



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:24 PM GMT

PDB ID : 1THS
Title : STRUCTURES OF THROMBIN COMPLEXES WITH A DESIGNED AND
A NATURAL EXOSITE INHIBITOR
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Deposited on : 1993-06-16
Resolution : 2.20 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

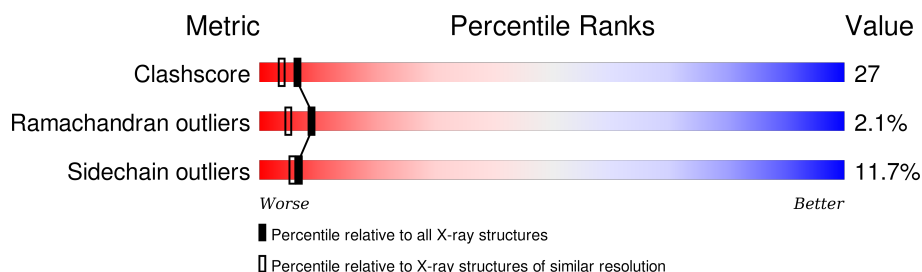
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	36	
2	H	259	
3	I	11	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2529 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 ALPHA-THROMBIN (SMALL SUBUNIT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	33	Total	C	N	O	S	0	0	0
			265	162	45	57	1			

- Molecule 2 is a protein called ALPHA-THROMBIN (LARGE SUBUNIT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	252	Total	C	N	O	S	0	0	0
			2039	1299	360	366	14			

- Molecule 3 is a protein called SYNTHETIC INHIBITOR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	11	Total	C	N	O	0	0	1
			85	56	10	19			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	123	Total	O	0	0
			123	123		
4	L	17	Total	O	0	0
			17	17		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

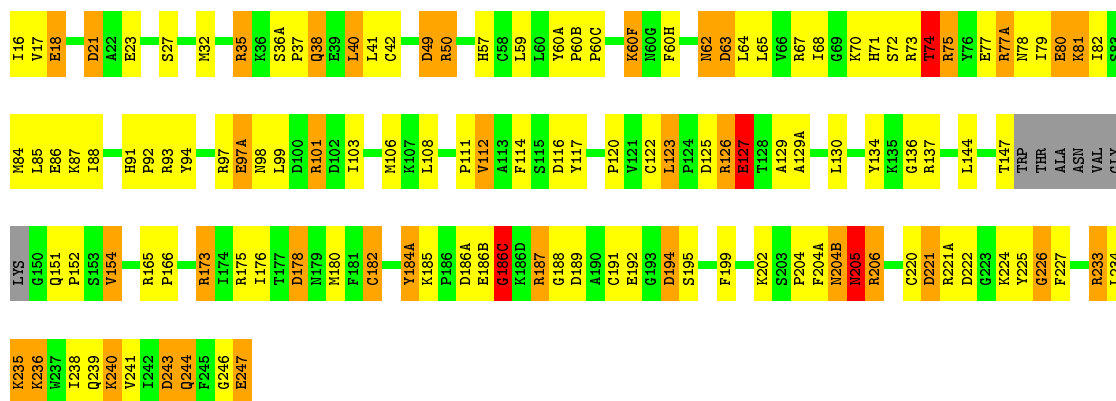
• Molecule 1: ALPHA-THROMBIN (SMALL SUBUNIT)

Chain L: 




• Molecule 2: ALPHA-THROMBIN (LARGE SUBUNIT)

Chain H: 



• Molecule 3: SYNTHETIC INHIBITOR

Chain I: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	72.28 Å 72.73 Å 73.56 Å 90.00° 100.55° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.161 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2529	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	L	1.15	0/267	2.34	12/353 (3.4%)
2	H	1.15	0/2091	2.32	85/2823 (3.0%)
3	I	1.10	0/68	2.59	7/93 (7.5%)
All	All	1.15	0/2426	2.33	104/3269 (3.2%)

There are no bond length outliers.

All (104) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	233	ARG	NE-CZ-NH1	24.05	132.32	120.30
2	H	187	ARG	NE-CZ-NH1	23.98	132.29	120.30
2	H	187	ARG	CD-NE-CZ	19.00	150.20	123.60
2	H	173	ARG	NE-CZ-NH1	17.83	129.22	120.30
2	H	187	ARG	NE-CZ-NH2	-16.06	112.27	120.30
2	H	93	ARG	NE-CZ-NH1	16.00	128.30	120.30
1	L	15	ARG	CD-NE-CZ	15.25	144.95	123.60
2	H	233	ARG	NE-CZ-NH2	-14.60	113.00	120.30
2	H	184(A)	TYR	CB-CG-CD1	-13.88	112.67	121.00
2	H	206	ARG	NE-CZ-NH1	13.71	127.15	120.30
2	H	93	ARG	NE-CZ-NH2	-13.42	113.59	120.30
2	H	184(A)	TYR	CB-CG-CD2	12.65	128.59	121.00
2	H	206	ARG	NE-CZ-NH2	-11.40	114.60	120.30
2	H	35	ARG	NE-CZ-NH1	11.32	125.96	120.30
2	H	175	ARG	NE-CZ-NH2	10.68	125.64	120.30
2	H	233	ARG	CD-NE-CZ	10.34	138.08	123.60
2	H	243	ASP	CA-CB-CG	10.26	135.97	113.40
2	H	93	ARG	CD-NE-CZ	10.03	137.64	123.60
2	H	243	ASP	CB-CG-OD1	9.84	127.16	118.30
2	H	35	ARG	NE-CZ-NH2	-9.69	115.45	120.30
2	H	125	ASP	CB-CG-OD1	9.64	126.97	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	97	ARG	CD-NE-CZ	-9.36	110.50	123.60
2	H	60(A)	TYR	CB-CG-CD1	-9.04	115.58	121.00
2	H	192	GLU	OE1-CD-OE2	-8.91	112.61	123.30
2	H	221	ASP	CB-CG-OD2	8.84	126.25	118.30
2	H	225	TYR	CB-CG-CD2	-8.63	115.82	121.00
2	H	186(C)	GLY	C-N-CA	8.27	142.38	121.70
1	L	1(A)	ASP	CB-CG-OD2	8.15	125.64	118.30
3	I	61	GLU	CA-CB-CG	8.07	131.16	113.40
2	H	221	ASP	CB-CG-OD1	-8.04	111.06	118.30
2	H	97	ARG	NE-CZ-NH1	-8.01	116.30	120.30
2	H	101	ARG	CD-NE-CZ	-7.92	112.52	123.60
3	I	62	GLU	CB-CG-CD	7.91	135.55	114.20
2	H	27	SER	CB-CA-C	7.90	125.11	110.10
2	H	80	GLU	CG-CD-OE1	7.85	134.01	118.30
2	H	77(A)	ARG	CA-C-O	-7.75	103.82	120.10
2	H	77(A)	ARG	CA-C-N	7.64	134.02	117.20
2	H	194	ASP	CB-CG-OD2	-7.61	111.45	118.30
3	I	56	TYR	CB-CG-CD1	7.60	125.56	121.00
2	H	27	SER	N-CA-CB	-7.59	99.11	110.50
2	H	221(A)	ARG	NE-CZ-NH2	7.51	124.06	120.30
3	I	56	TYR	CB-CG-CD2	-7.46	116.53	121.00
2	H	49	ASP	CB-CG-OD2	7.38	124.95	118.30
2	H	178	ASP	CB-CG-OD1	7.38	124.94	118.30
3	I	56	TYR	N-CA-CB	7.29	123.73	110.60
2	H	21	ASP	CB-CG-OD2	-7.27	111.75	118.30
2	H	173	ARG	NH1-CZ-NH2	-7.25	111.43	119.40
2	H	117	TYR	CB-CG-CD2	-7.16	116.71	121.00
2	H	225	TYR	CB-CG-CD1	6.99	125.20	121.00
2	H	94	TYR	CB-CG-CD1	6.97	125.19	121.00
2	H	75	ARG	CA-CB-CG	-6.90	98.21	113.40
2	H	116	ASP	CB-CG-OD1	6.64	124.28	118.30
2	H	192	GLU	CG-CD-OE2	6.64	131.58	118.30
2	H	246	GLY	C-N-CA	6.53	138.03	121.70
2	H	94	TYR	CB-CG-CD2	-6.49	117.11	121.00
2	H	137	ARG	NE-CZ-NH1	-6.38	117.11	120.30
2	H	175	ARG	NE-CZ-NH1	-6.36	117.12	120.30
3	I	62	GLU	OE1-CD-OE2	-6.34	115.69	123.30
2	H	38	GLN	O-C-N	6.34	132.84	122.70
1	L	1(A)	ASP	CB-CG-OD1	-6.28	112.65	118.30
2	H	75	ARG	NE-CZ-NH2	-6.22	117.19	120.30
2	H	123	LEU	CB-CA-C	6.21	121.99	110.20
2	H	226	GLY	O-C-N	6.10	132.46	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	77(A)	ARG	N-CA-CB	6.08	121.54	110.60
2	H	205	ASN	CB-CA-C	6.04	122.48	110.40
2	H	84	MET	CB-CA-C	6.00	122.40	110.40
2	H	62	ASN	CA-CB-CG	-5.99	100.22	113.40
1	L	14(J)	TYR	CA-C-N	-5.93	104.16	117.20
2	H	234	LEU	CB-CA-C	5.80	121.22	110.20
2	H	127	GLU	CA-CB-CG	5.75	126.06	113.40
2	H	137	ARG	NE-CZ-NH2	5.68	123.14	120.30
2	H	77	GLU	OE1-CD-OE2	-5.67	116.50	123.30
2	H	247	GLU	CA-CB-CG	5.66	125.86	113.40
1	L	4	ARG	CG-CD-NE	5.65	123.66	111.80
2	H	73	ARG	CD-NE-CZ	5.65	131.51	123.60
2	H	125	ASP	CB-CG-OD2	-5.59	113.27	118.30
2	H	134	TYR	CB-CG-CD2	-5.58	117.65	121.00
3	I	62	GLU	N-CA-CB	5.56	120.62	110.60
1	L	14(G)	LEU	CA-CB-CG	5.56	128.09	115.30
2	H	42	CYS	CA-CB-SG	5.54	123.98	114.00
2	H	18	GLU	CG-CD-OE1	5.50	129.29	118.30
1	L	14(K)	ILE	CB-CA-C	5.40	122.40	111.60
2	H	233	ARG	NH1-CZ-NH2	-5.40	113.46	119.40
2	H	194	ASP	OD1-CG-OD2	5.39	133.54	123.30
2	H	63	ASP	O-C-N	5.32	131.21	122.70
2	H	129(A)	ALA	CB-CA-C	5.31	118.06	110.10
2	H	67	ARG	NE-CZ-NH2	5.30	122.95	120.30
2	H	84	MET	CA-CB-CG	-5.29	104.30	113.30
2	H	80	GLU	OE1-CD-OE2	-5.26	116.99	123.30
2	H	74	THR	N-CA-CB	-5.25	100.33	110.30
2	H	78	ASN	CA-CB-CG	5.22	124.90	113.40
1	L	14(A)	LYS	CA-C-O	-5.17	109.23	120.10
2	H	244	GLN	CB-CG-CD	5.17	125.05	111.60
2	H	220	CYS	CA-C-N	5.17	128.56	117.20
1	L	7	PHE	CB-CA-C	5.16	120.72	110.40
2	H	189	ASP	CB-CG-OD1	5.16	122.95	118.30
2	H	192	GLU	CB-CA-C	5.10	120.60	110.40
1	L	14(L)	ASP	CB-CG-OD2	5.09	122.88	118.30
2	H	224	LYS	CB-CA-C	5.09	120.59	110.40
2	H	64	LEU	CA-C-N	-5.06	106.08	117.20
1	L	14(E)	GLU	CA-CB-CG	5.05	124.52	113.40
2	H	97(A)	GLU	CA-CB-CG	5.05	124.50	113.40
2	H	40	LEU	N-CA-CB	5.03	120.46	110.40
1	L	14	ASP	CB-CG-OD1	-5.01	113.79	118.30

There are no chirality outliers.

There are no planarity outliers.

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	L	265	0	259	39	1
2	H	2039	0	2009	115	1
3	I	85	0	74	7	0
4	H	123	0	0	5	0
4	L	17	0	0	1	0
All	All	2529	0	2342	130	1

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 27.

All (130) 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:L:1(D):GLY:CA	2:H:123:LEU:H	1.51	1.24
2:H:126:ARG:CB	2:H:126:ARG:HH11	1.57	1.16
1:L:1(D):GLY:N	2:H:123:LEU:H	1.45	1.15
1:L:1(D):GLY:HA3	2:H:122:CYS:HA	1.30	1.12
1:L:1(E):SER:HB2	2:H:123:LEU:O	1.52	1.08
2:H:126:ARG:HB3	2:H:126:ARG:HH11	0.95	1.08
1:L:1(D):GLY:CA	2:H:123:LEU:N	2.18	1.07
2:H:126:ARG:HB3	2:H:126:ARG:NH1	1.71	1.06
2:H:50:ARG:NH1	2:H:86:GLU:OE1	1.92	1.01
1:L:14(J):TYR:C	1:L:14(K):ILE:HG13	1.80	0.97
1:L:1(D):GLY:H	2:H:123:LEU:H	1.12	0.94
1:L:1(D):GLY:HA3	2:H:122:CYS:CA	1.96	0.94
2:H:147:THR:HA	4:H:476:HOH:O	1.69	0.91
1:L:1(E):SER:CB	2:H:123:LEU:O	2.19	0.91
2:H:87:LYS:HD3	2:H:88:ILE:H	1.39	0.85
1:L:1(D):GLY:CA	2:H:122:CYS:HA	2.07	0.83
2:H:236:LYS:HD2	2:H:239:GLN:NE2	1.92	0.83
1:L:14(I):SER:C	1:L:14(K):ILE:H	1.79	0.82
1:L:1(D):GLY:H	2:H:123:LEU:N	1.79	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:49:ASP:OD2	2:H:111:PRO:HB3	1.83	0.79
2:H:50:ARG:HA	2:H:108:LEU:HD12	1.66	0.78
2:H:235:LYS:HD3	2:H:239:GLN:OE1	1.84	0.78
1:L:1(D):GLY:HA2	2:H:123:LEU:N	2.00	0.77
1:L:1(C):GLU:HG2	2:H:120:PRO:HG2	1.65	0.77
2:H:65:LEU:HD21	3:I:64:ALC:HD13	1.67	0.76
1:L:14(A):LYS:HG2	2:H:23:GLU:OE2	1.87	0.74
1:L:15:ARG:HD2	2:H:204:PRO:O	1.88	0.74
2:H:35:ARG:O	2:H:38:GLN:HA	1.89	0.72
1:L:1(D):GLY:HA3	2:H:123:LEU:N	2.05	0.72
2:H:71:HIS:CD2	2:H:154:VAL:HG22	2.25	0.72
2:H:127:GLU:OE2	4:H:533:HOH:O	2.08	0.72
2:H:50:ARG:C	2:H:108:LEU:HD12	2.11	0.71
1:L:14(A):LYS:HE2	2:H:23:GLU:CD	2.11	0.71
2:H:62:ASN:ND2	2:H:62:ASN:H	1.88	0.70
2:H:87:LYS:HD3	2:H:88:ILE:N	2.07	0.70
2:H:236:LYS:HD2	2:H:239:GLN:HE22	1.54	0.70
2:H:50:ARG:CA	2:H:108:LEU:HD12	2.25	0.66
1:L:1(D):GLY:HA3	2:H:122:CYS:C	2.16	0.66
2:H:240:LYS:HD3	2:H:244:GLN:OE1	1.94	0.66
1:L:1(C):GLU:OE2	1:L:1(B):ALA:HB3	1.96	0.66
2:H:126:ARG:CB	2:H:126:ARG:NH1	2.40	0.65
2:H:187:ARG:HD3	2:H:221:ASP:OD2	1.97	0.64
1:L:1(D):GLY:HA2	2:H:123:LEU:H	1.52	0.64
2:H:126:ARG:NH1	2:H:127:GLU:OE1	2.30	0.64
2:H:74:THR:HG22	2:H:75:ARG:HG3	1.80	0.63
2:H:185:LYS:HB3	2:H:186(A):ASP:OD1	1.99	0.62
2:H:70:LYS:HE3	2:H:72:SER:O	2.00	0.61
2:H:185:LYS:HB2	2:H:186(B):GLU:HG3	1.82	0.60
2:H:144:LEU:HD11	2:H:152:PRO:CA	2.31	0.60
1:L:1(C):GLU:HG2	2:H:120:PRO:CG	2.30	0.60
2:H:71:HIS:CD2	2:H:154:VAL:CG2	2.85	0.60
2:H:186(B):GLU:O	2:H:186(C):GLY:O	2.20	0.60
1:L:1(D):GLY:HA2	2:H:123:LEU:HB2	1.84	0.59
2:H:59:LEU:HD13	2:H:88:ILE:HD13	1.84	0.58
2:H:91:HIS:CE1	2:H:101:ARG:HD3	2.38	0.58
1:L:1(D):GLY:HA2	2:H:123:LEU:CB	2.33	0.58
2:H:236:LYS:HD3	2:H:236:LYS:N	2.13	0.58
1:L:14(A):LYS:HE2	2:H:23:GLU:OE1	2.03	0.58
1:L:1(D):GLY:N	2:H:123:LEU:N	2.29	0.58
2:H:186(B):GLU:O	2:H:186(C):GLY:C	2.41	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:60:PRO:C	3:I:62:GLU:N	2.57	0.57
1:L:14(J):TYR:O	1:L:14(K):ILE:HG13	2.04	0.57
1:L:1(E):SER:O	1:L:1(D):GLY:C	2.44	0.57
1:L:15:ARG:HB2	2:H:204:PRO:O	2.05	0.56
2:H:60(F):LYS:HD2	2:H:60(H):PHE:HE2	1.72	0.55
2:H:178:ASP:O	2:H:233:ARG:HD2	2.06	0.55
2:H:80:GLU:C	2:H:81:LYS:HD2	2.27	0.55
2:H:82:ILE:HD12	3:I:59:ILE:HD13	1.89	0.55
2:H:49:ASP:OD2	2:H:111:PRO:CB	2.55	0.55
2:H:80:GLU:O	2:H:81:LYS:HD2	2.07	0.54
3:I:63:ALA:C	3:I:65:GLU:N	2.56	0.54
2:H:60(F):LYS:HD2	2:H:60(H):PHE:CE2	2.42	0.54
2:H:165:ARG:N	2:H:166:PRO:HD2	2.23	0.54
2:H:191:CYS:O	2:H:194:ASP:HB2	2.07	0.54
2:H:144:LEU:HD11	2:H:152:PRO:HA	1.89	0.54
1:L:1(E):SER:O	1:L:1(C):GLU:N	2.42	0.53
2:H:129:ALA:O	2:H:130:LEU:HB2	2.09	0.53
1:L:1(E):SER:HB3	2:H:123:LEU:O	2.09	0.52
2:H:103:ILE:HD11	2:H:238:ILE:HD11	1.91	0.52
3:I:60:PRO:C	3:I:62:GLU:H	2.12	0.51
1:L:14(A):LYS:CG	2:H:23:GLU:OE2	2.57	0.50
2:H:21:ASP:HB3	2:H:154:VAL:CG1	2.42	0.50
1:L:1(D):GLY:CA	2:H:122:CYS:CA	2.76	0.49
2:H:17:VAL:O	2:H:18:GLU:HB2	2.12	0.49
4:L:526:HOH:O	2:H:123:LEU:HD12	2.12	0.49
2:H:68:ILE:HD12	2:H:112:VAL:HG21	1.94	0.49
2:H:87:LYS:CD	2:H:88:ILE:N	2.75	0.49
3:I:60:PRO:O	3:I:62:GLU:N	2.46	0.49
2:H:57:HIS:NE2	2:H:195:SER:OG	2.45	0.49
2:H:85:LEU:HD11	2:H:106:MET:CE	2.42	0.49
2:H:98:ASN:OD1	2:H:98:ASN:N	2.44	0.48
1:L:1(C):GLU:H	1:L:1:CYS:CB	2.26	0.48
1:L:5:PRO:HA	1:L:9:LYS:HB2	1.94	0.48
2:H:205:ASN:O	2:H:205:ASN:ND2	2.47	0.48
1:L:1(C):GLU:HG3	1:L:1(B):ALA:H	1.79	0.47
2:H:184(A):TYR:HB2	4:H:509:HOH:O	2.14	0.47
2:H:32:MET:HG3	2:H:40:LEU:CD1	2.44	0.47
2:H:17:VAL:O	2:H:188:GLY:HA2	2.14	0.47
2:H:136:GLY:HA3	2:H:199:PHE:CZ	2.50	0.47
1:L:15:ARG:NH2	2:H:204(A):PHE:O	2.31	0.47
1:L:14(G):LEU:HD21	2:H:202:LYS:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:36(A):SER:HA	2:H:37:PRO:C	2.34	0.47
2:H:204(B):ASN:ND2	2:H:206:ARG:HB2	2.30	0.47
2:H:205:ASN:ND2	2:H:205:ASN:C	2.69	0.46
2:H:16:ILE:N	2:H:194:ASP:OD2	2.49	0.46
2:H:16:ILE:O	2:H:144:LEU:HA	2.15	0.46
2:H:182:CYS:HA	2:H:226:GLY:O	2.16	0.46
2:H:126:ARG:HH11	2:H:126:ARG:CG	2.27	0.45
2:H:85:LEU:CD1	2:H:106:MET:HE3	2.45	0.45
2:H:185:LYS:N	2:H:186(B):GLU:OE1	2.34	0.45
2:H:205:ASN:ND2	4:H:508:HOH:O	2.49	0.45
3:I:55:SIN:O3	3:I:56:TYR:CD2	2.69	0.44
2:H:126:ARG:NH1	2:H:126:ARG:CG	2.80	0.44
2:H:144:LEU:HD21	2:H:152:PRO:HB3	1.98	0.44
2:H:204(B):ASN:HD22	2:H:204(B):ASN:C	2.20	0.44
2:H:114:PHE:HB3	4:H:403:HOH:O	2.18	0.44
2:H:85:LEU:CD1	2:H:106:MET:CE	2.95	0.43
2:H:57:HIS:CE1	2:H:195:SER:OG	2.72	0.43
2:H:60(B):PRO:N	2:H:60(C):PRO:CD	2.82	0.42
2:H:71:HIS:NE2	2:H:154:VAL:CG2	2.82	0.42
2:H:101:ARG:HD2	2:H:101:ARG:HH11	1.59	0.42
2:H:151:GLN:HA	2:H:152:PRO:HD3	1.91	0.42
2:H:176:ILE:HD12	2:H:227:PHE:CE2	2.55	0.41
2:H:165:ARG:NH2	2:H:180:MET:O	2.52	0.41
2:H:71:HIS:NE2	2:H:154:VAL:HG22	2.35	0.41
1:L:14(H):GLU:HA	1:L:14(L):ASP:HA	2.02	0.41
2:H:74:THR:CG2	2:H:75:ARG:HG3	2.49	0.41
2:H:130:LEU:HD23	2:H:130:LEU:HA	1.72	0.41
2:H:50:ARG:NH1	2:H:108:LEU:O	2.54	0.40
2:H:165:ARG:N	2:H:166:PRO:CD	2.85	0.40

All (1) 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:L:14(L):ASP:O	2:H:173:ARG:NH2[4_556]	1.83	0.37

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	L	31/36 (86%)	22 (71%)	6 (19%)	3 (10%)	1	0
2	H	248/259 (96%)	233 (94%)	13 (5%)	2 (1%)	24	22
3	I	7/11 (64%)	4 (57%)	2 (29%)	1 (14%)	0	0
All	All	286/306 (94%)	259 (91%)	21 (7%)	6 (2%)	9	5

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	1(D)	GLY
1	L	14(M)	GLY
2	H	186(C)	GLY
1	L	14(L)	ASP
3	I	63	ALA
2	H	77(A)	ARG

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	L	29/31 (94%)	23 (79%)	6 (21%)	1	1
2	H	220/225 (98%)	196 (89%)	24 (11%)	8	7
3	I	7/8 (88%)	7 (100%)	0	100	100
All	All	256/264 (97%)	226 (88%)	30 (12%)	7	5

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	1(C)	GLU
1	L	9	LYS
1	L	14(A)	LYS
1	L	14(F)	LEU
1	L	14(K)	ILE
1	L	14(L)	ASP
2	H	41	LEU
2	H	50	ARG
2	H	60(F)	LYS
2	H	63	ASP
2	H	74	THR
2	H	79	ILE
2	H	81	LYS
2	H	92	PRO
2	H	97(A)	GLU
2	H	99	LEU
2	H	112	VAL
2	H	126	ARG
2	H	127	GLU
2	H	154	VAL
2	H	182	CYS
2	H	204(B)	ASN
2	H	205	ASN
2	H	222	ASP
2	H	235	LYS
2	H	236	LYS
2	H	240	LYS
2	H	241	VAL
2	H	243	ASP
2	H	247	GLU

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

Mol	Chain	Res	Type
2	H	62	ASN
2	H	156	GLN
2	H	204(B)	ASN
2	H	205	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
3	ALC	I	64	3	10,11,12	0.50	0	10,13,15	0.57	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
3	ALC	I	64	3	-	0/4/14/16	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	64	ALC	1	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.