



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:29 PM UTC

PDB ID : 1A4Y / pdb_00001a4y
Title : RIBONUCLEASE INHIBITOR-ANGIOGENIN COMPLEX
Authors : Papageorgiou, A.C.; Acharya, K.R.
Deposited on : 1998-02-08
Resolution : 2.00 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

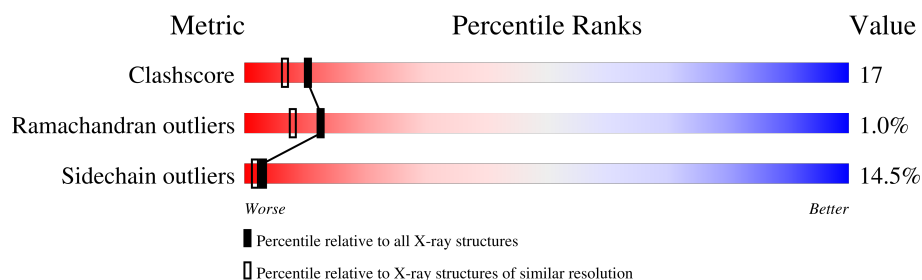
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	460	
1	D	460	
2	B	123	
2	E	123	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8939 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 RIBONUCLEASE INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	3	0	0
			3410	2106	590	680	34			
1	D	460	Total	C	N	O	S	3	0	0
			3410	2106	590	680	34			

- Molecule 2 is a protein called ANGIOGENIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	123	Total	C	N	O	S	0	0	0
			993	610	197	179	7			
2	E	123	Total	C	N	O	S	0	0	0
			993	610	197	179	7			

- Molecule 3 is water.

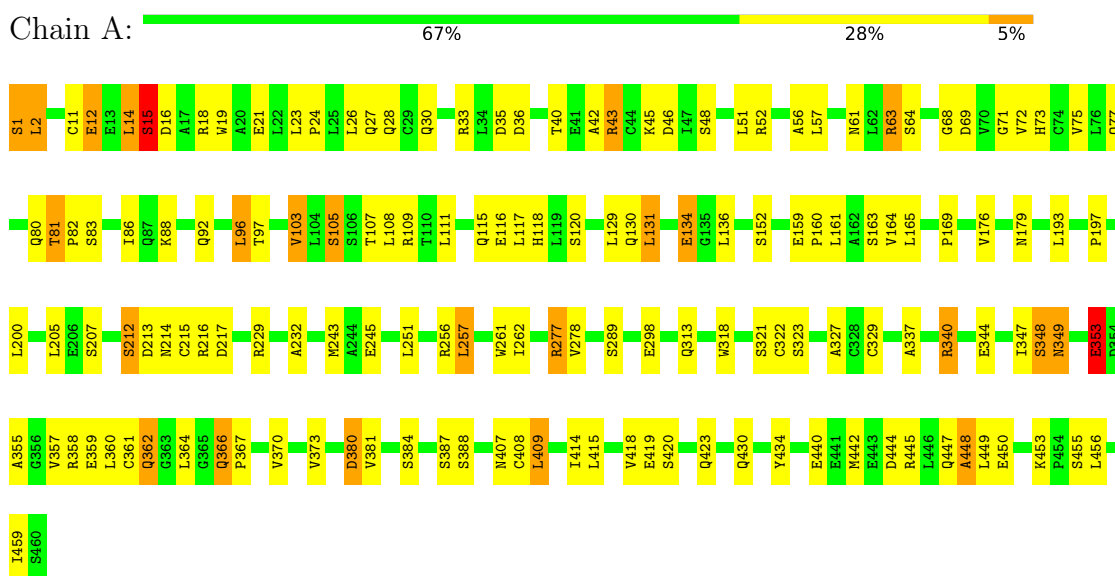
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	56	Total	O	0	0
			56	56		
3	B	18	Total	O	0	0
			18	18		
3	D	51	Total	O	0	0
			51	51		
3	E	8	Total	O	0	0
			8	8		

3 Residue-property plots

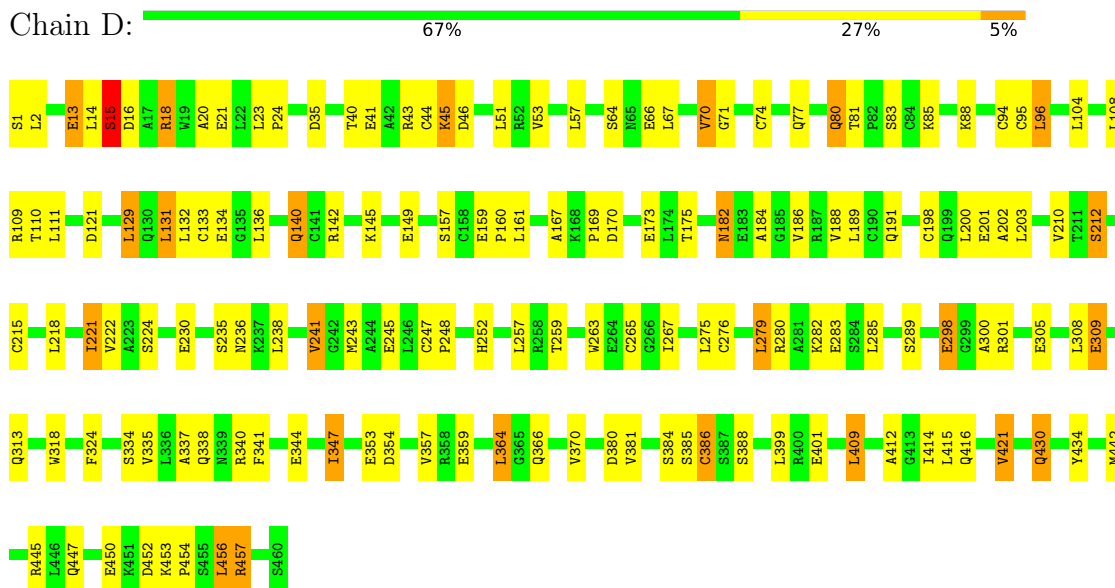
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

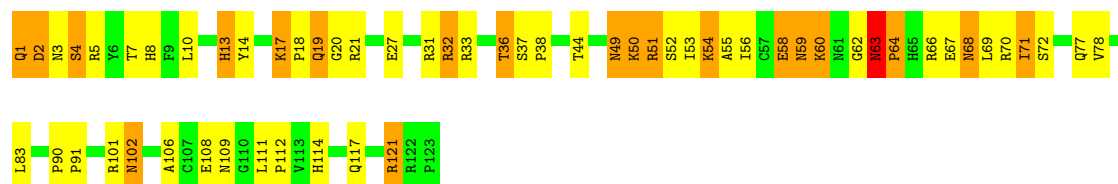


• Molecule 1: RIBONUCLEASE INHIBITOR



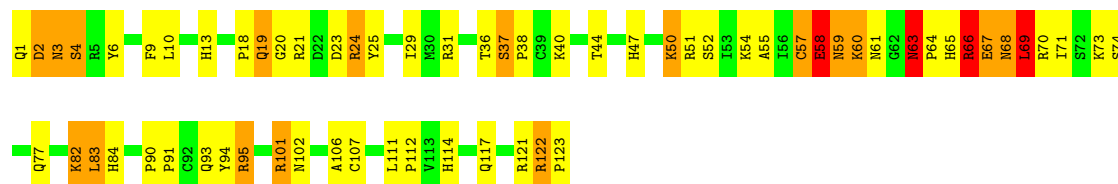
- Molecule 2: ANGIOGENIN

Chain B: 52% 31% 16%



- Molecule 2: ANGIOGENIN

Chain E:  48% 35% 14% 3%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.55 Å 105.61 Å 93.52 Å 90.00° 107.09° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	86.9 (20.00-2.00)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.193 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8939	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

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	0.56	2/3447 (0.1%)	1.18	20/4677 (0.4%)
1	D	0.66	2/3447 (0.1%)	1.05	19/4677 (0.4%)
2	B	0.53	0/1017	1.00	6/1370 (0.4%)
2	E	0.60	0/1017	1.08	9/1370 (0.7%)
All	All	0.60	4/8928 (0.0%)	1.10	54/12094 (0.4%)

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	A	1	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	380	ASP	CA-CB	-21.57	1.21	1.53
1	D	409	LEU	C-N	-7.29	1.25	1.33
1	A	380	ASP	CA-CB	6.26	1.63	1.53
1	A	409	LEU	C-N	-5.21	1.25	1.33

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	380	ASP	CA-CB-CG	37.31	149.91	112.60
1	D	380	ASP	CA-CB-CG	16.95	129.55	112.60
1	A	380	ASP	N-CA-CB	15.79	136.47	112.47
2	E	67	GLU	N-CA-C	-8.56	101.67	113.56
1	A	14	LEU	N-CA-C	8.39	120.34	111.03
1	A	409	LEU	CA-C-O	-8.04	112.23	121.47
1	D	380	ASP	N-CA-CB	7.99	125.01	112.46
1	A	370	VAL	N-CA-C	7.86	120.45	112.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	386	CYS	N-CA-C	7.52	120.35	111.71
1	D	370	VAL	N-CA-C	7.23	121.31	113.43
2	E	102	ASN	N-CA-C	-6.98	100.15	110.48
1	D	409	LEU	CA-C-O	-6.98	112.40	120.49
2	E	66	ARG	N-CA-C	6.85	120.09	109.07
1	D	13	GLU	N-CA-C	-6.82	98.91	109.76
1	D	453	LYS	CA-C-N	6.50	126.19	119.56
1	D	453	LYS	C-N-CA	6.50	126.19	119.56
1	A	448	ALA	N-CA-C	-6.36	103.97	111.03
2	E	69	LEU	N-CA-C	-6.09	100.08	109.76
1	D	409	LEU	CA-C-N	-6.03	116.09	122.30
1	D	409	LEU	C-N-CA	-6.03	116.09	122.30
1	A	179	ASN	N-CA-C	-6.03	98.81	109.06
1	A	384	SER	N-CA-C	5.94	117.76	111.28
1	A	2	LEU	N-CA-C	5.86	119.10	109.72
1	A	81	THR	CA-C-N	5.69	126.95	119.84
1	A	81	THR	C-N-CA	5.69	126.95	119.84
2	B	68	ASN	N-CA-C	-5.68	106.29	113.23
1	A	64	SER	N-CA-C	5.67	119.50	112.24
1	A	216	ARG	N-CA-C	-5.66	105.19	111.36
1	A	329	CYS	N-CA-C	5.65	118.21	111.71
2	E	63	ASN	CA-C-N	5.65	125.93	119.83
2	E	63	ASN	C-N-CA	5.65	125.93	119.83
1	D	121	ASP	N-CA-C	5.64	119.46	112.58
2	E	77	GLN	N-CA-C	-5.61	100.83	109.76
1	D	167	ALA	N-CA-C	5.40	119.87	113.12
2	E	3	ASN	N-CA-C	5.32	117.28	108.13
1	A	56	ALA	N-CA-C	5.31	119.91	113.38
1	D	111	LEU	CA-C-N	5.31	124.98	119.56
1	D	111	LEU	C-N-CA	5.31	124.98	119.56
1	A	298	GLU	N-CA-C	-5.30	105.58	111.36
1	D	2	LEU	N-CA-C	5.30	117.88	109.50
2	B	72	SER	N-CA-C	5.30	117.13	110.24
1	A	30	GLN	N-CA-C	-5.26	106.70	113.23
1	A	327	ALA	N-CA-C	5.26	117.76	111.71
2	B	13	HIS	N-CA-C	5.26	119.45	112.30
1	A	43	ARG	NE-CZ-NH2	5.25	123.93	119.20
2	B	63	ASN	CA-C-N	5.22	126.36	119.84
2	B	63	ASN	C-N-CA	5.22	126.36	119.84
1	D	347	ILE	CB-CA-C	-5.19	105.25	112.36
1	D	338	GLN	N-CA-C	5.17	119.80	112.93
1	D	224	SER	N-CA-C	5.13	119.82	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	64	SER	N-CA-C	5.13	118.31	111.24
2	E	57	CYS	N-CA-C	5.08	116.88	109.71
1	A	360	LEU	N-CA-C	-5.03	105.25	111.33
2	B	8	HIS	N-CA-C	-5.02	105.81	111.28

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	380	ASP	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	434	TYR	Sidechain

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	3410	0	3389	93	0
1	D	3410	0	3389	89	0
2	B	993	0	965	52	0
2	E	993	0	965	71	0
3	A	56	0	0	1	0
3	B	18	0	0	1	0
3	D	51	0	0	1	0
3	E	8	0	0	0	0
All	All	8939	0	8708	295	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 17.

All (295) 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:B:51:ARG:H	2:B:51:ARG:HD2	1.14	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:65:HIS:HE1	2:E:71:ILE:HG22	1.20	1.06
2:E:44:THR:H	2:E:117:GLN:HE22	1.08	0.97
2:E:65:HIS:HB2	2:E:69:LEU:O	1.65	0.97
2:B:44:THR:H	2:B:117:GLN:HE22	1.15	0.93
1:D:401:GLU:HG3	1:D:430:GLN:HB3	1.52	0.91
2:E:65:HIS:CE1	2:E:71:ILE:HG22	2.09	0.86
1:A:381:VAL:HG12	1:A:409:LEU:HD21	1.56	0.86
2:E:55:ALA:HB3	2:E:61:ASN:HB2	1.60	0.84
2:E:122:ARG:HD2	2:E:123:PRO:HD2	1.59	0.83
2:B:51:ARG:HD2	2:B:51:ARG:N	1.94	0.83
1:A:359:GLU:HA	1:A:362:GLN:HG3	1.59	0.82
2:E:66:ARG:O	2:E:69:LEU:HB2	1.79	0.81
2:B:49:ASN:HD21	2:B:51:ARG:HB2	1.45	0.81
1:D:140:GLN:HE22	1:D:142:ARG:HH22	1.29	0.79
1:D:14:LEU:O	1:D:15:SER:HB3	1.81	0.79
1:A:366:GLN:HE21	1:A:367:PRO:HD2	1.48	0.78
2:E:57:CYS:O	2:E:58:GLU:HB2	1.83	0.78
2:B:67:GLU:O	2:B:67:GLU:HG2	1.83	0.78
1:D:159:GLU:HB3	1:D:160:PRO:HD3	1.65	0.78
1:A:229:ARG:NH1	1:A:256:ARG:HB2	2.00	0.77
1:D:16:ASP:OD1	1:D:43:ARG:NH2	2.17	0.77
1:D:77:GLN:O	1:D:80:GLN:HB2	1.85	0.76
2:E:59:ASN:H	2:E:70:ARG:NH2	1.84	0.76
2:E:18:PRO:HG3	2:E:47:HIS:CG	2.21	0.76
1:D:140:GLN:HA	1:D:142:ARG:HH12	1.52	0.74
1:D:18:ARG:HH12	1:D:21:GLU:HG2	1.52	0.74
1:A:105:SER:O	1:A:109:ARG:HG3	1.88	0.74
1:D:51:LEU:HD22	1:D:57:LEU:HD22	1.67	0.74
2:E:68:ASN:HD21	2:E:70:ARG:HH11	1.37	0.72
1:D:357:VAL:HG21	1:D:381:VAL:HG22	1.72	0.72
2:E:59:ASN:H	2:E:70:ARG:HH21	1.38	0.72
1:A:313:GLN:HE22	1:D:313:GLN:HE22	1.39	0.71
2:E:122:ARG:HH11	2:E:123:PRO:HD2	1.56	0.71
2:B:44:THR:H	2:B:117:GLN:NE2	1.87	0.70
1:A:349:ASN:N	1:A:349:ASN:HD22	1.90	0.70
1:D:243:MET:HE1	1:D:275:LEU:HD13	1.73	0.70
2:E:2:ASP:HA	2:E:6:TYR:HD2	1.56	0.69
1:A:414:ILE:CG2	1:A:442:MET:HE2	2.22	0.69
3:D:509:HOH:O	2:E:114:HIS:HD2	1.75	0.69
1:A:414:ILE:HG22	1:A:442:MET:HE2	1.74	0.69
2:E:64:PRO:HG3	2:E:70:ARG:NH2	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:129:LEU:HD22	1:D:157:SER:HB3	1.74	0.68
2:E:101:ARG:HH11	2:E:101:ARG:HB3	1.57	0.68
1:D:243:MET:CE	1:D:275:LEU:HB2	2.24	0.68
1:D:300:ALA:HB2	1:D:324:PHE:CE1	2.29	0.68
2:B:17:LYS:O	2:B:19:GLN:HG2	1.93	0.68
2:E:68:ASN:OD1	2:E:107:CYS:HB2	1.94	0.67
2:B:21:ARG:NH2	2:B:77:GLN:OE1	2.28	0.66
2:E:55:ALA:HB1	2:E:60:LYS:HB3	1.76	0.66
2:B:44:THR:N	2:B:117:GLN:HE22	1.89	0.65
2:B:1:GLN:HB3	2:B:7:THR:HG21	1.79	0.65
1:D:35:ASP:CG	2:E:31:ARG:HH22	2.05	0.65
2:E:67:GLU:HG2	2:E:67:GLU:O	1.97	0.65
1:D:20:ALA:HA	1:D:23:LEU:HD12	1.79	0.65
1:D:140:GLN:NE2	1:D:142:ARG:HH22	1.94	0.65
1:A:14:LEU:O	1:A:15:SER:HB3	1.98	0.64
1:D:301:ARG:O	1:D:305:GLU:HG3	1.97	0.64
2:B:18:PRO:C	2:B:19:GLN:HG2	2.21	0.64
1:D:298:GLU:OE1	1:D:298:GLU:HA	1.97	0.64
1:A:344:GLU:HG2	1:A:373:VAL:HB	1.80	0.64
1:D:142:ARG:HG2	1:D:142:ARG:HH11	1.62	0.64
2:E:106:ALA:HB3	2:E:114:HIS:HB3	1.80	0.63
1:A:414:ILE:O	1:A:418:VAL:HG23	1.98	0.63
1:A:159:GLU:HB3	1:A:160:PRO:HD3	1.81	0.62
1:D:386:CYS:SG	1:D:409:LEU:HD22	2.39	0.62
2:E:121:ARG:HG3	2:E:121:ARG:HH11	1.64	0.62
2:B:101:ARG:HG3	2:B:102:ASN:N	2.15	0.61
2:E:6:TYR:OH	2:E:50:LYS:HD3	2.01	0.61
2:E:44:THR:N	2:E:117:GLN:HE22	1.89	0.61
2:E:101:ARG:HH11	2:E:101:ARG:CB	2.14	0.61
2:E:55:ALA:CB	2:E:61:ASN:HB2	2.28	0.61
1:A:18:ARG:NH1	1:A:21:GLU:HB2	2.16	0.60
2:B:49:ASN:ND2	2:B:51:ARG:HB2	2.14	0.60
1:A:214:ASN:O	1:A:217:ASP:HB2	2.02	0.60
1:D:18:ARG:NH1	1:D:21:GLU:HG2	2.16	0.60
1:A:337:ALA:O	1:A:340:ARG:NH2	2.35	0.59
2:B:56:ILE:O	2:B:62:GLY:HA3	2.03	0.59
1:D:212:SER:HB3	1:D:238:LEU:O	2.02	0.59
1:D:357:VAL:HG21	1:D:381:VAL:CG2	2.32	0.59
1:A:251:LEU:HD21	1:A:278:VAL:HA	1.85	0.59
1:A:24:PRO:HA	1:A:27:GLN:HG3	1.84	0.58
1:A:14:LEU:O	1:A:15:SER:CB	2.50	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:14:LEU:O	1:D:15:SER:CB	2.50	0.58
1:A:33:ARG:HG3	1:A:61:ASN:HB3	1.86	0.58
1:D:212:SER:O	1:D:215:CYS:HB2	2.03	0.58
2:E:44:THR:H	2:E:117:GLN:NE2	1.91	0.58
2:E:64:PRO:HA	2:E:70:ARG:NE	2.18	0.58
2:E:2:ASP:HA	2:E:6:TYR:CD2	2.36	0.57
2:E:20:GLY:O	2:E:21:ARG:HG3	2.04	0.57
2:B:54:LYS:NZ	2:B:111:LEU:HD23	2.20	0.56
2:B:67:GLU:O	2:B:68:ASN:HB2	2.05	0.56
1:D:44:CYS:SG	1:D:67:LEU:HD22	2.46	0.56
1:A:212:SER:O	1:A:215:CYS:HB2	2.06	0.56
2:B:71:ILE:HG23	2:B:71:ILE:O	2.05	0.56
1:A:322:CYS:O	1:A:323:SER:HB2	2.06	0.55
1:A:381:VAL:CG1	1:A:409:LEU:HD21	2.31	0.55
2:B:3:ASN:O	2:B:5:ARG:N	2.39	0.55
2:B:108:GLU:O	2:B:109:ASN:HB2	2.07	0.55
2:B:101:ARG:CG	2:B:102:ASN:N	2.69	0.55
1:D:430:GLN:HE21	1:D:457:ARG:HD2	1.71	0.55
1:D:169:PRO:O	1:D:198:CYS:HA	2.07	0.54
1:D:337:ALA:HB1	1:D:366:GLN:HG3	1.87	0.54
2:B:53:ILE:O	2:B:56:ILE:HG13	2.07	0.54
1:D:23:LEU:HD21	1:D:46:ASP:HB3	1.90	0.54
2:B:106:ALA:HB3	2:B:114:HIS:HB3	1.89	0.54
2:B:101:ARG:HG3	2:B:102:ASN:H	1.73	0.54
2:B:54:LYS:HZ3	2:B:111:LEU:HD23	1.72	0.53
1:A:23:LEU:HD21	1:A:46:ASP:HB3	1.90	0.53
1:D:241:VAL:O	1:D:245:GLU:HG3	2.09	0.53
1:A:251:LEU:HD11	1:A:277:ARG:HG2	1.91	0.53
1:D:452:ASP:O	1:D:454:PRO:HD3	2.08	0.53
2:E:94:TYR:C	2:E:95:ARG:HH11	2.17	0.52
1:A:14:LEU:HD12	1:A:19:TRP:HE3	1.74	0.52
1:D:243:MET:HE2	1:D:275:LEU:HB2	1.91	0.52
2:E:65:HIS:HD1	2:E:70:ARG:HA	1.74	0.52
2:E:63:ASN:N	2:E:73:LYS:HE2	2.25	0.52
1:D:94:CYS:O	1:D:95:CYS:HB2	2.09	0.52
1:A:36:ASP:OD2	2:B:32:ARG:HD3	2.10	0.51
1:A:353:GLU:OE1	1:A:380:ASP:OD2	2.29	0.51
1:D:182:ASN:O	1:D:186:VAL:HG23	2.10	0.51
1:D:243:MET:HG3	1:D:267:ILE:HG12	1.92	0.51
1:A:366:GLN:NE2	1:A:367:PRO:HD2	2.21	0.51
1:A:418:VAL:HG21	1:A:442:MET:HE1	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:173:GLU:HG3	1:D:202:ALA:HB3	1.93	0.51
1:A:229:ARG:CZ	1:A:256:ARG:HB2	2.40	0.51
2:B:66:ARG:HH21	2:B:69:LEU:HD12	1.76	0.51
2:E:66:ARG:O	2:E:67:GLU:HB3	2.11	0.50
1:D:131:LEU:O	1:D:134:GLU:HB2	2.11	0.50
1:D:415:LEU:HD13	1:D:445:ARG:HH12	1.76	0.50
1:A:357:VAL:HG21	1:A:381:VAL:HG22	1.93	0.50
2:E:13:HIS:HD2	2:E:44:THR:O	1.95	0.50
2:B:64:PRO:HD3	2:B:70:ARG:NH2	2.27	0.50
1:A:176:VAL:HG23	1:A:205:LEU:HD23	1.94	0.50
2:B:101:ARG:HG2	2:B:102:ASN:O	2.12	0.49
1:A:129:LEU:HD21	1:A:161:LEU:HG	1.93	0.49
1:A:407:ASN:C	1:A:409:LEU:H	2.20	0.49
2:E:68:ASN:ND2	2:E:70:ARG:HD2	2.27	0.49
1:D:104:LEU:O	1:D:108:LEU:HG	2.12	0.49
1:D:230:GLU:HG3	1:D:259:THR:HB	1.94	0.49
1:A:318:TRP:CH2	1:A:344:GLU:OE1	2.64	0.49
2:E:82:LYS:HE3	2:E:83:LEU:N	2.27	0.49
1:A:318:TRP:CZ3	1:A:344:GLU:OE1	2.65	0.49
2:B:20:GLY:O	2:B:21:ARG:HG2	2.12	0.48
2:B:56:ILE:C	2:B:58:GLU:H	2.21	0.48
2:E:65:HIS:ND1	2:E:70:ARG:HA	2.28	0.48
1:A:11:CYS:HB2	1:D:1:SER:HB2	1.94	0.48
1:A:349:ASN:N	1:A:349:ASN:ND2	2.54	0.48
1:A:11:CYS:HB2	1:D:1:SER:CB	2.44	0.48
1:D:70:VAL:HG23	1:D:71:GLY:H	1.78	0.48
2:E:18:PRO:HG3	2:E:47:HIS:CD2	2.48	0.48
2:B:13:HIS:HD2	2:B:44:THR:O	1.96	0.48
1:A:81:THR:O	1:A:83:SER:N	2.46	0.48
1:D:81:THR:C	1:D:83:SER:H	2.20	0.48
1:D:186:VAL:HG21	1:D:210:VAL:HG22	1.96	0.48
1:D:276:CYS:O	1:D:280:ARG:HG2	2.13	0.48
2:E:63:ASN:O	2:E:70:ARG:HG2	2.14	0.48
1:A:414:ILE:HG21	1:A:442:MET:HE2	1.96	0.48
2:E:18:PRO:O	2:E:19:GLN:HG2	2.14	0.48
1:A:72:VAL:HG21	1:A:96:LEU:HG	1.96	0.47
1:D:21:GLU:HG3	1:D:21:GLU:O	2.13	0.47
1:D:149:GLU:HG2	1:D:175:THR:HG22	1.96	0.47
1:A:35:ASP:OD1	1:A:35:ASP:C	2.57	0.47
1:A:35:ASP:OD2	2:B:31:ARG:NH2	2.47	0.47
2:B:114:HIS:HD2	3:B:140:HOH:O	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:GLU:O	2:B:67:GLU:CG	2.57	0.47
1:A:14:LEU:HD12	1:A:19:TRP:CE3	2.50	0.47
1:D:96:LEU:HD11	1:D:104:LEU:HD12	1.96	0.47
1:D:159:GLU:HB3	1:D:160:PRO:CD	2.41	0.47
1:D:279:LEU:CD1	1:D:285:LEU:HD23	2.45	0.47
1:A:381:VAL:HG12	1:A:409:LEU:CD2	2.37	0.47
1:D:142:ARG:HH11	1:D:142:ARG:CG	2.28	0.47
1:A:169:PRO:HB3	1:A:197:PRO:HG2	1.98	0.46
1:D:414:ILE:CG2	1:D:442:MET:HE2	2.44	0.46
1:D:421:VAL:HG13	1:D:456:LEU:HD22	1.95	0.46
2:E:84:HIS:O	2:E:93:GLN:HB2	2.13	0.46
1:A:423:GLN:O	1:A:453:LYS:NZ	2.48	0.46
2:E:82:LYS:C	2:E:94:TYR:HD1	2.23	0.46
2:B:56:ILE:O	2:B:70:ARG:HD3	2.16	0.46
1:D:318:TRP:CH2	1:D:344:GLU:OE1	2.68	0.46
2:B:63:ASN:HA	2:B:64:PRO:HD2	1.80	0.46
2:E:63:ASN:ND2	2:E:73:LYS:NZ	2.64	0.46
1:A:35:ASP:OD2	1:A:63:ARG:HD3	2.15	0.46
1:A:73:HIS:HA	1:A:103:VAL:HG11	1.97	0.46
1:A:289:SER:HB2	1:A:318:TRP:HD1	1.78	0.46
1:D:45:LYS:HB3	1:D:45:LYS:HE2	1.53	0.46
2:E:95:ARG:HD3	2:E:95:ARG:HA	1.52	0.46
1:D:247:CYS:N	1:D:248:PRO:CD	2.78	0.46
1:A:48:SER:O	1:A:52:ARG:HG3	2.16	0.46
1:A:165:LEU:HD13	1:A:193:LEU:CD2	2.46	0.46
1:D:415:LEU:CD1	1:D:445:ARG:HH12	2.29	0.46
1:A:81:THR:C	1:A:83:SER:H	2.23	0.46
1:A:36:ASP:CG	2:B:32:ARG:HH11	2.22	0.46
1:A:108:LEU:HD13	1:A:136:LEU:HD23	1.97	0.46
2:E:122:ARG:HA	2:E:123:PRO:HD2	1.80	0.46
1:A:12:GLU:O	1:A:12:GLU:HG2	2.16	0.45
1:A:355:ALA:O	1:A:359:GLU:HG3	2.17	0.45
2:E:25:TYR:O	2:E:29:ILE:HG22	2.15	0.45
2:E:122:ARG:HD2	2:E:122:ARG:HA	1.47	0.45
1:A:21:GLU:O	1:A:24:PRO:HD2	2.17	0.45
1:A:420:SER:O	1:A:423:GLN:HG2	2.17	0.45
2:E:58:GLU:OE1	2:E:58:GLU:HA	2.14	0.45
2:E:122:ARG:HH11	2:E:123:PRO:CD	2.25	0.45
1:D:401:GLU:HG3	1:D:430:GLN:CB	2.36	0.45
2:E:51:ARG:HH11	2:E:54:LYS:HE2	1.81	0.45
2:E:69:LEU:O	2:E:70:ARG:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:GLY:O	1:A:72:VAL:HG23	2.17	0.45
1:D:129:LEU:HD21	1:D:161:LEU:HG	1.97	0.45
1:D:243:MET:HE1	1:D:275:LEU:HB2	1.97	0.45
1:D:452:ASP:C	1:D:454:PRO:HD3	2.42	0.45
2:E:66:ARG:C	2:E:68:ASN:N	2.71	0.45
2:B:53:ILE:HG22	2:B:112:PRO:HG3	1.98	0.44
1:A:418:VAL:HG13	1:A:449:LEU:HD22	2.00	0.44
1:D:354:ASP:HA	1:D:385:SER:OG	2.16	0.44
1:A:51:LEU:HD22	1:A:57:LEU:HD22	2.00	0.44
1:A:232:ALA:HA	1:A:261:TRP:HB2	1.98	0.44
2:E:63:ASN:HA	2:E:64:PRO:HD3	1.82	0.44
1:A:348:SER:C	1:A:349:ASN:HD22	2.25	0.44
2:E:66:ARG:C	2:E:68:ASN:H	2.19	0.44
1:A:131:LEU:O	1:A:134:GLU:HB2	2.17	0.44
1:A:358:ARG:O	1:A:361:CYS:HB2	2.18	0.44
1:A:366:GLN:HB3	1:A:367:PRO:HD2	2.00	0.44
1:D:300:ALA:HB2	1:D:324:PHE:CD1	2.52	0.44
2:E:94:TYR:O	2:E:95:ARG:NH1	2.50	0.44
1:D:184:ALA:O	1:D:188:VAL:HG23	2.18	0.44
1:D:236:ASN:O	1:D:265:CYS:HA	2.18	0.44
2:B:2:ASP:OD1	2:B:2:ASP:N	2.41	0.43
1:D:308:LEU:HD21	1:D:335:VAL:HA	2.00	0.43
2:E:64:PRO:HA	2:E:70:ARG:HG2	1.99	0.43
1:A:116:GLU:OE2	1:A:118:HIS:HE1	2.01	0.43
2:E:23:ASP:O	2:E:24:ARG:C	2.62	0.43
1:A:18:ARG:HD2	1:A:18:ARG:HA	1.71	0.43
1:D:221:ILE:N	1:D:221:ILE:HD13	2.33	0.43
1:A:107:THR:CG2	1:A:111:LEU:HD12	2.49	0.43
1:A:19:TRP:CZ2	1:A:43:ARG:HB3	2.54	0.43
1:A:40:THR:C	1:A:42:ALA:N	2.71	0.43
1:D:133:CYS:HA	1:D:136:LEU:HD12	2.00	0.43
2:E:37:SER:HA	2:E:38:PRO:HA	1.86	0.43
2:B:21:ARG:NH1	2:B:78:VAL:O	2.52	0.43
1:D:161:LEU:HD23	1:D:161:LEU:HA	1.78	0.43
1:A:23:LEU:HD23	1:A:26:LEU:HD12	2.00	0.43
2:E:51:ARG:NH1	2:E:54:LYS:HE2	2.34	0.42
1:A:36:ASP:OD1	2:B:32:ARG:NH1	2.52	0.42
2:B:36:THR:O	2:B:36:THR:HG23	2.19	0.42
1:D:414:ILE:HG22	1:D:442:MET:HE2	2.01	0.42
1:A:18:ARG:HH12	1:A:21:GLU:HB2	1.81	0.42
1:A:115:GLN:HG2	3:A:501:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:MET:HE3	1:A:442:MET:HA	2.01	0.42
2:E:65:HIS:CE1	2:E:71:ILE:H	2.38	0.42
1:A:415:LEU:HD12	1:A:415:LEU:HA	1.82	0.42
1:D:23:LEU:N	1:D:24:PRO:HD2	2.35	0.42
1:A:69:ASP:OD2	1:A:97:THR:OG1	2.37	0.42
2:E:6:TYR:O	2:E:9:PHE:HB3	2.19	0.42
1:A:1:SER:O	1:A:2:LEU:HD23	2.20	0.42
1:A:445:ARG:O	1:A:448:ALA:HB3	2.20	0.42
2:B:17:LYS:HB3	2:B:19:GLN:NE2	2.35	0.42
2:E:63:ASN:ND2	2:E:73:LYS:HZ3	2.18	0.42
1:A:71:GLY:O	1:A:75:VAL:HG23	2.20	0.42
1:D:200:LEU:HD21	1:D:203:LEU:HB2	2.02	0.42
1:D:434:TYR:CD1	2:E:40:LYS:HE2	2.55	0.41
1:A:366:GLN:HE21	1:A:366:GLN:HB3	1.62	0.41
2:E:90:PRO:HA	2:E:91:PRO:C	2.45	0.41
1:A:92:GLN:HG3	1:A:120:SER:HB2	2.03	0.41
1:A:414:ILE:O	1:A:415:LEU:C	2.63	0.41
1:A:442:MET:HE3	1:A:442:MET:CA	2.50	0.41
2:B:37:SER:HA	2:B:38:PRO:HA	1.72	0.41
2:B:58:GLU:CB	2:B:60:LYS:HE3	2.51	0.41
1:D:412:ALA:O	1:D:416:GLN:HG3	2.20	0.41
2:B:14:TYR:CZ	2:B:50:LYS:HG2	2.55	0.41
1:D:218:LEU:O	1:D:222:VAL:HG23	2.20	0.41
2:E:63:ASN:CA	2:E:73:LYS:HE2	2.51	0.41
1:D:140:GLN:HA	1:D:142:ARG:NH1	2.26	0.41
2:E:111:LEU:HA	2:E:112:PRO:HD3	1.93	0.41
2:B:55:ALA:HA	2:B:60:LYS:NZ	2.35	0.41
2:B:69:LEU:HD23	2:B:69:LEU:HA	1.81	0.41
1:A:257:LEU:HD23	1:A:257:LEU:HA	1.96	0.41
2:B:59:ASN:HD21	2:B:63:ASN:ND2	2.18	0.41
1:D:280:ARG:NE	1:D:309:GLU:OE1	2.54	0.41
1:D:313:GLN:HG2	1:D:341:PHE:CZ	2.56	0.41
1:A:193:LEU:HD22	1:A:200:LEU:HD22	2.03	0.41
2:B:33:ARG:HA	2:B:33:ARG:HD3	1.89	0.41
1:D:35:ASP:C	1:D:35:ASP:OD1	2.63	0.41
1:D:35:ASP:OD1	2:E:31:ARG:NH2	2.52	0.41
2:B:17:LYS:HD2	2:B:17:LYS:HA	1.88	0.41
1:D:289:SER:HB2	1:D:318:TRP:HD1	1.86	0.41
2:E:121:ARG:HH11	2:E:121:ARG:CG	2.29	0.41
1:A:108:LEU:HD21	1:A:117:LEU:HD22	2.03	0.40
1:A:430:GLN:HE21	1:A:430:GLN:HB2	1.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:263:TRP:CD1	1:D:263:TRP:H	2.39	0.40
1:D:318:TRP:CZ3	1:D:344:GLU:OE1	2.74	0.40
1:D:430:GLN:NE2	1:D:457:ARG:HH11	2.19	0.40
2:E:82:LYS:HB3	2:E:82:LYS:HE2	1.92	0.40
1:A:318:TRP:HH2	1:A:344:GLU:CD	2.29	0.40
2:B:90:PRO:HA	2:B:91:PRO:C	2.46	0.40
1:D:364:LEU:HD23	1:D:364:LEU:HA	1.96	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	458/460 (100%)	437 (95%)	17 (4%)	4 (1%)	14	9
1	D	458/460 (100%)	439 (96%)	17 (4%)	2 (0%)	30	27
2	B	121/123 (98%)	109 (90%)	9 (7%)	3 (2%)	4	1
2	E	121/123 (98%)	109 (90%)	9 (7%)	3 (2%)	4	1
All	All	1158/1166 (99%)	1094 (94%)	52 (4%)	12 (1%)	12	8

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	4	SER
2	E	58	GLU
2	E	59	ASN
1	A	82	PRO
1	D	15	SER
2	E	4	SER
1	A	15	SER
2	B	121	ARG

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Mol	Chain	Res	Type
1	D	182	ASN
1	A	16	ASP
1	A	353	GLU
2	B	64	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	382/396 (96%)	335 (88%)	47 (12%)	4	3
1	D	382/396 (96%)	331 (87%)	51 (13%)	4	2
2	B	110/110 (100%)	88 (80%)	22 (20%)	1	0
2	E	110/110 (100%)	87 (79%)	23 (21%)	1	0
All	All	984/1012 (97%)	841 (86%)	143 (14%)	3	2

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	12	GLU
1	A	15	SER
1	A	28	GLN
1	A	45	LYS
1	A	63	ARG
1	A	77	GLN
1	A	80	GLN
1	A	86	ILE
1	A	88	LYS
1	A	96	LEU
1	A	103	VAL
1	A	105	SER
1	A	130	GLN
1	A	131	LEU
1	A	134	GLU
1	A	152	SER

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Mol	Chain	Res	Type
1	A	163	SER
1	A	164	VAL
1	A	207	SER
1	A	212	SER
1	A	213	ASP
1	A	243	MET
1	A	245	GLU
1	A	257	LEU
1	A	262	ILE
1	A	277	ARG
1	A	321	SER
1	A	340	ARG
1	A	347	ILE
1	A	348	SER
1	A	349	ASN
1	A	353	GLU
1	A	362	GLN
1	A	364	LEU
1	A	366	GLN
1	A	387	SER
1	A	388	SER
1	A	408	CYS
1	A	419	GLU
1	A	440	GLU
1	A	444	ASP
1	A	447	GLN
1	A	450	GLU
1	A	455	SER
1	A	456	LEU
1	A	459	ILE
2	B	1	GLN
2	B	2	ASP
2	B	4	SER
2	B	10	LEU
2	B	17	LYS
2	B	19	GLN
2	B	27	GLU
2	B	32	ARG
2	B	36	THR
2	B	49	ASN
2	B	50	LYS
2	B	51	ARG

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Mol	Chain	Res	Type
2	B	52	SER
2	B	54	LYS
2	B	58	GLU
2	B	59	ASN
2	B	60	LYS
2	B	63	ASN
2	B	71	ILE
2	B	83	LEU
2	B	102	ASN
2	B	121	ARG
1	D	13	GLU
1	D	15	SER
1	D	18	ARG
1	D	40	THR
1	D	41	GLU
1	D	45	LYS
1	D	53	VAL
1	D	66	GLU
1	D	70	VAL
1	D	74	CYS
1	D	80	GLN
1	D	85	LYS
1	D	88	LYS
1	D	96	LEU
1	D	109	ARG
1	D	110	THR
1	D	129	LEU
1	D	131	LEU
1	D	132	LEU
1	D	140	GLN
1	D	145	LYS
1	D	170	ASP
1	D	189	LEU
1	D	191	GLN
1	D	201	GLU
1	D	212	SER
1	D	221	ILE
1	D	235	SER
1	D	241	VAL
1	D	252	HIS
1	D	257	LEU
1	D	279	LEU

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Mol	Chain	Res	Type
1	D	282	LYS
1	D	283	GLU
1	D	298	GLU
1	D	309	GLU
1	D	334	SER
1	D	340	ARG
1	D	347	ILE
1	D	353	GLU
1	D	359	GLU
1	D	364	LEU
1	D	384	SER
1	D	388	SER
1	D	399	LEU
1	D	421	VAL
1	D	430	GLN
1	D	447	GLN
1	D	450	GLU
1	D	456	LEU
1	D	457	ARG
2	E	1	GLN
2	E	2	ASP
2	E	3	ASN
2	E	4	SER
2	E	10	LEU
2	E	19	GLN
2	E	24	ARG
2	E	36	THR
2	E	37	SER
2	E	50	LYS
2	E	52	SER
2	E	58	GLU
2	E	60	LYS
2	E	63	ASN
2	E	66	ARG
2	E	68	ASN
2	E	69	LEU
2	E	74	SER
2	E	82	LYS
2	E	83	LEU
2	E	95	ARG
2	E	101	ARG
2	E	122	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	118	HIS
1	A	140	GLN
1	A	182	ASN
1	A	313	GLN
1	A	349	ASN
1	A	366	GLN
1	A	406	ASN
1	A	430	GLN
2	B	13	HIS
2	B	19	GLN
2	B	49	ASN
2	B	59	ASN
2	B	63	ASN
2	B	84	HIS
2	B	117	GLN
1	D	10	GLN
1	D	118	HIS
1	D	140	GLN
1	D	349	ASN
1	D	406	ASN
1	D	430	GLN
2	E	12	GLN
2	E	13	HIS
2	E	63	ASN
2	E	65	HIS
2	E	68	ASN
2	E	84	HIS
2	E	114	HIS
2	E	117	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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.