



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:41 AM UTC

PDB ID : 4D7D / pdb_00004d7d
Title : Cytochrome P450 3A4 bound to an inhibitor
Authors : Sevrioukova, I.; Poulos, T.
Deposited on : 2014-11-22
Resolution : 2.76 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

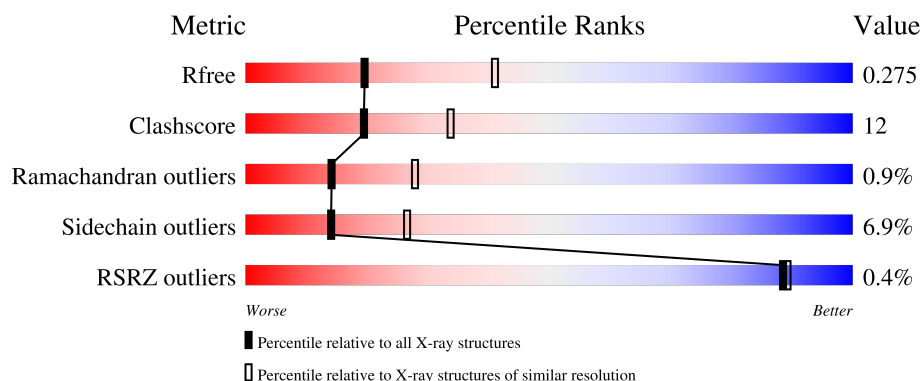
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.76 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	487	 68% 23% • 6%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3775 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.

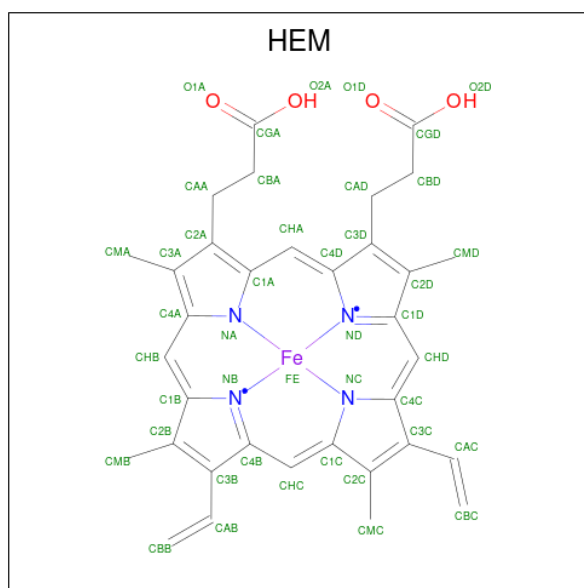
- Molecule 1 is a protein called CYTOCHROME P450 3A4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	S	0	0	1
			3689	2400	607	658	24			

There are 6 discrepancies between the modelled and reference sequences:

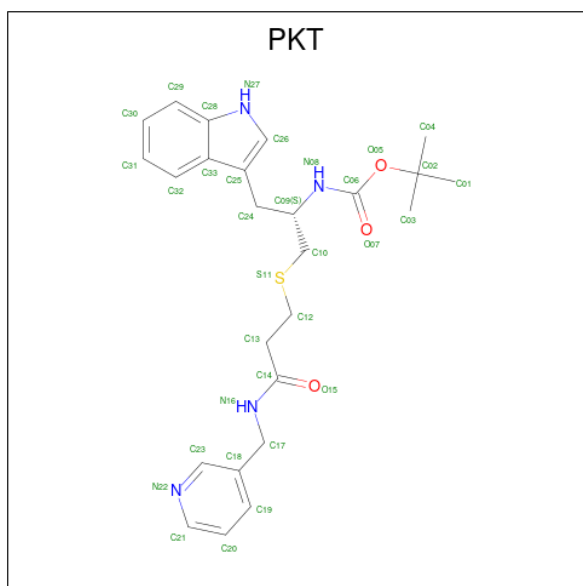
Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MET	-	expression tag	UNP P08684
A	22	ALA	-	expression tag	UNP P08684
A	504	HIS	-	expression tag	UNP P08684
A	505	HIS	-	expression tag	UNP P08684
A	506	HIS	-	expression tag	UNP P08684
A	507	HIS	-	expression tag	UNP P08684

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is tert-butyl [(2S)-1-(1H-indol-3-yl)-3-({3-oxo-3-[(pyridin-3-ylmethyl)amino]propyl}sulfanyl)propan-2-yl]carbamate (CCD ID: PKT) (formula: C₂₅H₃₂N₄O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			33	25	4	3	1		

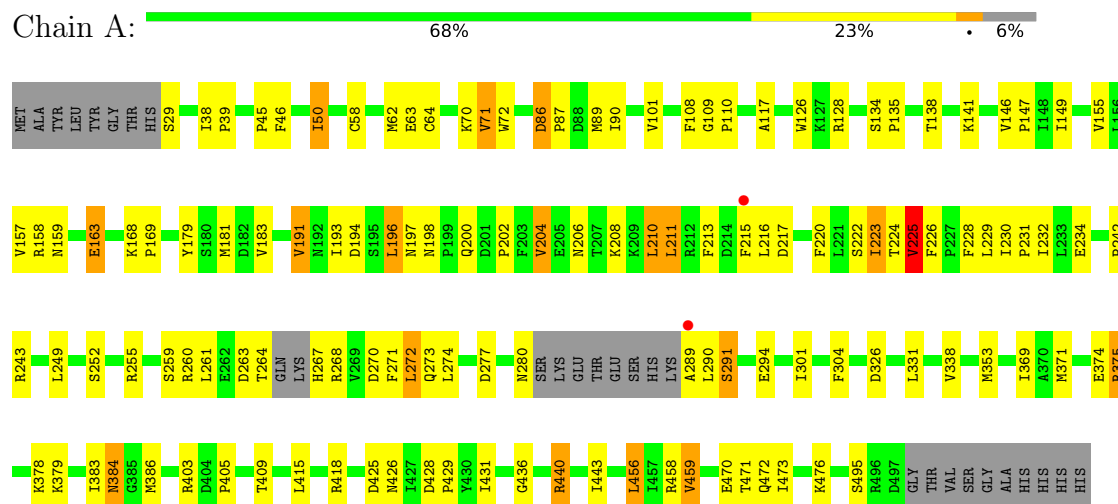
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	10	Total	O	0	0
			10	10		

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: CYTOCHROME P450 3A4



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	78.14Å 101.33Å 127.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.44 – 2.76 37.44 – 2.76	Depositor EDS
% Data completeness (in resolution range)	97.2 (37.44-2.76) 97.3 (37.44-2.76)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.6	Depositor
R, R_{free}	0.200 , 0.278 0.208 , 0.275	Depositor DCC
R_{free} test set	645 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	96.6	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 53.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3775	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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

5.1 Standard geometry

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

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	0.70	0/3778	1.05	13/5111 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	223	ILE	N-CA-C	8.30	118.30	110.74
1	A	86	ASP	CA-C-N	7.61	127.65	119.28
1	A	86	ASP	C-N-CA	7.61	127.65	119.28
1	A	168	LYS	CA-C-N	7.30	128.97	119.84
1	A	168	LYS	C-N-CA	7.30	128.97	119.84
1	A	470	GLU	N-CA-C	-6.43	105.09	113.12
1	A	291	SER	N-CA-C	5.93	116.10	108.34
1	A	210	LEU	N-CA-C	5.80	117.60	111.28
1	A	108	PHE	N-CA-C	5.52	117.10	111.14
1	A	211	LEU	N-CA-C	5.40	118.28	109.59
1	A	197	ASN	CB-CA-C	5.22	120.82	110.17
1	A	109	GLY	N-CA-C	-5.17	101.80	112.34
1	A	263	ASP	N-CA-C	5.13	116.62	108.67

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	268	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3689	0	3771	80	0
2	A	43	0	30	10	0
3	A	33	0	32	8	0
4	A	10	0	0	1	0
All	All	3775	0	3833	88	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (88) 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:A:249:LEU:HA	1:A:252:SER:HB2	1.54	0.86
1:A:403:ARG:O	1:A:405:PRO:HD3	1.85	0.77
1:A:58:CYS:SG	1:A:371:MET:HE2	2.30	0.71
1:A:126:TRP:CZ2	1:A:440:ARG:HG2	2.26	0.70
1:A:87:PRO:HG3	1:A:431:ILE:HD11	1.74	0.68
1:A:117:ALA:HB1	1:A:301:ILE:HG13	1.77	0.67
1:A:89:MET:CG	1:A:383:ILE:HD12	2.26	0.65
1:A:149:ILE:HG12	1:A:183:VAL:HG13	1.79	0.64
1:A:222:SER:O	1:A:226:PHE:HB2	1.97	0.64
1:A:71:VAL:HG21	1:A:386:MET:HE1	1.79	0.63
1:A:202:PRO:O	1:A:206:ASN:ND2	2.29	0.62
2:A:1500:HEM:NA	3:A:1600:PKT:H23	2.11	0.61
1:A:234:GLU:HA	1:A:234:GLU:OE1	2.01	0.61
1:A:45:PRO:O	1:A:46:PHE:HB2	2.01	0.61
1:A:428:ASP:HB3	1:A:431:ILE:HG12	1.84	0.60
1:A:223:ILE:HG13	1:A:224:THR:H	1.67	0.60
1:A:260:ARG:HG3	1:A:272:LEU:CD1	2.32	0.60
1:A:271:PHE:O	1:A:272:LEU:C	2.43	0.59
2:A:1500:HEM:C4A	3:A:1600:PKT:H23	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:THR:C	1:A:267:HIS:CE1	2.81	0.59
1:A:89:MET:HG2	1:A:383:ILE:HD12	1.84	0.59
1:A:138:THR:OG1	1:A:141:LYS:HG2	2.04	0.58
1:A:146:VAL:HB	1:A:147:PRO:HD3	1.85	0.57
1:A:204:VAL:O	1:A:208:LYS:HG2	2.04	0.57
1:A:216:LEU:O	1:A:216:LEU:HG	2.05	0.57
1:A:270:ASP:O	1:A:273:GLN:N	2.40	0.55
1:A:193:ILE:HG22	1:A:193:ILE:O	2.07	0.54
1:A:409:THR:O	1:A:418:ARG:NH2	2.40	0.54
1:A:29:SER:N	4:A:2001:HOH:O	2.40	0.54
1:A:191:VAL:O	1:A:191:VAL:HG12	2.09	0.52
1:A:415:LEU:HB2	1:A:418:ARG:HH11	1.73	0.52
1:A:179:TYR:HA	1:A:196:LEU:HD21	1.92	0.52
1:A:383:ILE:O	1:A:383:ILE:HG13	2.09	0.52
1:A:117:ALA:HB1	1:A:301:ILE:CG1	2.39	0.52
1:A:101:VAL:O	1:A:378:LYS:HG2	2.10	0.52
2:A:1500:HEM:NC	3:A:1600:PKT:C21	2.73	0.51
1:A:89:MET:HG3	1:A:383:ILE:HD12	1.92	0.51
1:A:290:LEU:HG	1:A:291:SER:H	1.76	0.51
1:A:277:ASP:O	1:A:280:ASN:ND2	2.45	0.50
1:A:415:LEU:HB2	1:A:418:ARG:HD2	1.93	0.50
2:A:1500:HEM:C1D	3:A:1600:PKT:H21	2.46	0.50
1:A:338:VAL:HB	1:A:353:MET:HE2	1.94	0.49
1:A:134:SER:OG	1:A:135:PRO:HD3	2.11	0.49
1:A:230:ILE:HB	1:A:231:PRO:HD3	1.93	0.49
1:A:384:ASN:N	1:A:384:ASN:OD1	2.45	0.49
1:A:220:PHE:HA	1:A:223:ILE:HG12	1.95	0.49
1:A:198:ASN:C	1:A:200:GLN:H	2.20	0.49
1:A:224:THR:O	1:A:225:VAL:HG23	2.12	0.48
1:A:291:SER:OG	1:A:294:GLU:HB2	2.12	0.48
1:A:134:SER:N	1:A:135:PRO:CD	2.76	0.48
1:A:252:SER:O	1:A:255:ARG:HB3	2.14	0.47
1:A:375:ARG:NH2	2:A:1500:HEM:O1A	2.47	0.47
1:A:128:ARG:NH2	1:A:289:ALA:O	2.48	0.47
1:A:220:PHE:HD1	1:A:223:ILE:HD11	1.80	0.46
2:A:1500:HEM:C1B	3:A:1600:PKT:H23	2.51	0.46
1:A:436:GLY:HA3	2:A:1500:HEM:HBA1	1.97	0.46
1:A:456:LEU:O	1:A:459:VAL:HG12	2.14	0.46
1:A:86:ASP:HA	1:A:87:PRO:HD3	1.77	0.46
1:A:38:ILE:HG23	1:A:39:PRO:HD2	1.98	0.45
2:A:1500:HEM:CHD	3:A:1600:PKT:H21	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:ASN:ND2	1:A:196:LEU:HD12	2.32	0.44
1:A:193:ILE:HD11	1:A:255:ARG:HH22	1.80	0.44
1:A:228:PHE:C	1:A:231:PRO:HD2	2.43	0.43
1:A:290:LEU:HG	1:A:291:SER:N	2.32	0.43
1:A:62:MET:O	1:A:63:GLU:C	2.62	0.43
1:A:471:THR:HG22	1:A:473:ILE:HG13	2.00	0.43
1:A:101:VAL:HG22	1:A:379:LYS:HD2	2.00	0.42
2:A:1500:HEM:C4C	3:A:1600:PKT:H21	2.54	0.42
1:A:86:ASP:O	1:A:90:ILE:HG13	2.18	0.42
1:A:155:VAL:HG12	1:A:196:LEU:HB3	2.01	0.42
1:A:211:LEU:HD22	1:A:213:PHE:HB2	2.02	0.42
1:A:415:LEU:HD12	1:A:418:ARG:NH1	2.35	0.42
1:A:226:PHE:HB3	1:A:229:LEU:HD12	2.01	0.42
1:A:374:GLU:C	1:A:375:ARG:HG2	2.45	0.42
1:A:157:VAL:CG2	1:A:158:ARG:N	2.83	0.42
2:A:1500:HEM:CHB	3:A:1600:PKT:H23	2.50	0.41
1:A:213:PHE:CE2	1:A:215:PHE:HE1	2.38	0.41
1:A:64:CYS:HB3	1:A:72:TRP:CE2	2.55	0.41
1:A:472:GLN:OE1	1:A:476:LYS:HB2	2.21	0.41
1:A:50:ILE:HD12	1:A:50:ILE:HA	1.66	0.41
1:A:181:MET:HG2	1:A:204:VAL:HG23	2.02	0.41
1:A:223:ILE:HG13	1:A:224:THR:N	2.34	0.41
1:A:428:ASP:HA	1:A:429:PRO:HD2	1.83	0.41
1:A:211:LEU:HD12	1:A:304:PHE:CZ	2.57	0.40
1:A:101:VAL:HG22	1:A:379:LYS:CG	2.51	0.40
1:A:163:GLU:N	1:A:163:GLU:CD	2.79	0.40
1:A:270:ASP:O	1:A:271:PHE:C	2.64	0.40
1:A:110:PRO:HA	1:A:234:GLU:OE2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	453/487 (93%)	413 (91%)	36 (8%)	4 (1%)	14	28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	VAL
1	A	242	PRO
1	A	261	LEU
1	A	169	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	419/443 (95%)	390 (93%)	29 (7%)	14	26

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	ILE
1	A	70	LYS
1	A	71	VAL
1	A	163	GLU
1	A	191	VAL
1	A	194	ASP
1	A	196	LEU
1	A	204	VAL
1	A	210	LEU
1	A	217	ASP
1	A	225	VAL
1	A	232	ILE
1	A	243	ARG
1	A	259	SER
1	A	272	LEU
1	A	274	LEU
1	A	326	ASP

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Mol	Chain	Res	Type
1	A	331	LEU
1	A	369	ILE
1	A	375	ARG
1	A	384	ASN
1	A	425	ASP
1	A	426	ASN
1	A	440	ARG
1	A	443	ILE
1	A	456	LEU
1	A	458	ARG
1	A	459	VAL
1	A	495	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	A	159	ASN
1	A	192	ASN
1	A	197	ASN
1	A	237	ASN
1	A	279	GLN
1	A	451	ASN
1	A	462	ASN

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	HEM	A	1500	3,1	50,50,50	2.54	23 (46%)	67,82,82	3.18	33 (49%)
3	PKT	A	1600	2	34,35,35	1.61	3 (8%)	45,47,47	1.74	12 (26%)

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	HEM	A	1500	3,1	-	2/14/54/54	-
3	PKT	A	1600	2	-	11/25/25/25	0/3/3/3

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1600	PKT	O05-C06	6.46	1.47	1.34
2	A	1500	HEM	FE-NB	5.74	2.12	1.94
2	A	1500	HEM	C3C-C2C	5.12	1.47	1.37
2	A	1500	HEM	C3D-C2D	4.64	1.46	1.36
3	A	1600	PKT	C33-C28	4.51	1.47	1.41
2	A	1500	HEM	C3B-C2B	4.32	1.45	1.37
2	A	1500	HEM	C4D-ND	-4.22	1.32	1.40
2	A	1500	HEM	FE-ND	4.11	2.07	1.94
2	A	1500	HEM	CHD-C4C	3.96	1.46	1.38
2	A	1500	HEM	CHC-C1C	3.79	1.45	1.38
2	A	1500	HEM	CHD-C1D	3.75	1.47	1.39
2	A	1500	HEM	C4A-NA	3.75	1.46	1.39
2	A	1500	HEM	C1C-NC	3.58	1.46	1.39
2	A	1500	HEM	C4C-NC	3.51	1.46	1.39
2	A	1500	HEM	C1A-NA	3.49	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1500	HEM	CHB-C1B	3.24	1.45	1.38
2	A	1500	HEM	CHA-C4D	2.96	1.44	1.38
2	A	1500	HEM	CHC-C4B	2.92	1.45	1.39
2	A	1500	HEM	C1B-NB	-2.80	1.35	1.40
2	A	1500	HEM	C1D-C2D	2.71	1.50	1.44
2	A	1500	HEM	C2A-C3A	2.64	1.45	1.38
3	A	1600	PKT	C33-C25	2.37	1.47	1.44
2	A	1500	HEM	CHB-C4A	2.20	1.44	1.39
2	A	1500	HEM	CHA-C1A	2.19	1.44	1.39
2	A	1500	HEM	C4A-C3A	2.07	1.48	1.43
2	A	1500	HEM	C1A-C2A	2.03	1.48	1.44

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1500	HEM	C3B-C4B-NB	9.72	116.45	109.47
2	A	1500	HEM	C3B-C2B-C1B	-8.49	100.04	106.41
2	A	1500	HEM	C2B-C1B-NB	7.58	118.55	109.84
2	A	1500	HEM	C2A-C1A-NA	7.07	117.99	110.15
2	A	1500	HEM	C3D-C4D-ND	6.55	117.36	110.17
2	A	1500	HEM	C4A-NA-C1A	-5.95	96.13	105.82
2	A	1500	HEM	C1D-C2D-C3D	-5.10	101.61	106.98
3	A	1600	PKT	C29-C28-C33	-5.03	117.32	122.19
2	A	1500	HEM	C2D-C1D-ND	4.73	115.37	109.90
2	A	1500	HEM	C3C-C2C-C1C	-4.44	102.84	107.05
2	A	1500	HEM	C3A-C4A-NA	4.29	117.03	110.14
3	A	1600	PKT	O05-C06-N08	4.23	116.95	110.03
2	A	1500	HEM	CBD-CAD-C3D	-4.00	101.48	112.53
2	A	1500	HEM	CHA-C4D-C3D	-3.95	117.94	125.23
2	A	1500	HEM	C1B-NB-C4B	-3.95	100.53	105.21
2	A	1500	HEM	CHA-C1A-C2A	-3.55	117.52	125.30
3	A	1600	PKT	O05-C06-O07	-3.48	119.45	125.64
2	A	1500	HEM	CHB-C4A-C3A	-3.45	117.42	127.43
2	A	1500	HEM	CMD-C2D-C1D	3.41	130.37	125.03
2	A	1500	HEM	CHC-C4B-C3B	-3.28	118.53	125.07
2	A	1500	HEM	C4B-C3B-C2B	-3.16	104.37	107.28
2	A	1500	HEM	C2C-C1C-NC	3.05	115.27	109.64
3	A	1600	PKT	C02-O05-C06	3.00	125.52	120.97
3	A	1600	PKT	C10-S11-C12	3.00	111.16	102.26
3	A	1600	PKT	C32-C33-C28	2.87	121.81	118.84
2	A	1500	HEM	CHD-C1D-C2D	-2.82	120.57	125.03
2	A	1500	HEM	CHB-C1B-C2B	-2.81	118.96	126.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1600	PKT	C29-C28-N27	2.80	135.23	130.74
2	A	1500	HEM	C4D-C3D-C2D	-2.78	102.84	106.89
3	A	1600	PKT	C09-C24-C25	-2.67	108.75	113.63
2	A	1500	HEM	C4C-NC-C1C	-2.66	101.49	105.82
2	A	1500	HEM	CMB-C2B-C1B	2.58	129.07	125.03
2	A	1500	HEM	CHC-C1C-C2C	-2.58	120.12	125.49
3	A	1600	PKT	C28-N27-C26	2.47	111.27	109.08
2	A	1500	HEM	C4A-CHB-C1B	-2.46	120.47	126.25
2	A	1500	HEM	CMA-C3A-C4A	2.43	129.12	125.42
2	A	1500	HEM	CAA-C2A-C1A	2.41	129.64	124.94
2	A	1500	HEM	C1A-C2A-C3A	-2.37	103.20	106.87
2	A	1500	HEM	O2A-CGA-CBA	2.18	120.89	114.00
2	A	1500	HEM	C4D-ND-C1D	-2.17	102.64	105.21
3	A	1600	PKT	C19-C18-C23	2.17	120.29	117.10
3	A	1600	PKT	C20-C19-C18	-2.09	117.67	120.61
2	A	1500	HEM	C1A-CHA-C4D	-2.08	121.36	126.25
2	A	1500	HEM	CMC-C2C-C1C	2.01	128.26	124.73
3	A	1600	PKT	C28-C33-C25	-2.00	105.14	107.17

There are no chirality outliers.

All (13) torsion outliers are listed below:

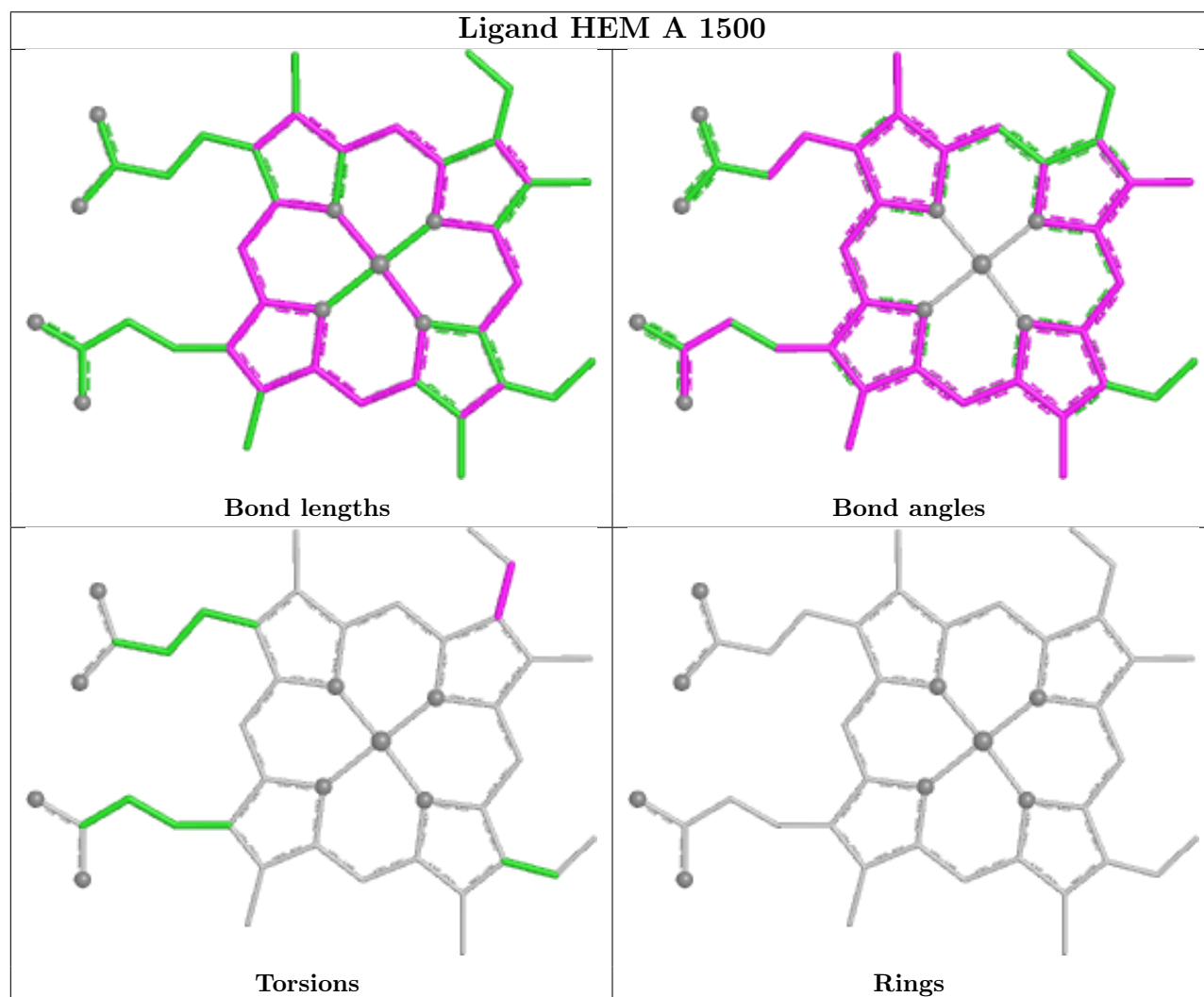
Mol	Chain	Res	Type	Atoms
3	A	1600	PKT	C24-C09-N08-C06
3	A	1600	PKT	N08-C09-C24-C25
3	A	1600	PKT	C10-C09-C24-C25
3	A	1600	PKT	C13-C14-N16-C17
3	A	1600	PKT	O15-C14-N16-C17
3	A	1600	PKT	O05-C06-N08-C09
3	A	1600	PKT	O07-C06-O05-C02
3	A	1600	PKT	O07-C06-N08-C09
3	A	1600	PKT	N08-C06-O05-C02
2	A	1500	HEM	C2C-C3C-CAC-CBC
2	A	1500	HEM	C4C-C3C-CAC-CBC
3	A	1600	PKT	C09-C10-S11-C12
3	A	1600	PKT	S11-C12-C13-C14

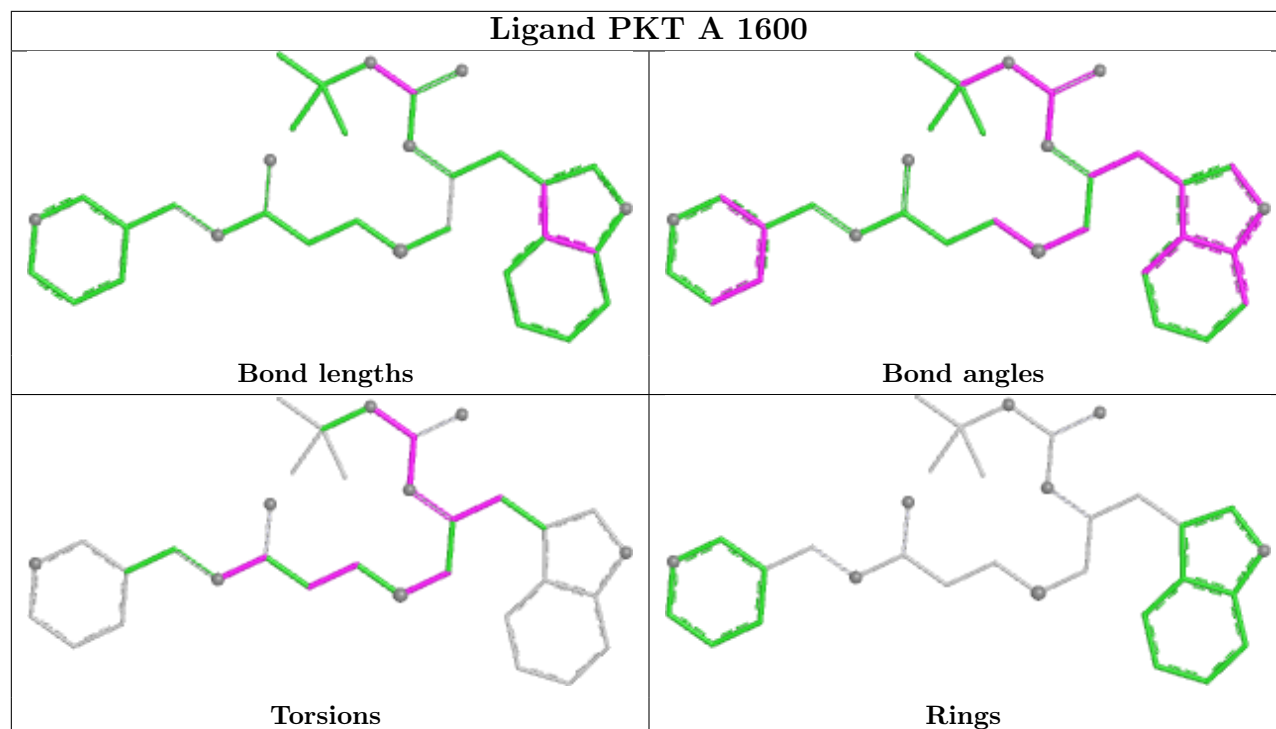
There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1500	HEM	10	0
3	A	1600	PKT	8	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	459/487 (94%)	-0.39	2 (0%) 88 89	63, 104, 164, 195	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	289	ALA	2.5
1	A	215	PHE	2.1

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.

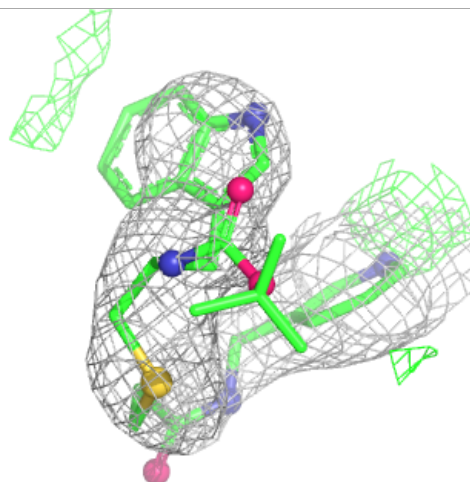
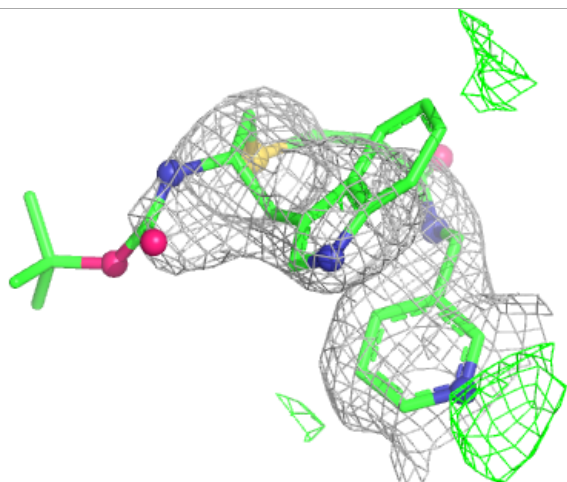
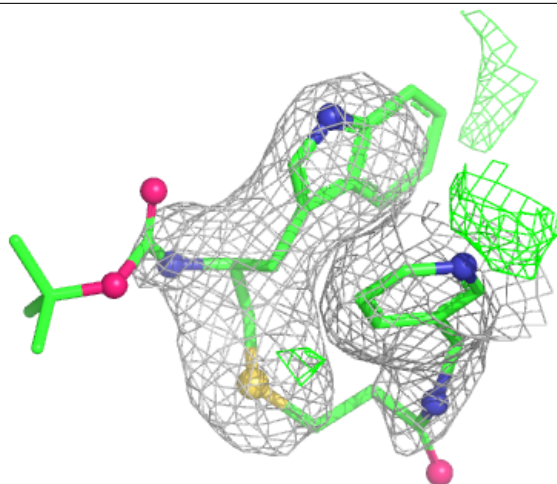
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PKT	A	1600	33/33	0.93	0.15	60,128,163,167	0
2	HEM	A	1500	43/43	0.98	0.08	62,70,77,83	0

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.

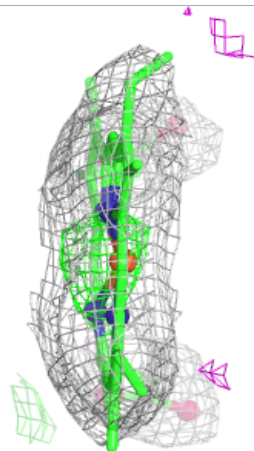
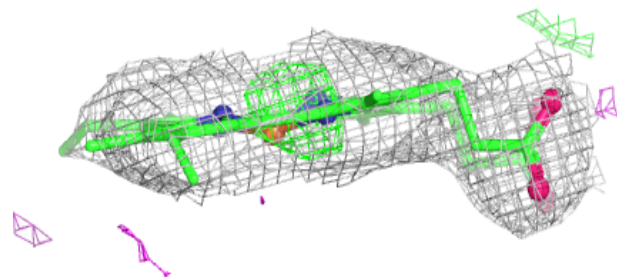
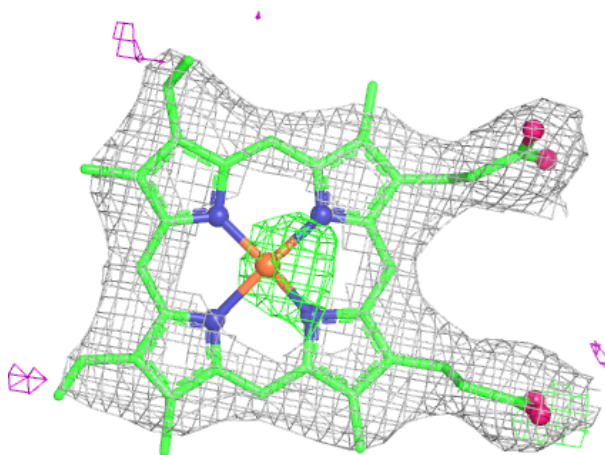
Electron density around PKT A 1600:

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



Electron density around HEM A 1500:

$2mF_o-DF_c$ (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.