



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:04 AM UTC

PDB ID : 1OMP / pdb_00001omp
Title : CRYSTALLOGRAPHIC EVIDENCE OF A LARGE LIGAND-INDUCED HINGE-TWIST MOTION BETWEEN THE TWO DOMAINS OF THE MALTODEXTRIN-BINDING PROTEIN INVOLVED IN ACTIVE TRANSPORT AND CHEMOTAXIS
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Deposited on : 1992-09-14
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
Xtriage (Phenix) : 2.0
EDS : 3.0
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

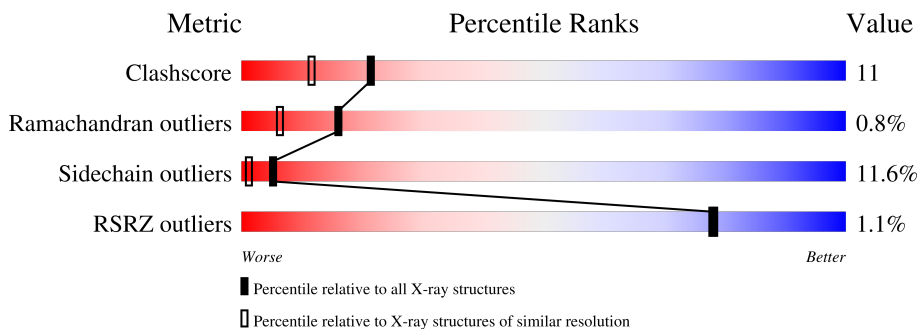
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
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	370	 % 65% 29% 6% •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2935 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 D-MALTODEXTRIN BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	370	2862	1843	468	545	6	0	0	0

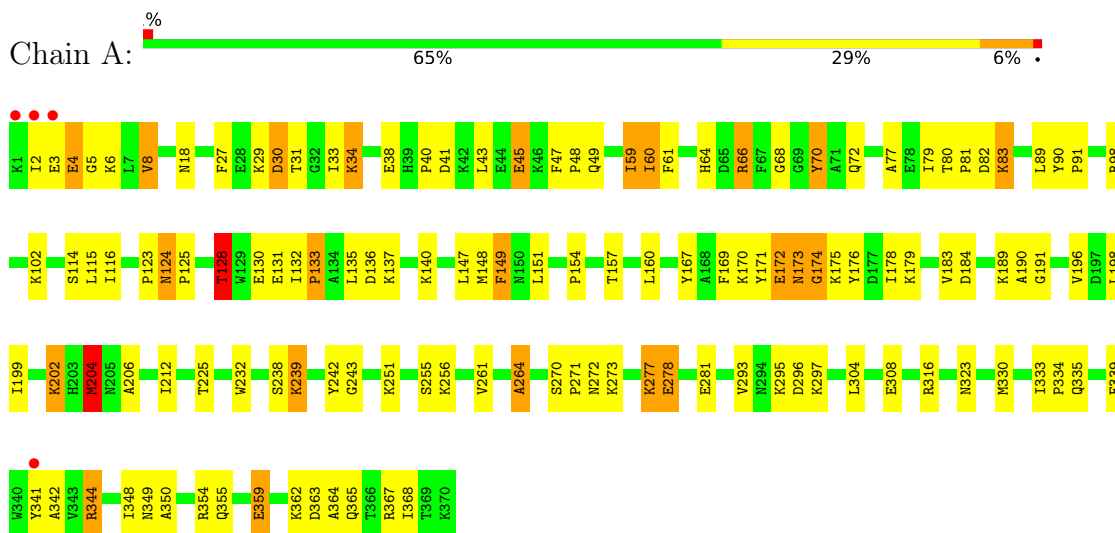
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	73	Total	O	0	0
			73	73		

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: D-MALTODEXTRIN BINDING PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	38.35Å 44.44Å 58.25Å 101.00° 100.40° 104.20°	Depositor
Resolution (Å)	10.00 – 1.80 10.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-1.80) 95.5 (10.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.53 (at 1.70Å)	Xtrriage
Refinement program	PROLSQ, X-PLOR	Depositor
R, R_{free}	0.210 , (Not available) 0.203 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	19.9	Xtrriage
Anisotropy	0.130	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 64.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2935	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.00% 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

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	1.19	4/2931 (0.1%)	1.87	57/3979 (1.4%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	GLY	CA-C	8.09	1.58	1.51
1	A	80	THR	CA-CB	5.54	1.60	1.53
1	A	61	PHE	C-N	-5.11	1.27	1.33
1	A	8	VAL	CA-CB	-5.02	1.48	1.54

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	242	TYR	CA-C-N	8.11	127.85	121.61
1	A	242	TYR	C-N-CA	8.11	127.85	121.61
1	A	98	ARG	NE-CZ-NH2	7.63	126.07	119.20
1	A	8	VAL	CB-CA-C	7.36	121.52	110.63
1	A	8	VAL	N-CA-CB	7.35	121.55	111.41
1	A	278	GLU	CB-CG-CD	7.10	124.67	112.60
1	A	133	PRO	CA-C-N	7.08	129.76	120.28
1	A	133	PRO	C-N-CA	7.08	129.76	120.28
1	A	70	TYR	CA-C-N	6.86	129.48	120.28
1	A	70	TYR	C-N-CA	6.86	129.48	120.28
1	A	125	PRO	O-C-N	6.68	124.29	121.15
1	A	149	PHE	CA-CB-CG	6.45	120.25	113.80
1	A	68	GLY	CA-C-N	6.36	127.00	120.00
1	A	68	GLY	C-N-CA	6.36	127.00	120.00
1	A	124	ASN	O-C-N	6.33	127.46	121.38
1	A	116	ILE	CA-C-O	-6.32	113.78	120.48
1	A	323	ASN	O-C-N	6.27	129.29	122.15
1	A	72	GLN	CA-C-O	-6.23	114.28	120.82
1	A	114	SER	O-C-N	6.17	130.73	122.96
1	A	264	ALA	CA-C-N	-6.07	117.99	122.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	264	ALA	C-N-CA	-6.07	117.99	122.18
1	A	354	ARG	CD-NE-CZ	6.01	132.81	124.40
1	A	27	PHE	CA-CB-CG	5.91	119.71	113.80
1	A	128	THR	N-CA-CB	-5.91	100.62	111.37
1	A	243	GLY	O-C-N	5.84	128.51	123.37
1	A	174	GLY	N-CA-C	-5.70	107.78	115.36
1	A	191	GLY	N-CA-C	5.63	119.03	112.50
1	A	196	VAL	O-C-N	5.59	127.29	121.87
1	A	66	ARG	CD-NE-CZ	5.58	132.22	124.40
1	A	198	LEU	O-C-N	5.57	128.10	122.09
1	A	114	SER	CA-C-O	-5.45	115.41	121.51
1	A	232	TRP	CA-C-O	-5.44	115.08	120.90
1	A	359	GLU	CB-CG-CD	5.44	121.85	112.60
1	A	304	LEU	CA-C-O	-5.42	114.17	120.62
1	A	3	GLU	CB-CA-C	-5.39	110.38	116.63
1	A	147	LEU	N-CA-CB	-5.34	101.56	111.13
1	A	308	GLU	CB-CG-CD	5.32	121.65	112.60
1	A	349	ASN	CA-C-O	-5.28	115.27	120.70
1	A	204	MET	CA-C-N	5.26	129.98	122.72
1	A	204	MET	C-N-CA	5.26	129.98	122.72
1	A	293	VAL	O-C-N	5.24	127.35	121.90
1	A	190	ALA	CA-C-N	5.24	125.75	119.94
1	A	190	ALA	C-N-CA	5.24	125.75	119.94
1	A	167	TYR	CA-C-O	-5.21	115.66	121.23
1	A	255	SER	N-CA-C	-5.19	103.19	110.50
1	A	225	THR	CA-CB-CG2	5.16	119.27	110.50
1	A	83	LYS	CA-C-N	5.12	127.14	120.28
1	A	83	LYS	C-N-CA	5.12	127.14	120.28
1	A	98	ARG	NE-CZ-NH1	-5.09	116.41	121.50
1	A	169	PHE	CA-CB-CG	5.08	118.88	113.80
1	A	255	SER	CA-C-O	-5.07	116.03	121.56
1	A	157	THR	CA-CB-OG1	-5.05	102.02	109.60
1	A	316	ARG	CD-NE-CZ	5.03	131.45	124.40
1	A	196	VAL	CA-C-O	-5.02	115.73	120.95
1	A	349	ASN	O-C-N	5.02	127.51	122.09
1	A	350	ALA	CA-C-N	5.00	127.39	120.29
1	A	350	ALA	C-N-CA	5.00	127.39	120.29

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	2862	0	2828	62	0
2	A	73	0	0	5	0
All	All	2935	0	2828	62	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 11.

All (62) 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:59:ILE:HG21	2:A:414:HOH:O	1.66	0.92
1:A:342:ALA:HB3	1:A:368:ILE:HD11	1.66	0.74
1:A:128:THR:HG21	2:A:428:HOH:O	1.91	0.70
1:A:64:HIS:HD2	1:A:261:VAL:H	1.44	0.64
1:A:47:PHE:HB3	1:A:48:PRO:HD3	1.79	0.64
1:A:136:ASP:O	1:A:140:LYS:HG2	1.97	0.63
1:A:31:THR:HG22	1:A:33:ILE:HG12	1.81	0.62
1:A:171:TYR:OH	1:A:174:GLY:HA2	1.98	0.62
1:A:128:THR:HG22	1:A:131:GLU:H	1.66	0.61
1:A:151:LEU:HD11	1:A:204:MET:HG2	1.83	0.60
1:A:278:GLU:HG3	2:A:441:HOH:O	2.01	0.60
1:A:173:ASN:ND2	1:A:175:LYS:HB3	2.16	0.59
1:A:43:LEU:HD13	1:A:60:ILE:HD11	1.85	0.57
1:A:135:LEU:HD13	2:A:426:HOH:O	2.03	0.57
1:A:43:LEU:CD1	1:A:60:ILE:HD11	2.34	0.57
1:A:333:ILE:HB	1:A:334:PRO:HD2	1.86	0.57
1:A:123:PRO:C	1:A:124:ASN:HD22	2.13	0.56
1:A:199:ILE:HG21	1:A:206:ALA:HB2	1.89	0.53
1:A:277:LYS:O	1:A:281:GLU:HG3	2.09	0.52
1:A:178:ILE:HG21	1:A:335:GLN:OE1	2.10	0.52
1:A:59:ILE:CD1	1:A:264:ALA:HB1	2.40	0.52
1:A:128:THR:HG22	1:A:131:GLU:HG2	1.91	0.51
1:A:363:ASP:HB3	1:A:367:ARG:HH21	1.75	0.51
1:A:364:ALA:O	1:A:368:ILE:HG12	2.11	0.50
1:A:171:TYR:HB2	1:A:176:TYR:CE1	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:HIS:CD2	1:A:261:VAL:H	2.27	0.49
1:A:128:THR:HG23	1:A:130:GLU:H	1.77	0.49
1:A:128:THR:HG23	1:A:130:GLU:N	2.28	0.49
1:A:270:SER:CB	2:A:438:HOH:O	2.61	0.49
1:A:184:ASP:HB2	1:A:365:GLN:HB2	1.94	0.49
1:A:6:LYS:HA	1:A:33:ILE:HG23	1.96	0.48
1:A:64:HIS:HE1	1:A:330:MET:O	1.96	0.48
1:A:154:PRO:HG3	1:A:344:ARG:HA	1.95	0.47
1:A:18:ASN:HB2	1:A:296:ASP:OD2	2.13	0.47
1:A:172:GLU:O	1:A:173:ASN:HB3	2.15	0.46
1:A:238:SER:O	1:A:239:LYS:HB2	2.14	0.46
1:A:6:LYS:HE2	1:A:34:LYS:HG3	1.97	0.46
1:A:149:PHE:CD1	1:A:204:MET:HE1	2.51	0.46
1:A:48:PRO:HG3	1:A:70:TYR:CE1	2.50	0.46
1:A:173:ASN:HD21	1:A:175:LYS:HB3	1.81	0.46
1:A:132:ILE:N	1:A:133:PRO:CD	2.79	0.46
1:A:31:THR:HG22	1:A:33:ILE:CG1	2.46	0.46
1:A:31:THR:CG2	1:A:33:ILE:HG12	2.46	0.46
1:A:4:GLU:H	1:A:272:ASN:HD21	1.63	0.45
1:A:45:GLU:OE1	1:A:66:ARG:NH2	2.40	0.45
1:A:40:PRO:HG2	1:A:43:LEU:HB3	1.98	0.45
1:A:48:PRO:HG3	1:A:70:TYR:HE1	1.82	0.45
1:A:251:LYS:NZ	1:A:251:LYS:HB3	2.31	0.45
1:A:173:ASN:CG	1:A:175:LYS:HB3	2.42	0.44
1:A:90:TYR:HA	1:A:91:PRO:HD3	1.88	0.44
1:A:342:ALA:CB	1:A:368:ILE:HD11	2.42	0.42
1:A:77:ALA:HB2	1:A:273:LYS:HE3	2.01	0.42
1:A:148:MET:CE	1:A:212:ILE:HG22	2.49	0.42
1:A:79:ILE:HD12	1:A:81:PRO:HD3	2.02	0.42
1:A:31:THR:HG22	1:A:33:ILE:H	1.84	0.42
1:A:355:GLN:HG2	1:A:359:GLU:OE1	2.20	0.42
1:A:123:PRO:HG2	1:A:124:ASN:H	1.86	0.41
1:A:30:ASP:OD1	1:A:30:ASP:N	2.53	0.41
1:A:199:ILE:O	1:A:202:LYS:NZ	2.46	0.41
1:A:5:GLY:O	1:A:33:ILE:HD12	2.20	0.41
1:A:339:PHE:HA	1:A:368:ILE:CD1	2.51	0.41
1:A:270:SER:HA	1:A:271:PRO:HD3	1.88	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	368/370 (100%)	351 (95%)	14 (4%)	3 (1%)	16 6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	173	ASN
1	A	4	GLU

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	292/297 (98%)	258 (88%)	34 (12%)	5 1

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	VAL
1	A	29	LYS
1	A	30	ASP
1	A	34	LYS
1	A	38	GLU
1	A	41	ASP
1	A	45	GLU
1	A	49	GLN

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Mol	Chain	Res	Type
1	A	59	ILE
1	A	60	ILE
1	A	82	ASP
1	A	83	LYS
1	A	89	LEU
1	A	102	LYS
1	A	115	LEU
1	A	128	THR
1	A	137	LYS
1	A	160	LEU
1	A	170	LYS
1	A	172	GLU
1	A	179	LYS
1	A	183	VAL
1	A	189	LYS
1	A	202	LYS
1	A	204	MET
1	A	239	LYS
1	A	256	LYS
1	A	277	LYS
1	A	295	LYS
1	A	297	LYS
1	A	341	TYR
1	A	344	ARG
1	A	348	ILE
1	A	362	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	39	HIS
1	A	64	HIS
1	A	72	GLN
1	A	124	ASN
1	A	201	ASN
1	A	203	HIS
1	A	218	ASN
1	A	282	ASN
1	A	365	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	370/370 (100%)	-0.20	4 (1%) 78 78	8, 20, 37, 57	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	LYS	3.9
1	A	2	ILE	3.4
1	A	341	TYR	2.4
1	A	3	GLU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.