU:HB2	1:G:163:PHE:CD1	2.55	0.42
2:E:201:PEU:OAQ	2:E:201:PEU:HAC1	2.20	0.42
1:F:44:PHE:CD1	1:F:153:GLN:HG2	2.55	0.42
1:G:128:TYR:CZ	1:G:162:LYS:HE3	2.54	0.42
1:G:112:TRP:CE2	2:G:201:PEU:HBK2	2.54	0.42
1:E:168:LYS:HD3	1:E:168:LYS:HA	1.71	0.42
1:G:24:PRO:HG3	1:G:136:SER:HB3	2.02	0.42
2:G:201:PEU:HBU2	1:H:142:ASP:HB2	2.02	0.42
1:E:69:VAL:HG22	1:E:79:LEU:HD13	2.01	0.41
1:B:156:ARG:HG3	1:B:158:GLU:HB2	2.02	0.41
2:E:201:PEU:HCI2	2:E:201:PEU:HCN1	2.01	0.41
1:D:79:LEU:HD23	1:D:94:MET:HE2	2.02	0.41
1:H:46:ALA:HB1	1:H:155:PRO:HG3	2.02	0.41
2:E:201:PEU:HCH1	2:E:201:PEU:HCK1	1.71	0.41
1:B:177:ILE:HG23	1:B:177:ILE:HD12	1.81	0.41
1:A:180:LEU:HA	1:A:181:PRO:HD3	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:PHE:HE2	1:B:92:ARG:HG3	1.84	0.41
1:C:88:GLN:HE21	1:C:89:CYS:H	1.68	0.41
1:B:85:ARG:NH1	1:B:90:GLU:OE1	2.55	0.41
1:C:102:LEU:HD12	1:C:102:LEU:HA	1.92	0.41
1:G:58:LYS:HA	1:G:58:LYS:HD3	1.82	0.41
1:B:128:TYR:CE1	1:B:162:LYS:HE2	2.57	0.40
1:D:63:SER:HB2	1:D:84:LEU:HB3	2.03	0.40
1:E:180:LEU:HA	1:E:181:PRO:HD3	1.96	0.40
1:D:85:ARG:HE	1:D:85:ARG:HB2	1.55	0.40
1:H:134:GLN:NE2	3:H:218:HOH:O	2.34	0.40
1:A:142:ASP:OD2	1:B:53:SER:N	2.40	0.40

All (3) 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)
3:E:331:HOH:O	3:F:217:HOH:O[1_455]	1.92	0.28
1:E:42:ARG:NH1	3:F:217:HOH:O[1_455]	2.16	0.04
1:A:93:THR:OG1	1:F:188:THR:OG1[1_455]	2.18	0.02

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	157/190 (83%)	152 (97%)	5 (3%)	0	100	100
1	B	159/190 (84%)	150 (94%)	8 (5%)	1 (1%)	21	11
1	C	158/190 (83%)	154 (98%)	3 (2%)	1 (1%)	21	11
1	D	155/190 (82%)	148 (96%)	7 (4%)	0	100	100
1	E	158/190 (83%)	155 (98%)	3 (2%)	0	100	100
1	F	165/190 (87%)	161 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	164/190 (86%)	161 (98%)	3 (2%)	0	100	100
1	H	156/190 (82%)	151 (97%)	5 (3%)	0	100	100
All	All	1272/1520 (84%)	1232 (97%)	38 (3%)	2 (0%)	43	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	56	ARG
1	C	110	PRO

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	134/157 (85%)	132 (98%)	2 (2%)	57	49
1	B	136/157 (87%)	128 (94%)	8 (6%)	18	7
1	C	135/157 (86%)	134 (99%)	1 (1%)	76	73
1	D	132/157 (84%)	127 (96%)	5 (4%)	29	17
1	E	135/157 (86%)	132 (98%)	3 (2%)	45	34
1	F	140/157 (89%)	137 (98%)	3 (2%)	47	36
1	G	139/157 (88%)	137 (99%)	2 (1%)	59	52
1	H	133/157 (85%)	131 (98%)	2 (2%)	57	49
All	All	1084/1256 (86%)	1058 (98%)	26 (2%)	43	31

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	149	TYR
1	A	184	ASP
1	B	53	SER
1	B	79	LEU
1	B	82	THR

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Mol	Chain	Res	Type
1	B	89	CYS
1	B	108	ARG
1	B	109	SER
1	B	144	ARG
1	B	161	GLU
1	C	188	THR
1	D	97	GLN
1	D	102	LEU
1	D	114	SER
1	D	115	THR
1	D	134	GLN
1	E	58	LYS
1	E	62	LEU
1	E	175	ASP
1	F	37	ASP
1	F	74	ASP
1	F	149	TYR
1	G	79	LEU
1	G	188	THR
1	H	29	SER
1	H	175	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	GLN
1	C	88	GLN
1	D	127	GLN
1	E	87	ASN
1	F	97	GLN
1	F	153	GLN
1	G	36	GLN
1	G	88	GLN
1	H	127	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

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	$\# Z > 2$
2	PEU	G	201	-	75,75,82	0.49	0	74,74,81	0.35	0
2	PEU	E	201	-	75,75,82	0.50	0	74,74,81	0.29	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PEU	G	201	-	-	40/73/73/80	-
2	PEU	E	201	-	-	38/73/73/80	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (78) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	201	PEU	CAM-CAL-OAK-CAJ
2	G	201	PEU	OCJ-CCK-CCL-OCM

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Mol	Chain	Res	Type	Atoms
2	E	201	PEU	OCJ-CCK-CCL-OCM
2	G	201	PEU	OAN-CAO-CAP-OAQ
2	G	201	PEU	OAQ-CAR-CAS-OAT
2	G	201	PEU	OBV-CBW-CBX-OBY
2	G	201	PEU	OCS-CCT-CCU-OCV
2	E	201	PEU	OBJ-CBK-CBL-OBM
2	E	201	PEU	OAK-CAL-CAM-OAN
2	G	201	PEU	OCP-CCQ-CCR-OCS
2	E	201	PEU	OBM-CBN-CBO-OBP
2	G	201	PEU	OBP-CBQ-CBR-OBS
2	E	201	PEU	CCQ-CCR-OCS-CCT
2	G	201	PEU	OBD-CCH-CCI-OCJ
2	E	201	PEU	OAW-CAX-CAY-OAZ
2	E	201	PEU	OAE-CAF-CAG-OAH
2	G	201	PEU	OAK-CAL-CAM-OAN
2	E	201	PEU	OAZ-CBA-CBB-OBC
2	G	201	PEU	OBJ-CBK-CBL-OBM
2	E	201	PEU	OAN-CAO-CAP-OAQ
2	G	201	PEU	OCB-CCC-CCD-OCE
2	G	201	PEU	CCQ-CCR-OCS-CCT
2	G	201	PEU	OAT-CAU-CAV-OAW
2	E	201	PEU	OAT-CAU-CAV-OAW
2	G	201	PEU	OAE-CAF-CAG-OAH
2	E	201	PEU	OCS-CCT-CCU-OCV
2	G	201	PEU	OAH-CAI-CAJ-OAK
2	G	201	PEU	OBD-CBE-CBF-OBG
2	G	201	PEU	CCO-CCN-OCM-CCL
2	G	201	PEU	CCR-CCQ-OCP-CCO
2	E	201	PEU	OCB-CCC-CCD-OCE
2	G	201	PEU	OAW-CAX-CAY-OAZ
2	E	201	PEU	CAF-CAG-OAH-CAI
2	E	201	PEU	CAG-CAF-OAE-CAD
2	G	201	PEU	CCD-CCC-OCB-CCA
2	E	201	PEU	OCE-CCF-CCG-OBC
2	E	201	PEU	CBU-CBT-OBS-CBR
2	E	201	PEU	OCM-CCN-CCO-OCP
2	E	201	PEU	CCH-CCI-OCJ-CCK
2	E	201	PEU	CBI-CBH-OBG-CBF
2	G	201	PEU	CBE-CBF-OBG-CBH
2	E	201	PEU	CBO-CBN-OBM-CBL
2	G	201	PEU	OAZ-CBA-CBB-OBC
2	G	201	PEU	CBH-CBI-OBJ-CBK

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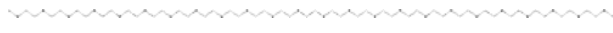
Mol	Chain	Res	Type	Atoms
2	G	201	PEU	CCH-CCI-OCJ-CCK
2	E	201	PEU	CBA-CBB-OBC-CCG
2	G	201	PEU	CBI-CBH-OBG-CBF
2	G	201	PEU	OCM-CCN-CCO-OCP
2	E	201	PEU	CCN-CCO-OCP-CCQ
2	E	201	PEU	CAJ-CAI-OAH-CAG
2	G	201	PEU	OBG-CBH-CBI-OBJ
2	G	201	PEU	CAJ-CAI-OAH-CAG
2	E	201	PEU	CCT-CCU-OCV-CCW
2	G	201	PEU	CBK-CBL-OBM-CBN
2	E	201	PEU	CAS-CAR-OAQ-CAP
2	E	201	PEU	CAI-CAJ-OAK-CAL
2	G	201	PEU	CCI-CCH-OB-DBE
2	G	201	PEU	CBT-CBU-OBV-CBW
2	E	201	PEU	OAQ-CAR-CAS-OAT
2	E	201	PEU	CBX-CBW-OBV-CBU
2	E	201	PEU	CAX-CAY-OAZ-CBA
2	G	201	PEU	CCL-CCK-OCJ-CCI
2	E	201	PEU	CBB-CBA-OAZ-CAY
2	G	201	PEU	CBR-CBQ-OBP-CBO
2	G	201	PEU	OAB-CAC-CAD-OAE
2	E	201	PEU	CAO-CAP-OAQ-CAR
2	E	201	PEU	CCD-CCC-OCB-CCA
2	G	201	PEU	CAG-CAF-OAE-CAD
2	G	201	PEU	CAP-CAO-OAN-CAM
2	E	201	PEU	CCL-CCK-OCJ-CCI
2	G	201	PEU	CBX-CBW-OBV-CBU
2	E	201	PEU	OB-DCCH-CCI-OCJ
2	G	201	PEU	OCE-CCF-CCG-OBC
2	E	201	PEU	OCP-CCQ-CCR-OCS
2	E	201	PEU	CBK-CBL-OBM-CBN
2	G	201	PEU	CBU-CBT-OBS-CBR
2	E	201	PEU	OAH-CAI-CAJ-OAK
2	E	201	PEU	OB-DCBZ-CCA-OCB

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	201	PEU	6	0
2	E	201	PEU	9	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.

Ligand PEU G 201	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand PEU E 201	
 Bond lengths	 Bond angles
 Torsions	 Rings

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

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	159/190 (83%)	0.34	4 (2%) 58 58	21, 33, 59, 71	0
1	B	161/190 (84%)	1.65	49 (30%) 1 1	42, 60, 80, 89	0
1	C	160/190 (84%)	0.88	16 (10%) 12 11	26, 45, 69, 90	0
1	D	157/190 (82%)	1.90	63 (40%) 0 0	46, 61, 83, 105	0
1	E	160/190 (84%)	0.31	9 (5%) 30 29	16, 31, 59, 72	0
1	F	167/190 (87%)	0.09	3 (1%) 67 68	17, 27, 48, 68	0
1	G	166/190 (87%)	0.17	4 (2%) 59 60	17, 29, 49, 74	0
1	H	158/190 (83%)	0.58	7 (4%) 39 38	24, 40, 63, 76	0
All	All	1288/1520 (84%)	0.73	155 (12%) 9 7	16, 39, 71, 105	0

All (155) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	112	TRP	6.3
1	B	89	CYS	5.6
1	C	113	GLY	5.1
1	C	112	TRP	4.7
1	C	110	PRO	4.6
1	F	73	THR	4.5
1	B	157	ALA	4.5
1	B	154	THR	4.5
1	D	99	ALA	4.4
1	B	29	SER	4.3
1	D	113	GLY	4.2
1	D	165	ALA	4.0
1	D	65	ALA	3.9
1	D	135	GLY	3.9
1	D	100	GLY	3.9
1	B	112	TRP	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	187	MET	3.7
1	B	91	THR	3.7
1	B	60	ALA	3.5
1	B	110	PRO	3.5
1	D	30	VAL	3.5
1	D	75	GLY	3.4
1	E	62	LEU	3.4
1	B	186	CYS	3.4
1	D	79	LEU	3.4
1	F	23	ALA	3.3
1	D	96	LEU	3.3
1	D	101	SER	3.3
1	B	55	LEU	3.3
1	C	103	GLY	3.3
1	D	115	THR	3.2
1	G	188	THR	3.1
1	H	59	ALA	3.1
1	B	180	LEU	3.1
1	E	186	CYS	3.1
1	B	183	THR	3.1
1	B	109	SER	3.0
1	C	72	ALA	3.0
1	D	157	ALA	3.0
1	D	90	GLU	3.0
1	B	176	THR	3.0
1	D	76	GLY	3.0
1	B	152	THR	3.0
1	E	187	MET	3.0
1	D	70	ALA	2.9
1	C	102	LEU	2.9
1	E	175	ASP	2.9
1	E	188	THR	2.9
1	B	65	ALA	2.9
1	D	155	PRO	2.9
1	C	99	ALA	2.9
1	B	48	LEU	2.8
1	B	43	TRP	2.8
1	H	174	GLU	2.8
1	D	132	TYR	2.8
1	B	82	THR	2.8
1	D	116	TYR	2.7
1	B	49	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	83	PHE	2.7
1	D	119	SER	2.7
1	D	134	GLN	2.7
1	B	86	LYS	2.7
1	B	44	PHE	2.7
1	D	34	PHE	2.7
1	D	110	PRO	2.7
1	G	26	ALA	2.7
1	D	186	CYS	2.7
1	H	89	CYS	2.7
1	B	184	ASP	2.7
1	B	53	SER	2.7
1	B	167	CYS	2.6
1	F	74	ASP	2.6
1	D	117	SER	2.6
1	D	111	HIS	2.6
1	D	37	ASP	2.6
1	D	67	SER	2.6
1	D	133	SER	2.6
1	B	73	THR	2.6
1	B	111	HIS	2.5
1	D	38	LYS	2.5
1	D	33	ASN	2.5
1	D	72	ALA	2.5
1	D	84	LEU	2.5
1	C	109	SER	2.5
1	B	62	LEU	2.4
1	C	188	THR	2.4
1	C	74	ASP	2.4
1	E	89	CYS	2.4
1	D	105	TYR	2.4
1	D	118	VAL	2.4
1	C	111	HIS	2.4
1	D	41	GLY	2.4
1	E	87	ASN	2.4
1	B	159	LEU	2.3
1	D	95	LEU	2.3
1	D	159	LEU	2.3
1	D	183	THR	2.3
1	H	186	CYS	2.3
1	D	169	ALA	2.3
1	B	155	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	29	SER	2.3
1	D	174	GLU	2.3
1	B	164	THR	2.3
1	B	165	ALA	2.3
1	D	146	ALA	2.3
1	D	81	SER	2.3
1	A	184	ASP	2.3
1	B	74	ASP	2.3
1	B	84	LEU	2.3
1	C	154	THR	2.3
1	D	91	THR	2.3
1	D	83	PHE	2.2
1	D	138	GLY	2.2
1	B	37	ASP	2.2
1	D	175	ASP	2.2
1	D	184	ASP	2.2
1	G	184	ASP	2.2
1	B	143	PHE	2.2
1	C	166	PHE	2.2
1	B	51	ASN	2.2
1	D	167	CYS	2.2
1	D	88	GLN	2.2
1	G	110	PRO	2.2
1	B	87	ASN	2.2
1	D	114	SER	2.2
1	D	136	SER	2.2
1	B	181	PRO	2.2
1	B	132	TYR	2.1
1	D	107	TYR	2.1
1	E	174	GLU	2.1
1	B	68	VAL	2.1
1	D	68	VAL	2.1
1	D	98	PRO	2.1
1	A	60	ALA	2.1
1	D	78	ASN	2.1
1	B	45	SER	2.1
1	B	100	GLY	2.1
1	D	158	GLU	2.1
1	C	187	MET	2.1
1	H	84	LEU	2.1
1	C	169	ALA	2.1
1	B	149	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	80	THR	2.1
1	A	171	GLY	2.1
1	D	145	MET	2.1
1	E	111	HIS	2.1
1	H	175	ASP	2.1
1	B	123	THR	2.0
1	B	187	MET	2.0
1	H	173	THR	2.0
1	D	120	VAL	2.0
1	B	147	THR	2.0
1	D	31	GLN	2.0
1	B	128	TYR	2.0
1	D	32	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

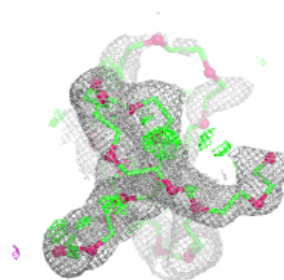
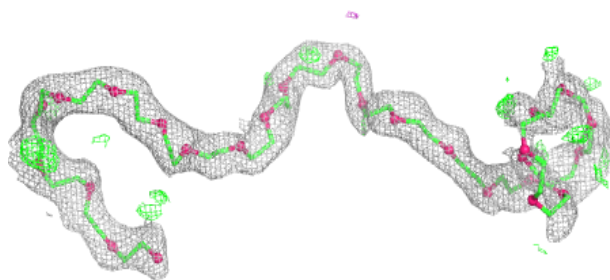
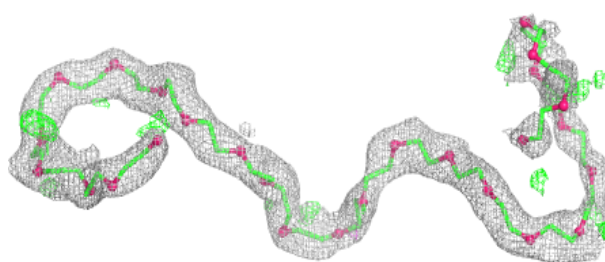
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PEU	G	201	76/83	0.84	0.15	28,62,91,104	0
2	PEU	E	201	76/83	0.85	0.14	27,60,102,115	0

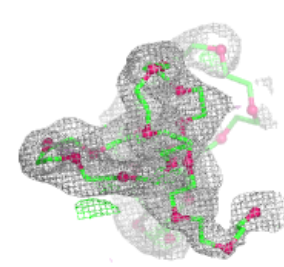
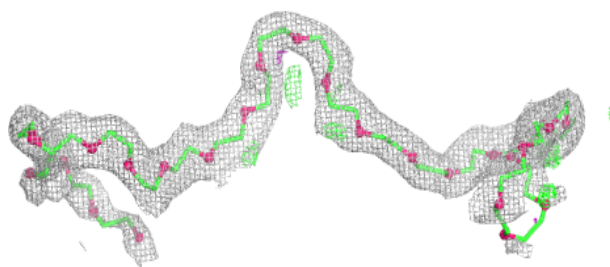
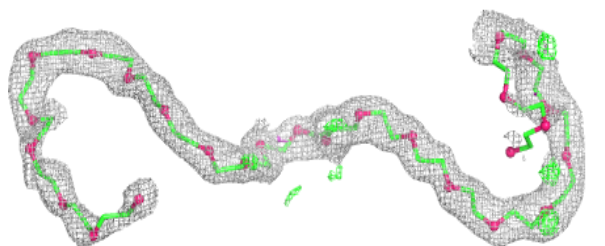
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PEU G 201:

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

**Electron density around PEU E 201:**

$2mF_o-DF_c$ (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.