



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:06 AM UTC

PDB ID : 1FPH / pdb_00001fph
Title : THE INTERACTION OF THROMBIN WITH FIBRINOGEN: A STRUCTURAL BASIS FOR ITS SPECIFICITY
Authors : Stubbs, M.T.; Bode, W.
Deposited on : 1993-04-21
Resolution : 2.50 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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

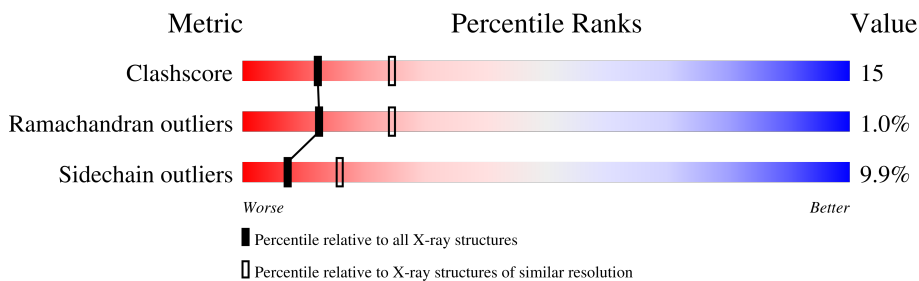
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	36	53% (green), 33% (yellow), 14% (orange)
2	H	259	51% (green), 42% (yellow), 7% (orange)
3	I	12	33% (green), 33% (yellow), 25% (orange), 8% (red)
4	F	12	50% (green), 33% (yellow), 8% (orange), 8% (red)

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2727 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
			Total	C	N	O	S			
1	L	36	287	177	48	61	1	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	259	2093	1334	370	375	14	0	0	0

- Molecule 3 is a protein called HIRUDIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	I	12	104	66	13	25	0	0	0

- Molecule 4 is a protein called FIBRINOPEPTIDE A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	F	12	75	47	13	15	0	0	1

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	22	Total	O	0	0
			22	22		
5	H	140	Total	O	0	0
			140	140		
5	I	4	Total	O	0	0
			4	4		
5	F	2	Total	O	0	0
			2	2		

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. 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. 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.

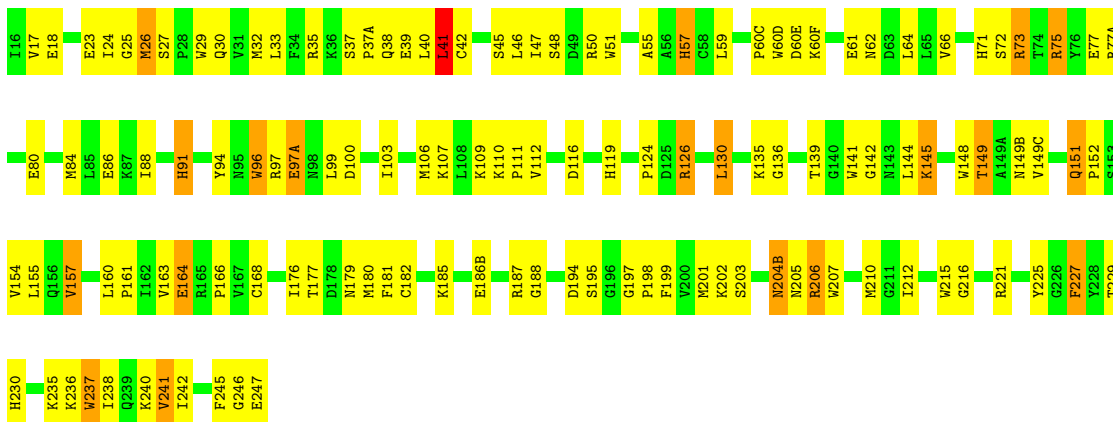
- Molecule 1: ALPHA-THROMBIN (SMALL SUBUNIT)

Chain L: 



- Molecule 2: ALPHA-THROMBIN (LARGE SUBUNIT)

Chain H: 



- Molecule 3: HIRUDIN

Chain I: 



- Molecule 4: FIBRINOPEPTIDE A

Chain F: 



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	90.34Å 90.34Å 132.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	EREF	Depositor
R, R_{free}	0.166 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2727	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

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: ACE, 0QE, AR7

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	0.96	0/290	1.69	3/384 (0.8%)
2	H	1.34	19/2148 (0.9%)	1.75	32/2903 (1.1%)
3	I	0.99	0/106	2.15	3/141 (2.1%)
4	F	0.76	0/61	2.17	3/81 (3.7%)
All	All	1.28	19/2605 (0.7%)	1.77	41/3509 (1.2%)

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	L	0	1
2	H	0	8
3	I	0	2
All	All	0	11

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	91	HIS	CE1-NE2	10.86	1.43	1.32
2	H	119	HIS	CE1-NE2	9.65	1.42	1.32
2	H	57	HIS	CE1-NE2	9.48	1.42	1.32
2	H	96	TRP	NE1-CE2	-9.28	1.27	1.37
2	H	148	TRP	NE1-CE2	-9.09	1.27	1.37
2	H	51	TRP	NE1-CE2	-8.85	1.27	1.37
2	H	91	HIS	ND1-CE1	8.78	1.41	1.32
2	H	215	TRP	NE1-CE2	-8.71	1.27	1.37
2	H	71	HIS	ND1-CE1	8.65	1.41	1.32
2	H	237	TRP	NE1-CE2	-8.38	1.28	1.37
2	H	60(D)	TRP	NE1-CE2	-8.35	1.28	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	29	TRP	NE1-CE2	-8.28	1.28	1.37
2	H	141	TRP	NE1-CE2	-8.08	1.28	1.37
2	H	207	TRP	NE1-CE2	-7.92	1.28	1.37
2	H	119	HIS	ND1-CE1	7.73	1.40	1.32
2	H	57	HIS	ND1-CE1	7.73	1.40	1.32
2	H	230	HIS	CE1-NE2	7.00	1.39	1.32
2	H	71	HIS	CE1-NE2	6.08	1.38	1.32
2	H	230	HIS	ND1-CE1	5.48	1.38	1.32

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	27	SER	O-C-N	9.64	129.04	121.23
2	H	60(E)	ASP	CA-CB-CG	-8.37	104.23	112.60
2	H	221	ARG	CD-NE-CZ	-8.02	113.17	124.40
1	L	4	ARG	N-CA-CB	-7.71	97.44	110.01
2	H	179	ASN	CA-CB-CG	-7.60	105.00	112.60
4	F	7	ASP	CA-CB-CG	-7.25	105.34	112.60
2	H	27	SER	CB-CA-C	-7.13	100.80	111.27
3	I	59	ILE	N-CA-CB	6.97	120.97	111.21
2	H	216	GLY	CA-C-O	-6.81	114.92	121.87
1	L	14(H)	GLU	CB-CG-CD	-6.73	101.16	112.60
2	H	35	ARG	CD-NE-CZ	-6.55	115.23	124.40
2	H	41	LEU	N-CA-C	6.54	121.38	113.41
2	H	142	GLY	O-C-N	6.39	129.17	122.59
2	H	235	LYS	N-CA-C	6.18	118.10	111.36
2	H	91	HIS	CA-CB-CG	-6.17	107.63	113.80
2	H	42	CYS	CA-C-N	-5.97	117.11	122.43
2	H	42	CYS	C-N-CA	-5.97	117.11	122.43
2	H	194	ASP	CA-CB-CG	-5.90	106.70	112.60
2	H	27	SER	CA-C-O	-5.88	114.81	121.28
2	H	75	ARG	N-CA-CB	5.87	118.62	110.17
2	H	39	GLU	CB-CG-CD	-5.79	102.76	112.60
2	H	245	PHE	CA-CB-CG	-5.74	108.06	113.80
4	F	7	ASP	CA-C-N	5.67	127.82	120.44
4	F	7	ASP	C-N-CA	5.67	127.82	120.44
3	I	58	GLU	CB-CA-C	-5.62	99.24	110.42
2	H	59	LEU	N-CA-C	-5.53	106.58	113.55
2	H	50	ARG	CB-CA-C	-5.49	100.26	109.27
2	H	149	THR	CA-C-O	5.45	126.81	120.49
2	H	86	GLU	CB-CG-CD	-5.44	103.35	112.60
2	H	181	PHE	CA-CB-CG	5.32	119.11	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	38	GLN	CB-CG-CD	-5.29	103.62	112.60
2	H	149	THR	CA-CB-CG2	5.26	119.44	110.50
2	H	168	CYS	O-C-N	5.23	127.66	122.12
3	I	56	PHE	CA-CB-CG	-5.19	108.61	113.80
2	H	207	TRP	N-CA-C	5.16	117.65	109.24
2	H	227	PHE	CA-CB-CG	-5.14	108.66	113.80
2	H	73	ARG	O-C-N	5.13	128.00	122.15
2	H	204(B)	ASN	O-C-N	5.13	128.45	122.24
1	L	1(A)	ASP	N-CA-CB	-5.08	103.24	110.46
2	H	145	LYS	CA-C-O	-5.02	115.73	121.40
2	H	145	LYS	N-CA-CB	-5.01	102.97	111.69

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	124	PRO	Mainchain
2	H	157	VAL	Mainchain
2	H	180	MET	Mainchain
2	H	187	ARG	Mainchain
2	H	206	ARG	Mainchain
2	H	238	ILE	Mainchain
2	H	246	GLY	Mainchain
2	H	55	ALA	Mainchain
3	I	58	GLU	Peptide,Mainchain
1	L	1(F)	GLY	Mainchain

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	L	287	0	278	11	6
2	H	2093	0	2064	67	5
3	I	104	0	85	7	0
4	F	75	0	68	9	0
5	F	2	0	0	0	0
5	H	140	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	I	4	0	0	0	0
5	L	22	0	0	0	1
All	All	2727	0	2495	78	7

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 15.

All (78) 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)
2:H:195:SER:OG	4:F:16:AR7:C	1.84	1.24
2:H:99:LEU:HD11	4:F:15:VAL:HG12	1.25	1.12
2:H:185:LYS:HB2	2:H:186(B):GLU:HG3	1.40	1.02
2:H:45:SER:HB3	2:H:198:PRO:HG3	1.51	0.93
2:H:23:GLU:H	2:H:26:MET:HE3	1.34	0.91
2:H:195:SER:OG	4:F:17:0QE:C1	2.18	0.91
1:L:6:LEU:HD23	2:H:25:GLY:HA3	1.65	0.79
2:H:73:ARG:HH22	3:I:55:ASP:CG	1.99	0.69
2:H:33:LEU:HD21	2:H:106:MET:HE1	1.76	0.67
2:H:32:MET:SD	2:H:40:LEU:HD12	2.37	0.64
2:H:195:SER:CB	4:F:16:AR7:C	2.75	0.64
2:H:97(A):GLU:HG3	4:F:6:ACE:H2	1.81	0.62
2:H:164:GLU:HB2	2:H:166:PRO:HD2	1.83	0.60
2:H:203:SER:HB3	2:H:204(B):ASN:HD21	1.67	0.60
2:H:144:LEU:HD21	2:H:152:PRO:HB3	1.85	0.59
2:H:204(B):ASN:C	2:H:204(B):ASN:HD22	2.11	0.58
2:H:33:LEU:HB3	2:H:41:LEU:HD12	1.85	0.58
2:H:72:SER:CB	2:H:75:ARG:HG2	2.35	0.56
2:H:237:TRP:O	2:H:241:VAL:HG13	2.05	0.55
1:L:6:LEU:CD2	2:H:25:GLY:HA3	2.33	0.55
2:H:212:ILE:HB	2:H:229:THR:HB	1.90	0.54
2:H:135:LYS:HA	2:H:161:PRO:HA	1.91	0.52
2:H:61:GLU:HG3	2:H:88:ILE:HG13	1.92	0.52
2:H:24:ILE:HD12	2:H:24:ILE:H	1.75	0.52
2:H:99:LEU:HD11	4:F:15:VAL:CG1	2.18	0.51
2:H:163:VAL:HG21	2:H:225:TYR:CD1	2.45	0.51
2:H:149:THR:HG22	2:H:149(C):VAL:HG23	1.93	0.50
2:H:136:GLY:HA3	2:H:199:PHE:CZ	2.45	0.50
2:H:204(B):ASN:HD22	2:H:205:ASN:N	2.09	0.50
1:L:3:LEU:HG	2:H:206:ARG:HG2	1.95	0.49
2:H:139:THR:HG22	2:H:157:VAL:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:195:SER:CB	4:F:17:0QE:C1	2.90	0.49
2:H:110:LYS:HG2	2:H:111:PRO:HD2	1.95	0.49
2:H:18:GLU:HB2	2:H:188:GLY:HA2	1.95	0.49
2:H:203:SER:HB3	2:H:204(B):ASN:ND2	2.27	0.49
2:H:60(C):PRO:HD3	2:H:96:TRP:CZ3	2.48	0.48
1:L:7:PHE:CE2	1:L:14:ASP:HB3	2.48	0.48
2:H:164:GLU:H	2:H:164:GLU:CD	2.20	0.48
2:H:17:VAL:O	2:H:188:GLY:HA2	2.13	0.48
2:H:94:TYR:CZ	2:H:96:TRP:HB3	2.48	0.48
2:H:182:CYS:HB3	2:H:227:PHE:CE2	2.49	0.47
2:H:240:LYS:HE2	2:H:241:VAL:HG12	1.95	0.47
2:H:47:ILE:HD11	2:H:242:ILE:HD11	1.96	0.46
2:H:91:HIS:HB2	2:H:103:ILE:HG23	1.97	0.46
2:H:23:GLU:N	2:H:26:MET:HE3	2.17	0.46
1:L:6:LEU:HD11	2:H:116:ASP:HB3	1.99	0.45
2:H:202:LYS:HE2	2:H:205:ASN:ND2	2.32	0.44
3:I:59:ILE:HG12	3:I:64:LEU:HD21	1.99	0.44
2:H:84:MET:CB	2:H:109:LYS:HD2	2.47	0.44
2:H:135:LYS:O	2:H:201:MET:HE3	2.18	0.43
2:H:149:THR:HG22	2:H:149(C):VAL:CG2	2.49	0.42
2:H:99:LEU:HD12	4:F:8:PHE:CZ	2.54	0.42
2:H:100:ASP:CG	2:H:177:THR:HG21	2.44	0.42
2:H:130:LEU:HD11	2:H:210:MET:HG3	2.02	0.42
2:H:204(B):ASN:C	2:H:204(B):ASN:ND2	2.77	0.42
1:L:3:LEU:HD11	2:H:206:ARG:HE	1.84	0.42
3:I:59:ILE:HB	3:I:60:PRO:HD2	2.02	0.42
1:L:14(B):THR:O	1:L:14(E):GLU:HB3	2.19	0.42
2:H:96:TRP:HA	2:H:99:LEU:HD23	2.02	0.42
2:H:37:SER:HA	2:H:37(A):PRO:HA	1.71	0.42
1:L:1(H):THR:N	2:H:126:ARG:HB2	2.35	0.42
2:H:195:SER:C	2:H:197:GLY:H	2.27	0.42
2:H:201:MET:HB2	2:H:210:MET:CE	2.50	0.42
1:L:14(D):ARG:HB3	1:L:15:ARG:HH22	1.84	0.42
2:H:151:GLN:HE21	2:H:151:GLN:HB3	1.46	0.42
2:H:197:GLY:HA2	2:H:198:PRO:HD3	1.69	0.41
3:I:59:ILE:HD13	3:I:59:ILE:HG21	1.83	0.41
2:H:77:GLU:O	2:H:80:GLU:HG2	2.21	0.41
2:H:110:LYS:HE3	2:H:110:LYS:HB2	1.82	0.41
3:I:60:PRO:HG2	3:I:63:TYR:CE2	2.56	0.41
2:H:57:HIS:CD2	4:F:15:VAL:HB	2.56	0.40
1:L:14(H):GLU:OE1	1:L:15:ARG:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:84:MET:HB3	2:H:109:LYS:HD2	2.03	0.40
3:I:57:GLU:HB3	3:I:58:GLU:H	1.69	0.40
2:H:57:HIS:O	2:H:60(F):LYS:HE3	2.21	0.40
3:I:64:LEU:HD13	3:I:64:LEU:HA	1.92	0.40
1:L:4:ARG:HA	1:L:5:PRO:HD3	1.94	0.40
2:H:30:GLN:HG2	2:H:155:LEU:HD11	2.02	0.40

All (7) 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:1(F):GLY:O	2:H:149(B):ASN:ND2[6_565]	0.69	1.51
5:L:534:HOH:O	5:H:460:HOH:O[3_654]	0.85	1.35
1:L:1(F):GLY:O	2:H:149(B):ASN:CG[6_565]	1.40	0.80
1:L:1(F):GLY:C	2:H:149(B):ASN:ND2[6_565]	1.42	0.78
1:L:1(F):GLY:O	2:H:149(B):ASN:CB[6_565]	2.06	0.14
1:L:1(E):SER:N	2:H:149(B):ASN:ND2[6_565]	2.06	0.14
1:L:1(G):PHE:CE1	1:L:1(G):PHE:CZ[7_555]	2.16	0.04

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	L	34/36 (94%)	29 (85%)	4 (12%)	1 (3%)	3	5
2	H	257/259 (99%)	243 (95%)	13 (5%)	1 (0%)	30	49
3	I	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
4	F	9/12 (75%)	7 (78%)	1 (11%)	1 (11%)	0	0
All	All	310/319 (97%)	288 (93%)	19 (6%)	3 (1%)	12	24

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	1(C)	GLU
2	H	77(A)	ARG
4	F	7	ASP

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	L	31/31 (100%)	29 (94%)	2 (6%)	15	32
2	H	225/225 (100%)	203 (90%)	22 (10%)	7	16
3	I	11/11 (100%)	9 (82%)	2 (18%)	2	3
4	F	5/5 (100%)	4 (80%)	1 (20%)	1	2
All	All	272/272 (100%)	245 (90%)	27 (10%)	7	16

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	6	LEU
1	L	15	ARG
2	H	26	MET
2	H	41	LEU
2	H	46	LEU
2	H	48	SER
2	H	62	ASN
2	H	64	LEU
2	H	66	VAL
2	H	97	ARG
2	H	97(A)	GLU
2	H	107	LYS
2	H	112	VAL
2	H	126	ARG
2	H	130	LEU
2	H	145	LYS
2	H	151	GLN
2	H	154	VAL
2	H	160	LEU

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Mol	Chain	Res	Type
2	H	164	GLU
2	H	176	ILE
2	H	236	LYS
2	H	241	VAL
2	H	247	GLU
3	I	55	ASP
3	I	64	LEU
4	F	7	ASP

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

Mol	Chain	Res	Type
2	H	62	ASN
2	H	71	HIS
2	H	78	ASN
2	H	95	ASN
2	H	151	GLN
2	H	204(B)	ASN
2	H	205	ASN
2	H	239	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](#)

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	$\# Z > 2$
4	AR7	F	16	-	10,10,11	1.48	1 (10%)	9,11,13	1.61	2 (22%)

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
4	AR7	F	16	-	-	2/9/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	16	AR7	O-C	-4.25	1.24	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	F	16	AR7	O-C-CA	3.18	123.74	111.52
4	F	16	AR7	CB-CA-C	-2.35	109.04	112.25

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	16	AR7	O-C-CA-N
4	F	16	AR7	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	16	AR7	2	0

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](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.