



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:13 AM UTC

PDB ID : 1FVU / pdb_00001fvu
Title : CRYSTAL STRUCTURE OF BOTROCETIN
Authors : Sen, U.; Vasudevan, S.; Subbarao, G.; McClintoc, R.A.; Celikel, R.; Ruggeri, Z.M.; Varughese, K.I.
Deposited on : 2000-09-20
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) : **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

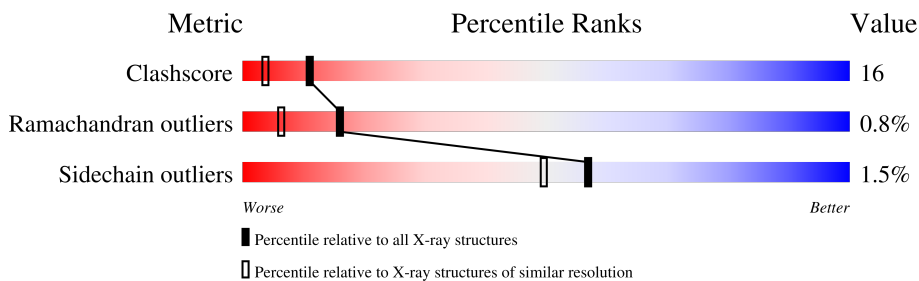
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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)

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	A	133	63% 34% ..
1	C	133	76% 24%
2	B	125	69% 26% ..
2	D	125	64% 31% ...

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4765 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 BOTROCETIN ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	133	Total	C	N	O	S	0	0	0
			1059	673	175	203	8			
1	C	133	Total	C	N	O	S	0	0	0
			1063	676	176	203	8			

- Molecule 2 is a protein called BOTROCETIN BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	121	Total	C	N	O	S	0	0	0
			1020	656	162	192	10			
2	D	121	Total	C	N	O	S	0	0	0
			1018	655	162	191	10			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is water.

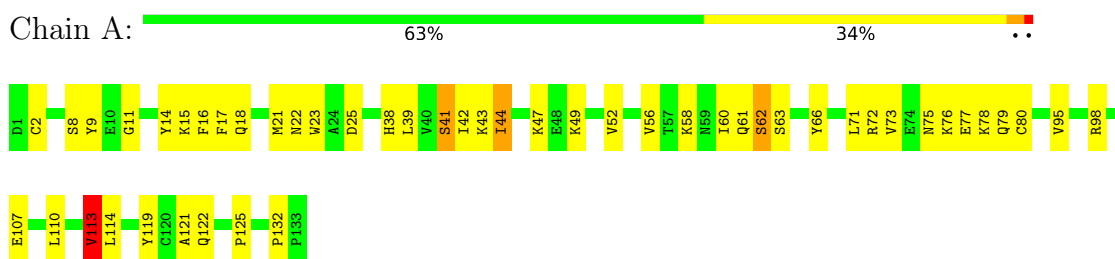
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	155	Total	O	0	0
			155	155		
4	B	145	Total	O	0	0
			145	145		
4	C	183	Total	O	0	0
			183	183		
4	D	120	Total	O	0	0
			120	120		

3 Residue-property plots

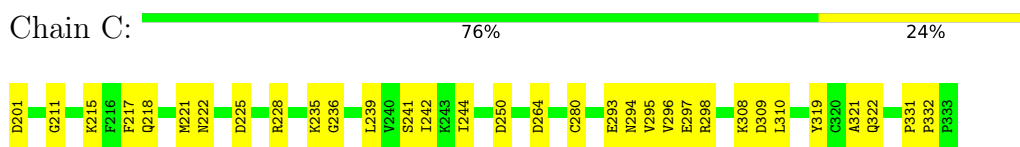
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

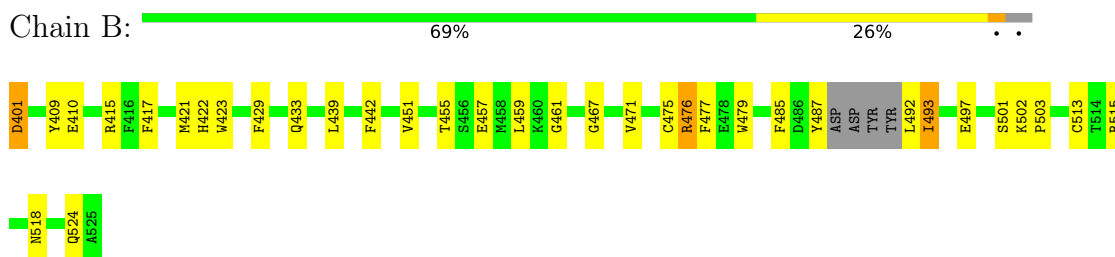
• Molecule 1: BOTROCETIN ALPHA CHAIN



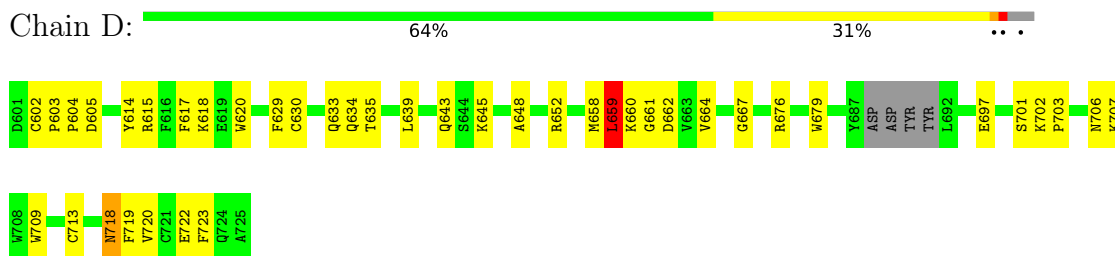
• Molecule 1: BOTROCETIN ALPHA CHAIN



• Molecule 2: BOTROCETIN BETA CHAIN



• Molecule 2: BOTROCETIN BETA CHAIN



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.83Å 69.67Å 103.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80	Depositor
% Data completeness (in resolution range)	87.7 (50.00-1.80)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.199 , 0.218	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4765	wwPDB-VP
Average B, all atoms (Å ²)	34.0	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: MG

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	0.34	0/1086	0.95	8/1465 (0.5%)
1	C	0.41	0/1090	1.01	7/1469 (0.5%)
2	B	0.38	0/1055	0.92	8/1429 (0.6%)
2	D	0.41	0/1053	0.95	6/1426 (0.4%)
All	All	0.39	0/4284	0.96	29/5789 (0.5%)

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	280	CYS	N-CA-C	8.82	124.10	113.16
1	A	39	LEU	N-CA-C	-8.34	98.73	110.50
1	A	80	CYS	N-CA-C	8.12	123.23	113.16
2	D	661	GLY	N-CA-C	-7.88	105.00	115.40
2	B	493	ILE	N-CA-C	7.21	117.34	110.42
2	B	518	ASN	N-CA-C	-7.17	101.28	110.53
2	D	718	ASN	N-CA-C	-6.66	101.94	110.53
2	B	455	THR	N-CA-C	6.64	121.09	112.92
2	D	659	LEU	N-CA-C	-6.17	102.57	110.53
1	A	63	SER	N-CA-C	-6.14	105.54	113.16
2	D	676	ARG	N-CA-C	-6.12	100.32	110.17
1	A	41	SER	N-CA-C	-6.05	100.77	110.14
1	C	239	LEU	N-CA-C	-5.94	101.62	110.23
2	B	467	GLY	N-CA-C	5.78	126.88	113.18
1	C	295	VAL	N-CA-C	5.51	117.24	108.87
2	B	476	ARG	N-CA-C	-5.50	101.32	110.17
1	A	66	TYR	N-CA-C	5.47	118.14	109.50
2	D	639	LEU	N-CA-C	-5.44	102.83	110.50
1	A	125	PRO	N-CA-C	-5.42	103.63	111.22
2	B	524	GLN	N-CA-C	-5.39	105.33	112.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	242	ILE	N-CA-C	5.35	115.83	108.12
2	B	423	TRP	N-CA-C	5.34	117.52	111.11
1	C	244	ILE	N-CA-C	5.32	116.68	110.62
2	D	667	GLY	N-CA-C	5.30	125.74	113.18
1	A	42	ILE	N-CA-C	5.27	115.63	107.78
1	C	236	GLY	N-CA-C	-5.10	108.29	115.32
2	B	439	LEU	N-CA-C	-5.01	103.43	110.50
1	A	113	VAL	N-CA-C	-5.01	108.62	113.53
1	C	331	PRO	N-CA-C	-5.00	104.60	110.70

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	A	1059	0	1005	42	0
1	C	1063	0	1013	22	0
2	B	1020	0	910	33	0
2	D	1018	0	905	47	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	155	0	0	10	0
4	B	145	0	0	11	0
4	C	183	0	0	13	0
4	D	120	0	0	20	0
All	All	4765	0	3833	131	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 16.

All (131) 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)
4:C:3539:HOH:O	2:D:648:ALA:HB3	1.64	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:634:GLN:HB3	4:D:3578:HOH:O	1.66	0.94
1:A:75:ASN:HD21	2:B:476:ARG:H	1.16	0.91
1:A:47:LYS:HB3	4:A:3472:HOH:O	1.70	0.90
1:C:201:ASP:HB2	4:C:3628:HOH:O	1.72	0.88
2:D:629:PHE:HD1	4:D:3552:HOH:O	1.57	0.87
1:A:76:LYS:HD3	4:A:3519:HOH:O	1.76	0.83
1:C:293:GLU:HG2	4:C:3244:HOH:O	1.82	0.78
2:B:401:ASP:HB2	4:B:3537:HOH:O	1.83	0.78
2:B:459:LEU:HD11	4:C:3536:HOH:O	1.84	0.77
2:D:709:TRP:HZ2	4:D:3527:HOH:O	1.67	0.76
2:B:409:TYR:CE2	4:B:3651:HOH:O	2.40	0.74
2:D:658:MET:HG3	4:D:3236:HOH:O	1.86	0.74
1:A:58:LYS:HE2	4:A:3227:HOH:O	1.89	0.71
1:A:38:HIS:NE2	4:A:3652:HOH:O	2.23	0.71
1:A:21:MET:HE2	1:A:25:ASP:HB3	1.72	0.70
2:B:487:TYR:HB2	4:B:3212:HOH:O	1.93	0.69
2:B:459:LEU:CD1	4:C:3536:HOH:O	2.42	0.67
4:C:3585:HOH:O	2:D:643:GLN:CG	2.43	0.66
1:A:44:ILE:HG13	1:A:49:LYS:HD3	1.77	0.65
2:D:659:LEU:HD11	4:D:3236:HOH:O	1.96	0.65
2:D:659:LEU:CD1	4:D:3236:HOH:O	2.44	0.65
1:A:75:ASN:ND2	2:B:476:ARG:H	1.94	0.64
2:D:635:THR:N	4:D:3578:HOH:O	2.31	0.63
2:B:492:LEU:HD23	2:B:492:LEU:O	1.99	0.63
1:A:98:ARG:NH1	1:A:98:ARG:HB2	2.14	0.62
1:A:47:LYS:HE3	4:A:3484:HOH:O	1.99	0.61
1:A:119:TYR:CE2	1:A:121:ALA:HB3	2.36	0.60
4:C:3585:HOH:O	2:D:643:GLN:HG2	2.00	0.60
2:D:629:PHE:CD1	4:D:3552:HOH:O	2.42	0.60
2:B:461:GLY:HA2	2:B:502:LYS:NZ	2.17	0.59
2:D:605:ASP:CG	4:D:3524:HOH:O	2.45	0.59
1:A:49:LYS:HD2	1:A:113:VAL:HG23	1.85	0.58
4:C:3539:HOH:O	2:D:648:ALA:CB	2.38	0.57
2:B:401:ASP:CG	4:B:3279:HOH:O	2.47	0.57
2:B:401:ASP:N	4:B:3537:HOH:O	2.38	0.56
1:C:294:ASN:HD21	2:D:707:LYS:NZ	2.04	0.56
2:D:718:ASN:ND2	4:D:3236:HOH:O	2.39	0.55
1:A:107:GLU:HG2	4:A:3514:HOH:O	2.07	0.54
2:B:442:PHE:HE2	2:B:451:VAL:HG21	1.71	0.54
1:A:113:VAL:HG13	1:A:114:LEU:CD2	2.37	0.54
2:B:410:GLU:CD	4:B:3651:HOH:O	2.51	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:319:TYR:CE2	1:C:321:ALA:HB3	2.42	0.54
2:B:415:ARG:HD3	2:B:417:PHE:CZ	2.41	0.54
2:D:664:VAL:CG2	2:D:719:PHE:HA	2.38	0.53
1:C:250:ASP:CG	4:C:3215:HOH:O	2.52	0.52
2:B:457:GLU:HG2	4:B:3098:HOH:O	2.10	0.52
1:A:15:LYS:HD3	1:A:17:PHE:CZ	2.45	0.52
1:A:23:TRP:CZ3	1:A:72:ARG:HD2	2.45	0.52
2:D:702:LYS:HG3	4:D:3516:HOH:O	2.10	0.51
2:B:421:MET:HE1	2:B:429:PHE:CD2	2.45	0.51
2:D:652:ARG:HB2	2:D:706:ASN:HD21	1.74	0.51
1:A:22:ASN:HA	1:A:122:GLN:O	2.11	0.50
2:B:515:ARG:CD	4:B:3558:HOH:O	2.59	0.50
1:C:309:ASP:O	1:C:310:LEU:HB2	2.10	0.50
1:A:98:ARG:NH2	1:C:308:LYS:HD3	2.27	0.50
2:D:603:PRO:HD2	2:D:634:GLN:HE22	1.76	0.50
1:C:296:VAL:HG21	2:D:709:TRP:CE2	2.47	0.50
1:C:308:LYS:NZ	4:C:3407:HOH:O	2.45	0.49
1:A:47:LYS:CE	4:A:3484:HOH:O	2.56	0.49
1:A:52:VAL:O	1:A:56:VAL:HG23	2.13	0.49
1:C:298:ARG:HH11	1:C:298:ARG:HG2	1.76	0.49
1:A:16:PHE:CE2	1:A:60:ILE:HA	2.47	0.49
2:D:602:CYS:SG	2:D:723:PHE:CZ	3.06	0.49
1:C:241:SER:HA	2:D:679:TRP:CZ3	2.47	0.48
4:C:3539:HOH:O	2:D:645:LYS:HA	2.13	0.48
2:D:618:LYS:HD2	4:D:3533:HOH:O	2.12	0.48
1:A:77:GLU:H	1:A:77:GLU:CD	2.22	0.48
1:A:79:GLN:HB2	2:B:471:VAL:HB	1.96	0.47
1:A:107:GLU:CG	4:A:3514:HOH:O	2.61	0.47
2:B:487:TYR:CB	4:B:3271:HOH:O	2.62	0.47
2:B:487:TYR:HB3	4:B:3271:HOH:O	2.13	0.47
2:D:664:VAL:HG23	2:D:719:PHE:HA	1.95	0.47
2:D:702:LYS:CG	4:D:3516:HOH:O	2.62	0.47
2:D:620:TRP:HH2	2:D:659:LEU:HD11	1.80	0.47
1:A:76:LYS:N	1:A:76:LYS:HD2	2.30	0.47
1:A:113:VAL:HG13	1:A:114:LEU:HD23	1.97	0.47
1:C:221:MET:HE2	1:C:225:ASP:HB3	1.97	0.47
2:D:664:VAL:HG21	2:D:720:VAL:HG23	1.97	0.47
2:D:722:GLU:HG2	2:D:723:PHE:N	2.30	0.46
1:C:222:ASN:HA	1:C:322:GLN:O	2.14	0.46
1:A:61:GLN:O	1:A:62:SER:CB	2.63	0.46
2:D:620:TRP:CH2	2:D:659:LEU:HD11	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:CYS:SG	1:A:8:SER:HB2	2.55	0.46
2:D:659:LEU:HD12	4:D:3236:HOH:O	2.12	0.46
1:A:47:LYS:HE2	4:A:3472:HOH:O	2.15	0.46
1:A:98:ARG:NH2	4:A:3376:HOH:O	2.48	0.46
1:C:294:ASN:HD21	2:D:707:LYS:HZ3	1.64	0.46
2:D:664:VAL:HG12	2:D:701:SER:O	2.15	0.46
2:D:629:PHE:O	2:D:633:GLN:HG2	2.16	0.46
1:C:228:ARG:NH1	4:C:3315:HOH:O	2.49	0.46
2:D:634:GLN:C	4:D:3578:HOH:O	2.56	0.46
2:D:658:MET:HG2	2:D:659:LEU:O	2.16	0.45
2:B:461:GLY:HA2	2:B:502:LYS:HZ1	1.82	0.45
2:D:634:GLN:CB	4:D:3578:HOH:O	2.42	0.45
2:B:422:HIS:HA	2:B:515:ARG:O	2.17	0.45
2:B:492:LEU:HD23	2:B:492:LEU:C	2.42	0.45
2:B:485:PHE:HA	4:B:3206:HOH:O	2.17	0.45
1:A:9:TYR:HB3	1:A:14:TYR:CE2	2.52	0.44
2:B:501:SER:O	2:B:503:PRO:HD3	2.17	0.44
1:C:215:LYS:HD3	1:C:217:PHE:CZ	2.52	0.44
2:D:630:CYS:N	4:D:3552:HOH:O	2.50	0.44
1:A:71:LEU:HD11	2:B:477:PHE:HB3	1.98	0.44
2:B:485:PHE:HD2	2:B:487:TYR:CE1	2.35	0.44
1:A:98:ARG:HB2	1:A:98:ARG:CZ	2.48	0.43
2:D:614:TYR:CD1	2:D:614:TYR:N	2.86	0.43
1:A:61:GLN:O	1:A:62:SER:HB3	2.17	0.43
2:D:604:PRO:O	2:D:605:ASP:HB2	2.19	0.43
2:D:615:ARG:HD3	2:D:617:PHE:CZ	2.54	0.43
1:C:298:ARG:HG2	1:C:298:ARG:NH1	2.34	0.43
1:C:241:SER:HA	2:D:679:TRP:CE3	2.53	0.42
2:B:476:ARG:HA	2:B:487:TYR:OH	2.19	0.42
1:A:11:GLY:O	1:A:132:PRO:HD3	2.20	0.42
1:A:41:SER:HA	2:B:479:TRP:CZ3	2.55	0.42
2:D:629:PHE:HB3	4:D:3552:HOH:O	2.20	0.42
1:A:41:SER:HA	2:B:479:TRP:CE3	2.55	0.42
2:B:429:PHE:O	2:B:433:GLN:HG2	2.20	0.41
1:A:43:LYS:HB2	1:A:43:LYS:NZ	2.35	0.41
2:D:697:GLU:C	2:D:713:CYS:SG	3.04	0.41
1:A:75:ASN:H	1:A:75:ASN:HD22	1.67	0.41
1:C:211:GLY:O	1:C:332:PRO:HD3	2.19	0.41
2:D:620:TRP:NE1	4:D:3533:HOH:O	2.36	0.41
1:A:73:VAL:HG13	2:B:475:CYS:HB3	2.03	0.41
1:A:75:ASN:ND2	1:A:75:ASN:H	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:218:GLN:NE2	1:C:264:ASP:OD2	2.53	0.41
1:C:310:LEU:HD23	1:C:310:LEU:HA	1.93	0.41
1:C:332:PRO:HG2	4:C:3229:HOH:O	2.21	0.41
2:B:497:GLU:C	2:B:513:CYS:SG	3.04	0.41
2:D:709:TRP:CZ2	4:D:3527:HOH:O	2.55	0.40
1:A:78:LYS:HD3	1:A:95:VAL:HB	2.03	0.40
2:D:660:LYS:C	2:D:662:ASP:H	2.27	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	131/133 (98%)	127 (97%)	2 (2%)	2 (2%)	8	2
1	C	131/133 (98%)	126 (96%)	4 (3%)	1 (1%)	16	6
2	B	117/125 (94%)	114 (97%)	3 (3%)	0	100	100
2	D	117/125 (94%)	110 (94%)	6 (5%)	1 (1%)	14	5
All	All	496/516 (96%)	477 (96%)	15 (3%)	4 (1%)	16	6

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	SER
1	A	44	ILE
1	C	297	GLU
2	D	703	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	117/119 (98%)	114 (97%)	3 (3%)	40	28
1	C	118/119 (99%)	117 (99%)	1 (1%)	73	70
2	B	110/114 (96%)	108 (98%)	2 (2%)	51	43
2	D	109/114 (96%)	108 (99%)	1 (1%)	70	67
All	All	454/466 (97%)	447 (98%)	7 (2%)	57	49

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	110	LEU
1	A	113	VAL
2	B	401	ASP
2	B	493	ILE
1	C	235	LYS
2	D	659	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	ASN
1	A	75	ASN
1	A	94	ASN
2	B	412	HIS
2	B	443	GLN
1	C	261	GLN
1	C	294	ASN
2	D	633	GLN
2	D	634	GLN
2	D	706	ASN
2	D	718	ASN

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.