



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 07:05 PM UTC

PDB ID : 5CTT / pdb_00005ctt
Title : Crystal structure of human SART3/TIP110 NLS-mouse importin alpha complex
Authors : Park, J.K.; Kim, E.E.
Deposited on : 2015-07-24
Resolution : 1.70 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

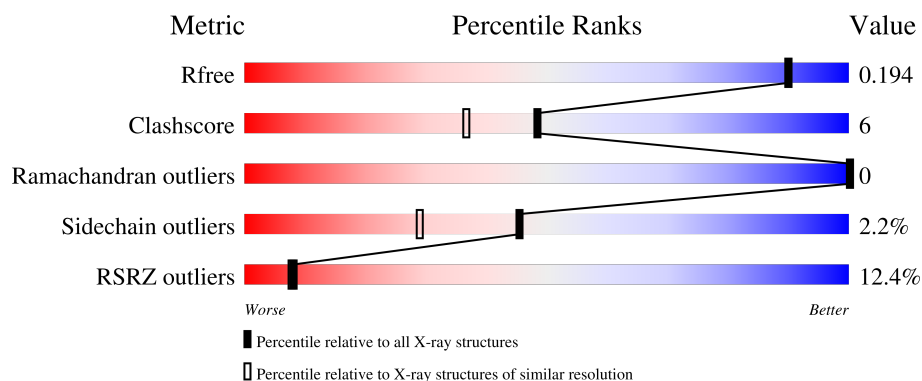
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	447	
2	B	55	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3874 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 Importin subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	426	3260	2075	555	620	10	0	2	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	MET	-	initiating methionine	UNP P52293
A	52	GLY	-	expression tag	UNP P52293
A	53	SER	-	expression tag	UNP P52293
A	54	SER	-	expression tag	UNP P52293
A	55	HIS	-	expression tag	UNP P52293
A	56	HIS	-	expression tag	UNP P52293
A	57	HIS	-	expression tag	UNP P52293
A	58	HIS	-	expression tag	UNP P52293
A	59	HIS	-	expression tag	UNP P52293
A	60	HIS	-	expression tag	UNP P52293
A	61	SER	-	expression tag	UNP P52293
A	62	SER	-	expression tag	UNP P52293
A	63	GLY	-	expression tag	UNP P52293
A	64	LEU	-	expression tag	UNP P52293
A	65	VAL	-	expression tag	UNP P52293
A	66	PRO	-	expression tag	UNP P52293
A	67	ARG	-	expression tag	UNP P52293
A	68	GLY	-	expression tag	UNP P52293
A	69	SER	-	expression tag	UNP P52293
A	70	HIS	-	expression tag	UNP P52293
A	71	MET	-	expression tag	UNP P52293

- Molecule 2 is a protein called Squamous cell carcinoma antigen recognized by T-cells 3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	16	Total	C	N	O	0	0	0
			142	82	37	23			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	595	LEU	-	expression tag	UNP Q15020
B	596	VAL	-	expression tag	UNP Q15020
B	597	PRO	-	expression tag	UNP Q15020
B	598	ARG	-	expression tag	UNP Q15020
B	599	GLY	-	expression tag	UNP Q15020
B	600	SER	-	expression tag	UNP Q15020

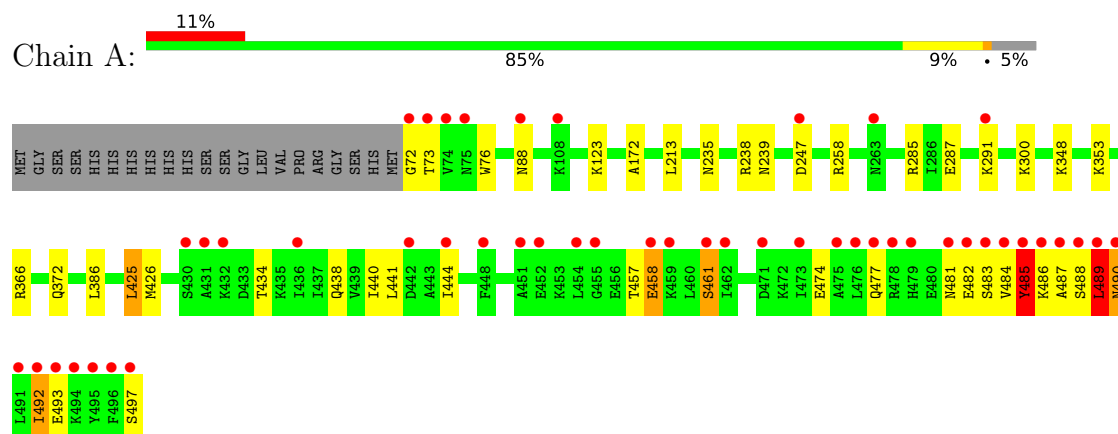
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	446	Total	O	0	0
			446	446		
3	B	26	Total	O	0	0
			26	26		

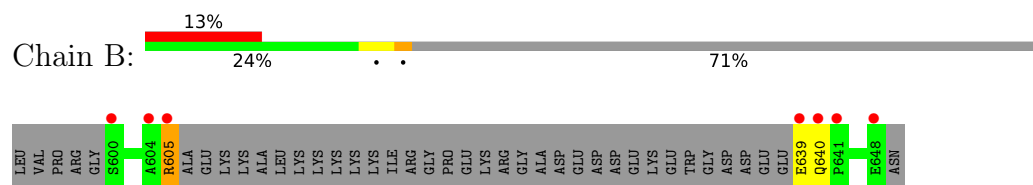
3 Residue-property plots [i](#)

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: Importin subunit alpha-1



• Molecule 2: Squamous cell carcinoma antigen recognized by T-cells 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.15Å 89.99Å 97.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.77 – 1.70 37.77 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.9 (37.77-1.70) 99.0 (37.77-1.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.7.3 _928	Depositor
R, R_{free}	0.191 , 0.219 0.195 , 0.194	Depositor DCC
R_{free} test set	3859 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 33.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3874	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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

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	0.94	26/3321 (0.8%)	0.85	10/4526 (0.2%)
2	B	0.54	0/141	0.98	1/181 (0.6%)
All	All	0.93	26/3462 (0.8%)	0.85	11/4707 (0.2%)

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	489	LEU	C-O	-15.20	1.06	1.24
1	A	488	SER	N-CA	-12.89	1.30	1.46
1	A	483	SER	C-O	-12.82	1.09	1.24
1	A	485	TYR	C-O	-11.14	1.10	1.24
1	A	485	TYR	CA-C	-9.79	1.40	1.52
1	A	488	SER	CA-CB	-9.69	1.37	1.53
1	A	487	ALA	C-O	-8.63	1.13	1.24
1	A	482	GLU	C-O	-8.44	1.14	1.24
1	A	488	SER	CB-OG	-8.24	1.25	1.42
1	A	484	VAL	N-CA	-8.19	1.36	1.46
1	A	481	ASN	C-O	-8.13	1.14	1.23
1	A	484	VAL	CB-CG1	-7.68	1.27	1.52
1	A	484	VAL	CB-CG2	-7.16	1.28	1.52
1	A	487	ALA	C-N	-7.06	1.24	1.33
1	A	490	ASN	C-O	-7.03	1.15	1.24
1	A	484	VAL	C-O	-6.93	1.16	1.24
1	A	488	SER	C-O	-6.60	1.16	1.24
1	A	489	LEU	C-N	-6.57	1.25	1.33
1	A	482	GLU	CA-C	-6.37	1.44	1.52
1	A	487	ALA	CA-C	-6.15	1.44	1.52
1	A	484	VAL	CA-CB	-5.92	1.47	1.54
1	A	490	ASN	N-CA	-5.73	1.39	1.46
1	A	489	LEU	CA-C	-5.63	1.45	1.52
1	A	489	LEU	CG-CD2	-5.48	1.34	1.52
1	A	490	ASN	CB-CG	-5.27	1.38	1.52
1	A	483	SER	CA-CB	-5.19	1.45	1.53

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	488	SER	N-CA-CB	-7.11	99.63	110.16
1	A	485	TYR	N-CA-CB	6.99	120.51	110.16
1	A	487	ALA	CA-C-O	6.26	127.17	119.97
1	A	492	ILE	CA-C-N	-6.16	112.44	120.44
1	A	492	ILE	C-N-CA	-6.16	112.44	120.44
1	A	489	LEU	CA-C-N	-6.00	112.24	120.28
1	A	489	LEU	C-N-CA	-6.00	112.24	120.28
2	B	640	GLN	N-CA-C	-5.85	101.14	109.62
1	A	487	ALA	CA-C-N	-5.25	112.83	120.29
1	A	487	ALA	C-N-CA	-5.25	112.83	120.29
1	A	488	SER	CA-CB-OG	-5.13	100.84	111.10

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	3260	0	3338	35	0
2	B	142	0	153	3	0
3	A	446	0	0	12	2
3	B	26	0	0	3	0
All	All	3874	0	3491	38	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 6.

All (38) 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:348:LYS:NZ	3:A:503:HOH:O	1.95	0.97
1:A:485:TYR:HD2	1:A:486:LYS:N	1.72	0.87
1:A:88:ASN:ND2	3:A:504:HOH:O	2.06	0.87
1:A:72:GLY:N	3:A:506:HOH:O	2.10	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:MET:HE1	1:A:444:ILE:HD11	1.73	0.70
1:A:247:ASP:OD1	3:A:505:HOH:O	2.09	0.70
1:A:287:GLU:OE2	1:A:291:LYS:HE3	1.92	0.69
1:A:386:LEU:HD21	1:A:425:LEU:HD13	1.75	0.69
1:A:485:TYR:CD2	1:A:486:LYS:N	2.61	0.69
1:A:426:MET:HE1	1:A:444:ILE:CD1	2.23	0.68
2:B:639:GLU:OE1	3:B:701:HOH:O	2.12	0.67
2:B:639:GLU:OE2	3:B:702:HOH:O	2.12	0.66
1:A:485:TYR:CD2	1:A:485:TYR:C	2.75	0.61
1:A:485:TYR:HD2	1:A:485:TYR:C	2.08	0.61
1:A:123:LYS:HG2	3:A:524:HOH:O	2.02	0.59
1:A:477:GLN:OE1	1:A:489:LEU:HD22	2.02	0.59
1:A:458:GLU:H	1:A:458:GLU:CD	2.13	0.56
1:A:73:THR:HA	1:A:76:TRP:NE1	2.23	0.53
1:A:172:ALA:HB2	3:A:809:HOH:O	2.08	0.53
1:A:366:ARG:NH2	3:A:507:HOH:O	2.14	0.52
1:A:490:ASN:O	1:A:490:ASN:OD1	2.29	0.51
1:A:492:ILE:O	1:A:493:GLU:C	2.48	0.50
2:B:605:ARG:HG3	3:B:704:HOH:O	2.12	0.50
1:A:489:LEU:CD1	1:A:493:GLU:OE2	2.61	0.48
1:A:434:THR:OG1	3:A:508:HOH:O	2.19	0.48
1:A:213:LEU:O	1:A:258[B]:ARG:NH1	2.46	0.48
1:A:490:ASN:OD1	1:A:490:ASN:C	2.48	0.47
1:A:493:GLU:HA	1:A:497:SER:HB2	1.97	0.47
1:A:474:GLU:HG3	3:A:924:HOH:O	2.16	0.46
1:A:489:LEU:O	1:A:490:ASN:C	2.48	0.45
1:A:238:ARG:O	1:A:239:ASN:HB2	2.17	0.45
1:A:441:LEU:HA	1:A:444:ILE:HD12	2.00	0.44
1:A:300:LYS:NZ	3:A:520:HOH:O	2.51	0.43
1:A:457:THR:O	1:A:461:SER:HB2	2.19	0.43
1:A:425:LEU:HG	1:A:440:ILE:HG23	2.03	0.41
1:A:235:ASN:OD1	3:A:501:HOH:O	2.22	0.41
1:A:285:ARG:HD2	3:A:624:HOH:O	2.22	0.40
1:A:434:THR:O	1:A:438:GLN:HG3	2.21	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:519:HOH:O	3:A:885:HOH:O[3_544]	1.77	0.43
3:A:632:HOH:O	3:A:699:HOH:O[3_544]	2.09	0.11

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	426/447 (95%)	422 (99%)	4 (1%)	0	100	100
2	B	12/55 (22%)	12 (100%)	0	0	100	100
All	All	438/502 (87%)	434 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	359/375 (96%)	352 (98%)	7 (2%)	50	34
2	B	15/47 (32%)	14 (93%)	1 (7%)	15	4
All	All	374/422 (89%)	366 (98%)	8 (2%)	45	30

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	353	LYS
1	A	372	GLN
1	A	425	LEU
1	A	458	GLU
1	A	461	SER
1	A	485	TYR
1	A	489	LEU
2	B	605	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	ASN
1	A	175	HIS
1	A	239	ASN
1	A	449	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

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	426/447 (95%)	0.27	48 (11%)	10 10	10, 23, 61, 79	2 (0%)
2	B	16/55 (29%)	1.47	7 (43%)	0 0	17, 33, 56, 61	0
All	All	442/502 (88%)	0.32	55 (12%)	8 8	10, 23, 61, 79	2 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	497	SER	9.0
1	A	486	LYS	7.5
1	A	485	TYR	6.4
2	B	600	SER	5.4
1	A	478	ARG	4.7
1	A	88	ASN	4.4
1	A	74	VAL	4.0
1	A	495	TYR	3.9
1	A	432	LYS	3.9
1	A	496	PHE	3.7
1	A	489	LEU	3.7
1	A	487	ALA	3.7
1	A	484	VAL	3.5
1	A	72	GLY	3.5
2	B	640	GLN	3.3
1	A	476	LEU	3.1
1	A	482	GLU	3.1
2	B	604	ALA	3.1
1	A	473	ILE	3.1
1	A	471	ASP	3.0
1	A	462	ILE	3.0
2	B	639	GLU	3.0
2	B	605	ARG	2.9
1	A	491	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	452	GLU	2.8
1	A	459	LYS	2.8
1	A	475	ALA	2.8
1	A	483	SER	2.7
1	A	451	ALA	2.7
1	A	493	GLU	2.7
2	B	641	PRO	2.6
1	A	477	GLN	2.6
1	A	490	ASN	2.6
1	A	479	HIS	2.6
1	A	75	ASN	2.6
1	A	291	LYS	2.6
1	A	494	LYS	2.6
1	A	448	PHE	2.6
1	A	492	ILE	2.6
1	A	488	SER	2.5
1	A	458	GLU	2.5
1	A	455	GLY	2.4
1	A	436	ILE	2.4
1	A	108	LYS	2.4
1	A	431	ALA	2.3
1	A	481	ASN	2.2
1	A	430	SER	2.2
1	A	442	ASP	2.2
1	A	444	ILE	2.2
1	A	247	ASP	2.1
2	B	648	GLU	2.1
1	A	263	ASN	2.1
1	A	73	THR	2.1
1	A	461	SER	2.0
1	A	454	LEU	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.