



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:45 AM GMT

PDB ID : 3PQ7
Title : Structure of I274C variant of E. coli KatE[] - Images 31-36
Authors : Loewen, P.C.; Jha, V.; Louis, S.; Chelikani, P.; Carpena, X.; Fita, I.
Deposited on : 2010-11-25
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
<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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

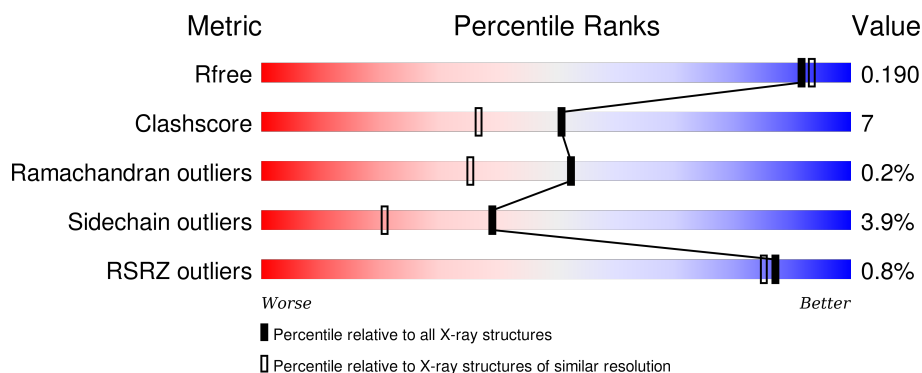
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
R_{free}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (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 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.

Mol	Chain	Length	Quality of chain
1	A	753	<div> <div></div> <div>83% 12% . .</div> </div>
1	B	753	<div> <div></div> <div>84% 11% . .</div> </div>
1	C	753	<div> <div></div> <div>86% 9% . .</div> </div>
1	D	753	<div> <div></div> <div>85% 10% . .</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	H2S	A	754	-	-	X	X
4	H2S	B	754	-	-	X	X
4	H2S	C	754	-	-	X	X
4	H2S	D	754	-	-	X	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 26809 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.

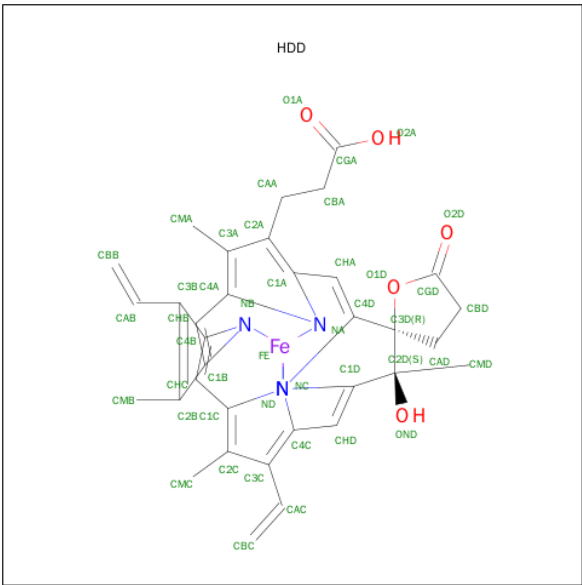
- Molecule 1 is a protein called Catalase HPIL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	726	Total	C	N	O	S	0	5	0
			5755	3652	1009	1083	11			
1	B	726	Total	C	N	O	S	0	5	0
			5757	3654	1009	1083	11			
1	C	726	Total	C	N	O	S	0	2	0
			5747	3649	1007	1080	11			
1	D	726	Total	C	N	O	S	0	9	0
			5771	3662	1013	1085	11			

There are 12 discrepancies between the modelled and reference sequences:

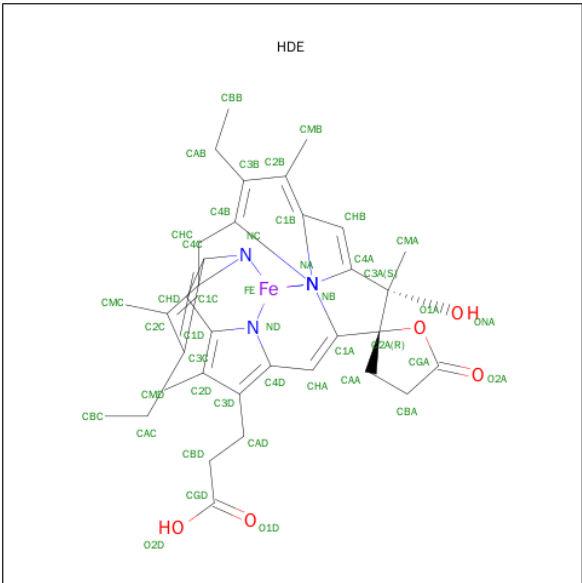
Chain	Residue	Modelled	Actual	Comment	Reference
A	274	CYS	ILE	ENGINEERED MUTATION	UNP P21179
A	438	ALA	CYS	ENGINEERED MUTATION	UNP P21179
A	669	ALA	CYS	ENGINEERED MUTATION	UNP P21179
B	274	CYS	ILE	ENGINEERED MUTATION	UNP P21179
B	438	ALA	CYS	ENGINEERED MUTATION	UNP P21179
B	669	ALA	CYS	ENGINEERED MUTATION	UNP P21179
C	274	CYS	ILE	ENGINEERED MUTATION	UNP P21179
C	438	ALA	CYS	ENGINEERED MUTATION	UNP P21179
C	669	ALA	CYS	ENGINEERED MUTATION	UNP P21179
D	274	CYS	ILE	ENGINEERED MUTATION	UNP P21179
D	438	ALA	CYS	ENGINEERED MUTATION	UNP P21179
D	669	ALA	CYS	ENGINEERED MUTATION	UNP P21179

- Molecule 2 is CIS-HEME D HYDROXYCHLORIN GAMMA-SPIROLACTONE (three-letter code: HDD) (formula: C₃₄H₃₂FeN₄O₅).



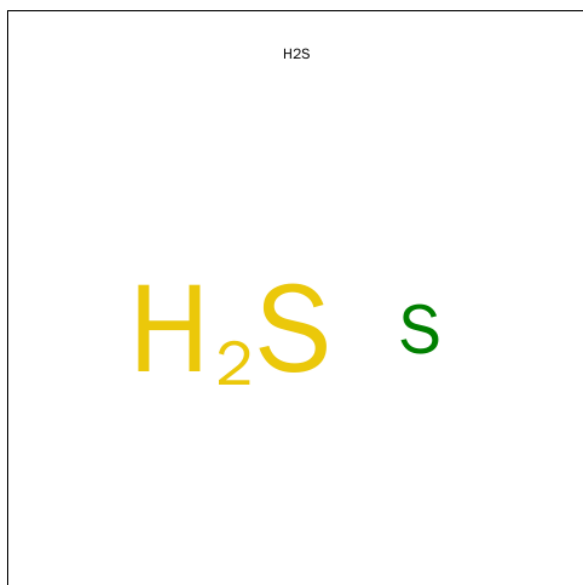
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
2	B	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
2	C	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
2	D	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		

- Molecule 3 is CIS-HEME D HYDROXYCHLORIN GAMMA-SPIROLACTONE 17R, 18S (three-letter code: HDE) (formula: C₃₄H₃₈FeN₄O₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
3	B	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
3	C	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		
3	D	1	Total	C	Fe	N	O	0	1
			44	34	1	4	5		

- Molecule 4 is HYDROSULFURIC ACID (three-letter code: H2S) (formula: H₂S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	S	0	0
			1	1		
4	B	1	Total	S	0	0
			1	1		
4	C	1	Total	S	0	0
			1	1		
4	D	1	Total	S	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	895	Total	O	0	0
			895	895		
5	B	779	Total	O	0	0
			779	779		

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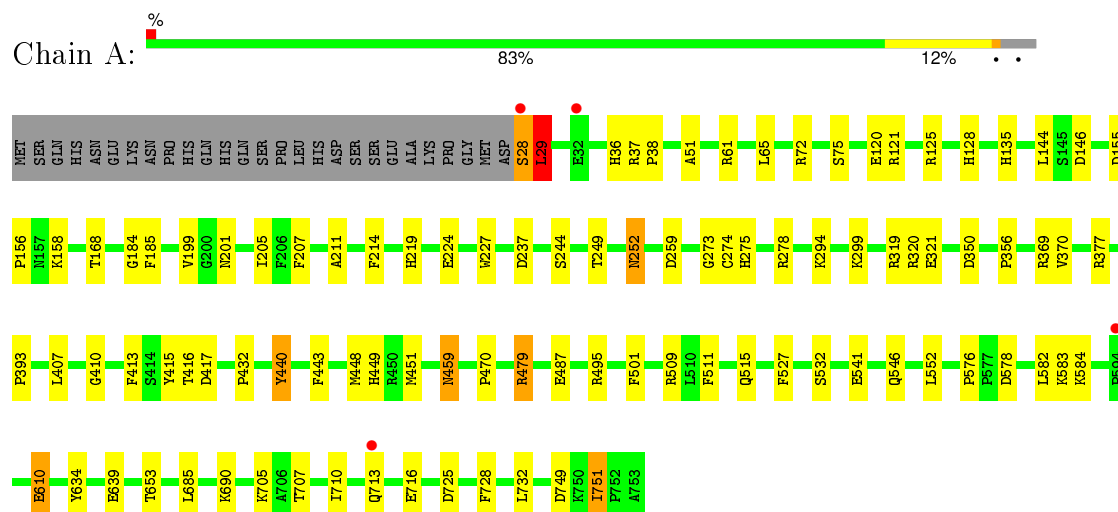
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	847	Total 847	O 847	0	0
5	D	902	Total 902	O 902	0	0

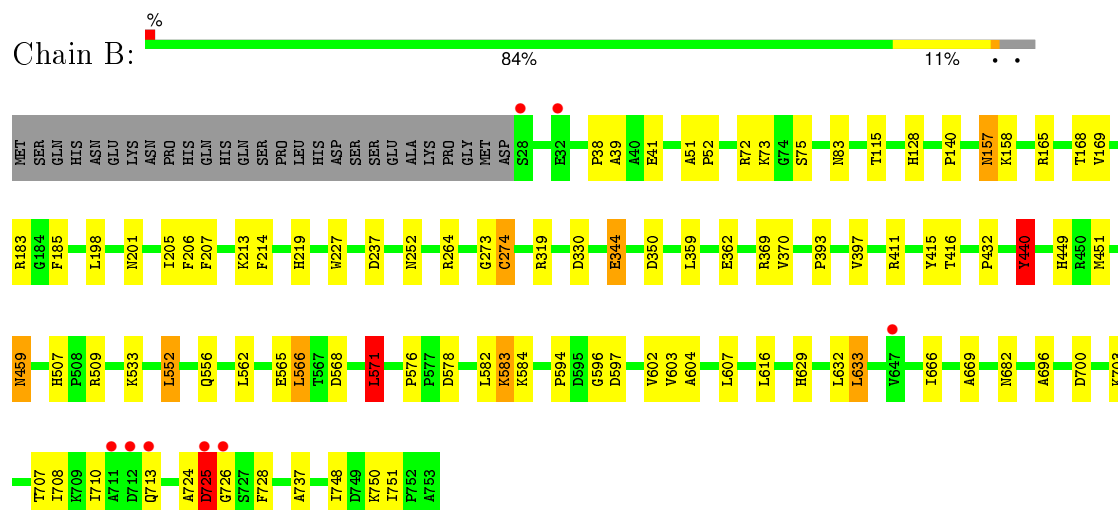
3 Residue-property plots

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.

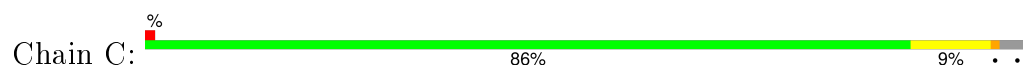
• Molecule 1: Catalase HP11

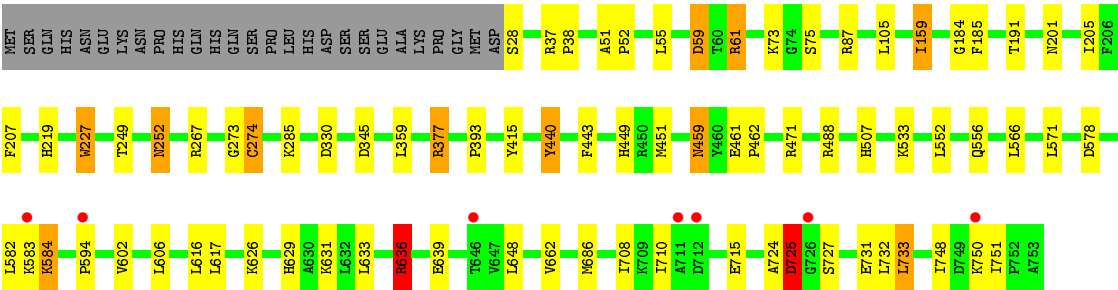


• Molecule 1: Catalase HP11



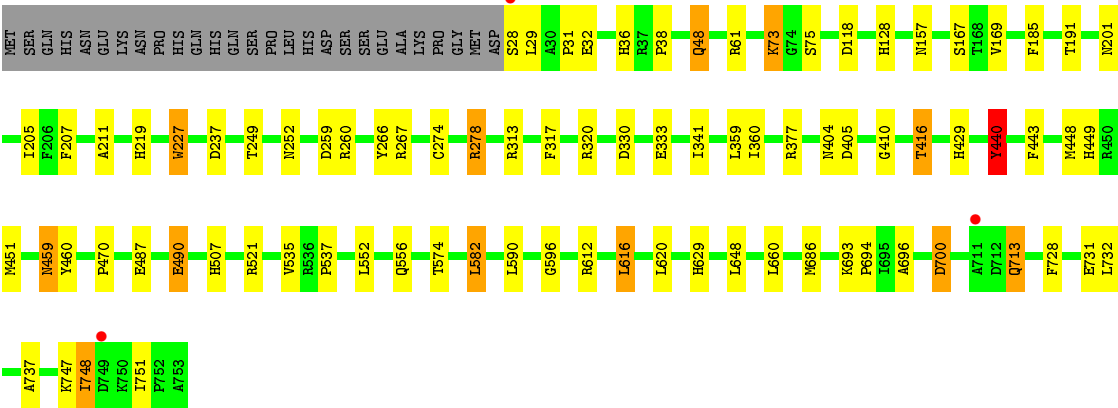
• Molecule 1: Catalase HP11





● Molecule 1: Catalase HP11

Chain D: 85% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.50Å 133.02Å 122.67Å 90.00° 109.40° 90.00°	Depositor
Resolution (Å)	34.25 – 1.80 31.28 – 1.80	Depositor EDS
% Data completeness (in resolution range)	92.5 (34.25-1.80) 92.5 (31.28-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.142 , 0.190 0.142 , 0.190	Depositor DCC
R_{free} test set	12169 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	11.8	Xtriage
Anisotropy	0.008	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.2	EDS
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 243264 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	26809	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HDE, HDD, H2S

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	1.14	8/5932 (0.1%)	0.95	10/8064 (0.1%)
1	B	1.10	3/5931 (0.1%)	0.94	7/8062 (0.1%)
1	C	1.11	1/5908 (0.0%)	0.97	12/8033 (0.1%)
1	D	1.17	7/5966 (0.1%)	0.95	12/8109 (0.1%)
All	All	1.13	19/23737 (0.1%)	0.95	41/32268 (0.1%)

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	C	0	2

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	440	TYR	CE1-CZ	7.40	1.48	1.38
1	B	440	TYR	CE1-CZ	6.98	1.47	1.38
1	A	440	TYR	CE1-CZ	6.15	1.46	1.38
1	D	460	TYR	CD2-CE2	5.87	1.48	1.39
1	A	29	LEU	N-CA	-5.78	1.34	1.46
1	A	501	PHE	CE2-CZ	5.75	1.48	1.37
1	B	397	VAL	CB-CG1	5.72	1.64	1.52
1	D	377	ARG	CZ-NH2	5.50	1.40	1.33
1	A	321	GLU	CD-OE1	5.48	1.31	1.25
1	D	333	GLU	CD-OE2	-5.38	1.19	1.25
1	A	224	GLU	CB-CG	5.25	1.62	1.52
1	C	443	PHE	CE1-CZ	5.22	1.47	1.37
1	B	362	GLU	CB-CG	5.21	1.62	1.52
1	A	120	GLU	CD-OE2	5.17	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	167	SER	CA-CB	5.13	1.60	1.52
1	D	317	PHE	CE2-CZ	5.10	1.47	1.37
1	D	266	TYR	CG-CD1	5.07	1.45	1.39
1	A	527	PHE	CE2-CZ	5.06	1.47	1.37
1	A	121	ARG	CG-CD	5.06	1.64	1.51

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	636	ARG	NE-CZ-NH2	-10.88	114.86	120.30
1	C	636	ARG	NE-CZ-NH1	9.81	125.20	120.30
1	D	377	ARG	NE-CZ-NH1	-7.64	116.48	120.30
1	C	471	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	C	37	ARG	NE-CZ-NH2	-7.17	116.72	120.30
1	C	87	ARG	NE-CZ-NH2	-7.09	116.75	120.30
1	A	320	ARG	NE-CZ-NH2	-6.91	116.84	120.30
1	A	495	ARG	NE-CZ-NH1	6.81	123.71	120.30
1	C	377	ARG	NE-CZ-NH1	-6.78	116.91	120.30
1	B	72	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	D	320	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	C	59	ASP	CB-CG-OD1	6.35	124.01	118.30
1	A	72	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	B	72	ARG	NE-CZ-NH1	6.20	123.40	120.30
1	B	350	ASP	CB-CG-OD1	-6.16	112.76	118.30
1	C	733	LEU	CA-CB-CG	6.14	129.43	115.30
1	D	582	LEU	CB-CG-CD1	6.07	121.32	111.00
1	A	294	LYS	CD-CE-NZ	-6.02	97.85	111.70
1	D	686	MET	CG-SD-CE	6.00	109.79	100.20
1	D	521	ARG	NE-CZ-NH2	-5.87	117.37	120.30
1	D	700	ASP	CB-CG-OD1	5.76	123.48	118.30
1	C	159	ILE	CB-CG1-CD1	-5.69	97.97	113.90
1	A	350	ASP	CB-CG-OD1	-5.58	113.28	118.30
1	A	685	LEU	CB-CG-CD1	-5.53	101.60	111.00
1	B	571	LEU	CA-CB-CG	5.45	127.82	115.30
1	A	479	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	B	597	ASP	CB-CG-OD1	5.41	123.16	118.30
1	B	264	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	D	259	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	259	ASP	CB-CG-OD2	5.21	122.98	118.30
1	D	377	ARG	CG-CD-NE	-5.19	100.90	111.80
1	C	636	ARG	CG-CD-NE	-5.16	100.97	111.80
1	D	61	ARG	NE-CZ-NH1	-5.16	117.72	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	612	ARG	NE-CZ-NH1	-5.16	117.72	120.30
1	A	495	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	D	278	ARG	NE-CZ-NH1	-5.10	117.75	120.30
1	C	725	ASP	N-CA-C	5.09	124.75	111.00
1	B	198	LEU	CB-CG-CD2	-5.09	102.35	111.00
1	D	612	ARG	NE-CZ-NH2	5.06	122.83	120.30
1	A	29	LEU	CA-CB-CG	5.05	126.91	115.30
1	C	345	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	724	ALA	Peptide
1	C	725	ASP	Peptide

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	5755	0	5582	83	0
1	B	5757	0	5587	76	0
1	C	5747	0	5577	63	2
1	D	5771	0	5598	52	0
2	A	44	0	31	16	0
2	B	44	0	31	17	0
2	C	44	0	31	18	0
2	D	44	0	31	9	0
3	A	44	0	36	8	0
3	B	44	0	36	12	0
3	C	44	0	36	13	0
3	D	44	0	36	9	0
4	A	1	0	0	8	0
4	B	1	0	0	5	0
4	C	1	0	0	7	0
4	D	1	0	0	7	0
5	A	895	0	0	20	3

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	779	0	0	10	2
5	C	847	0	0	22	0
5	D	902	0	0	22	2
All	All	26809	0	22612	318	5

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 7.

All (318) 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:C:274:CYS:HB3	4:C:754:H2S:S	1.29	1.70
2:C:760[A]:HDD:HBB2	4:C:754:H2S:S	1.29	1.68
1:A:274:CYS:HB3	4:A:754:H2S:S	1.42	1.56
2:B:760[A]:HDD:HBB2	4:B:754:H2S:S	1.44	1.54
1:D:274:CYS:HB3	4:D:754:H2S:S	1.45	1.52
1:B:274:CYS:HB3	4:B:754:H2S:S	1.51	1.49
2:C:760[A]:HDD:CBB	4:C:754:H2S:S	2.10	1.37
1:C:578:ASP:HB3	5:C:2919:HOH:O	1.30	1.27
1:C:449[B]:HIS:CE1	5:C:3610:HOH:O	1.75	1.27
3:B:761[B]:HDE:CBC	3:B:761[B]:HDE:HMC	1.66	1.25
1:C:274:CYS:CB	4:C:754:H2S:S	2.23	1.24
2:B:760[A]:HDD:CBB	4:B:754:H2S:S	2.27	1.23
1:A:716:GLU:HG2	5:A:3090:HOH:O	1.39	1.21
1:D:451:MET:SD	5:D:3617:HOH:O	1.95	1.21
2:C:760[A]:HDD:HBB1	2:C:760[A]:HDD:HMB1	1.24	1.19
2:D:760[A]:HDD:HBB2	4:D:754:H2S:S	1.88	1.14
1:A:274:CYS:CB	4:A:754:H2S:S	2.37	1.12
1:B:274:CYS:CB	4:B:754:H2S:S	2.38	1.12
1:A:29:LEU:HD22	5:C:2405:HOH:O	1.46	1.11
1:B:416:THR:HG21	5:D:2464:HOH:O	1.51	1.11
1:D:274:CYS:CB	4:D:754:H2S:S	2.39	1.11
3:D:761[B]:HDE:HMC	3:D:761[B]:HDE:HBCB	1.20	1.07
3:B:761[B]:HDE:HBCA	3:B:761[B]:HDE:HMC	1.15	1.07
1:B:201:ASN:CG	2:B:760[A]:HDD:HMB2	1.75	1.07
1:C:451:MET:SD	5:C:3612:HOH:O	2.13	1.04
1:D:201:ASN:CG	2:D:760[A]:HDD:HMB2	1.77	1.03
1:A:201:ASN:CG	2:A:760[A]:HDD:HMB2	1.78	1.03
3:C:761[B]:HDE:HBCB	3:C:761[B]:HDE:HMC	1.38	1.01
3:C:761[B]:HDE:CBC	3:C:761[B]:HDE:HMC	1.90	1.01
1:C:201:ASN:CG	2:C:760[A]:HDD:HMB2	1.81	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:CYS:SG	2:A:760[A]:HDD:CMB	2.49	1.00
3:B:761[B]:HDE:CMC	3:B:761[B]:HDE:HBCA	1.87	1.00
3:A:761[B]:HDE:HBCB	3:A:761[B]:HDE:HMC	1.45	0.98
2:A:760[A]:HDD:HBB2	4:A:754:H2S:S	2.04	0.97
3:B:761[B]:HDE:CMC	3:B:761[B]:HDE:CBC	2.40	0.97
1:A:610:GLU:HG2	5:A:3555:HOH:O	1.65	0.95
1:A:416[A]:THR:HG21	5:A:3313:HOH:O	1.65	0.95
2:D:760[A]:HDD:CBB	4:D:754:H2S:S	2.54	0.95
1:A:274:CYS:SG	2:A:760[A]:HDD:HMB3	2.07	0.94
1:C:267:ARG:HG3	5:C:2916:HOH:O	1.64	0.94
3:D:761[B]:HDE:HMC	3:D:761[B]:HDE:CBC	1.98	0.93
1:C:440:TYR:HD1	5:C:3454:HOH:O	1.53	0.91
1:A:274:CYS:SG	2:A:760[A]:HDD:HMB1	2.11	0.89
1:D:274:CYS:SG	2:D:760[A]:HDD:CMB	2.62	0.88
2:A:760[A]:HDD:CBB	4:A:754:H2S:S	2.62	0.87
1:B:451:MET:SD	5:B:3614:HOH:O	2.32	0.87
3:B:761[B]:HDE:HBCB	3:B:761[B]:HDE:HMC	1.57	0.87
1:C:751:ILE:HB	5:C:2367:HOH:O	1.74	0.86
3:D:761[B]:HDE:CMC	3:D:761[B]:HDE:HBCB	2.01	0.86
1:D:274:CYS:SG	2:D:760[A]:HDD:HMB1	2.17	0.83
1:A:751:ILE:O	1:A:751:ILE:HD12	1.80	0.82
1:A:28:SER:OG	1:A:28:SER:O	1.93	0.81
1:A:29:LEU:HD23	5:C:3144:HOH:O	1.80	0.81
1:A:541:GLU:OE2	5:A:2550:HOH:O	1.99	0.80
1:B:440:TYR:O	1:D:73[B]:LYS:HE3	1.81	0.80
2:C:760[A]:HDD:CMB	2:C:760[A]:HDD:HBB1	2.05	0.80
3:D:761[B]:HDE:HBBB	3:D:761[B]:HDE:HMB	1.66	0.78
1:C:725:ASP:O	5:C:2403:HOH:O	2.00	0.78
3:C:761[B]:HDE:CBB	3:C:761[B]:HDE:HMB	2.14	0.78
1:C:636:ARG:HD3	5:C:2717:HOH:O	1.84	0.78
1:D:274:CYS:SG	2:D:760[A]:HDD:HMB3	2.24	0.78
1:A:610:GLU:CG	5:A:3555:HOH:O	2.27	0.77
1:B:73:LYS:HE3	5:D:3517:HOH:O	1.85	0.77
3:B:761[B]:HDE:HBBB	3:B:761[B]:HDE:HMB	1.67	0.76
1:D:556:GLN:NE2	5:D:2773:HOH:O	2.17	0.76
1:A:201:ASN:ND2	2:A:760[A]:HDD:HMB2	2.01	0.76
3:C:761[B]:HDE:CMC	3:C:761[B]:HDE:CBC	2.63	0.75
3:C:761[B]:HDE:HBBA	3:C:761[B]:HDE:HMB	1.69	0.74
1:C:201:ASN:ND2	2:C:760[A]:HDD:HMB2	2.02	0.74
1:B:533[A]:LYS:HE2	5:B:3100:HOH:O	1.87	0.73
2:C:760[A]:HDD:CBB	2:C:760[A]:HDD:HMB1	2.12	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:761[B]:HDE:CMC	3:C:761[B]:HDE:HBCB	2.15	0.73
1:B:748:ILE:O	1:B:751:ILE:HG22	1.87	0.73
1:D:731:GLU:OE2	5:D:3028:HOH:O	2.04	0.73
1:B:201:ASN:ND2	2:B:760[A]:HDD:HMB2	2.05	0.72
1:C:449[A]:HIS:HD2	5:C:3611:HOH:O	1.72	0.71
1:B:330:ASP:OD1	1:B:629:HIS:HE1	1.73	0.71
1:D:201:ASN:ND2	2:D:760[A]:HDD:HMB2	2.06	0.70
1:D:28:SER:HA	5:D:2467:HOH:O	1.90	0.70
3:C:761[B]:HDE:HBCA	3:C:761[B]:HDE:HMC	1.74	0.69
3:D:761[B]:HDE:HMB	3:D:761[B]:HDE:CBB	2.22	0.69
1:B:700:ASP:HB2	5:B:3595:HOH:O	1.92	0.68
3:D:761[B]:HDE:CMC	3:D:761[B]:HDE:CBC	2.67	0.68
1:B:274:CYS:SG	2:B:760[A]:HDD:HMB3	2.33	0.68
1:B:583:LYS:NZ	1:B:583:LYS:H	1.92	0.67
1:C:449[B]:HIS:NE2	5:C:3610:HOH:O	2.00	0.67
1:B:552:LEU:HD21	1:B:571:LEU:HD12	1.77	0.67
3:B:761[B]:HDE:CMC	3:B:761[B]:HDE:HBCB	2.18	0.66
1:B:274:CYS:SG	2:B:760[A]:HDD:CMB	2.83	0.66
3:B:761[B]:HDE:CBB	3:B:761[B]:HDE:HMB	2.26	0.66
3:A:761[B]:HDE:HBBB	3:A:761[B]:HDE:HMB	1.78	0.66
1:C:274:CYS:HB3	2:C:760[A]:HDD:CBB	2.26	0.65
1:C:578:ASP:HB2	1:C:582:LEU:O	1.96	0.65
1:A:451:MET:SD	5:A:3609:HOH:O	2.53	0.65
1:C:274:CYS:SG	2:C:760[A]:HDD:CMB	2.84	0.65
1:A:532:SER:OG	5:A:2410:HOH:O	2.10	0.64
1:A:582:LEU:O	5:A:3093:HOH:O	2.15	0.63
2:A:760[A]:HDD:CAB	4:A:754:H2S:S	2.87	0.63
1:C:274:CYS:SG	2:C:760[A]:HDD:HMB3	2.39	0.63
1:B:724:ALA:O	1:B:725:ASP:O	2.17	0.62
2:B:760[A]:HDD:HBC1	2:B:760[A]:HDD:HMC1	1.80	0.62
1:C:59:ASP:OD2	5:C:2529:HOH:O	2.16	0.62
2:C:760[A]:HDD:CBC	2:C:760[A]:HDD:HMC1	2.30	0.62
1:D:330:ASP:OD1	1:D:629:HIS:HE1	1.81	0.62
1:D:490:GLU:OE1	5:D:2308:HOH:O	2.16	0.61
1:B:115:THR:HG21	5:D:3420:HOH:O	1.99	0.61
1:C:556:GLN:HG3	1:C:566:LEU:HD12	1.83	0.61
1:B:449[B]:HIS:HE1	5:D:1789:HOH:O	1.82	0.60
1:D:449[A]:HIS:HD2	5:D:3615:HOH:O	1.84	0.60
1:C:28:SER:N	5:C:2523:HOH:O	2.34	0.60
3:A:761[B]:HDE:CBB	3:A:761[B]:HDE:HMB	2.31	0.60
3:D:761[B]:HDE:HMC	4:D:754:H2S:S	2.42	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:416[B]:THR:HG22	5:D:1415:HOH:O	2.03	0.59
1:A:36:HIS:HE1	5:A:1872:HOH:O	1.86	0.59
1:D:748:ILE:O	1:D:751:ILE:HG22	2.02	0.58
1:A:639:GLU:HG3	5:A:2414:HOH:O	2.02	0.58
1:A:416[B]:THR:HG22	5:A:908:HOH:O	2.04	0.58
1:C:533:LYS:NZ	5:C:2231:HOH:O	2.37	0.58
2:B:760[A]:HDD:CBC	2:B:760[A]:HDD:HMC1	2.34	0.57
1:A:244:SER:HA	1:A:546[B]:GLN:NE2	2.18	0.57
1:A:278:ARG:HH12	1:A:487:GLU:CD	2.07	0.57
1:A:199:VAL:HG12	3:A:761[B]:HDE:HHDA	1.86	0.57
1:D:449[A]:HIS:HE1	5:D:1789:HOH:O	1.88	0.57
1:D:267:ARG:HG3	5:D:1920:HOH:O	2.04	0.56
2:C:760[A]:HDD:HMC1	2:C:760[A]:HDD:HBC1	1.88	0.56
1:A:690:LYS:HG3	1:A:751:ILE:HD11	1.86	0.56
1:B:726:GLY:HA2	5:B:3590:HOH:O	2.05	0.56
1:C:274:CYS:CA	4:C:754:H2S:S	2.94	0.56
1:C:274:CYS:SG	2:C:760[A]:HDD:HMB1	2.44	0.56
1:B:602:VAL:HG22	1:B:629:HIS:HB2	1.87	0.56
1:C:330:ASP:OD1	1:C:629:HIS:HE1	1.89	0.56
1:C:359:LEU:H	1:C:507:HIS:HD2	1.54	0.56
1:C:440:TYR:CD1	5:C:3454:HOH:O	2.38	0.55
1:A:610:GLU:CD	5:A:3555:HOH:O	2.41	0.55
1:A:459:ASN:ND2	1:B:219:HIS:HB3	2.22	0.55
1:D:616:LEU:HD22	1:D:620:LEU:HG	1.88	0.55
3:A:761[B]:HDE:CBC	3:A:761[B]:HDE:HMC	2.30	0.55
1:A:211:ALA:CB	1:A:410:GLY:HA3	2.37	0.55
1:D:440:TYR:CZ	5:D:3517:HOH:O	2.53	0.55
1:C:727:SER:O	1:C:731:GLU:HG3	2.07	0.55
2:C:760[A]:HDD:CMC	2:C:760[A]:HDD:HBC1	2.37	0.54
1:B:411:ARG:HG2	3:B:761[B]:HDE:C3B	2.37	0.54
1:C:273:GLY:C	1:C:274:CYS:SG	2.86	0.54
3:C:761[B]:HDE:CMC	3:C:761[B]:HDE:HBCA	2.36	0.54
1:B:449[B]:HIS:HD2	5:B:3613:HOH:O	1.89	0.53
1:B:440:TYR:CE1	1:D:73[B]:LYS:HE2	2.44	0.53
1:D:629:HIS:HD2	5:D:1554:HOH:O	1.90	0.53
1:B:274:CYS:SG	2:B:760[A]:HDD:HMB1	2.49	0.53
1:B:359:LEU:H	1:B:507:HIS:HD2	1.56	0.53
2:B:760[A]:HDD:HBC1	2:B:760[A]:HDD:CMC	2.39	0.53
1:C:583:LYS:O	1:C:584:LYS:HB3	2.07	0.52
3:C:761[B]:HDE:HBBB	3:C:761[B]:HDE:HMB	1.89	0.52
3:C:761[B]:HDE:HMC	4:C:754:H2S:S	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:761[B]:HDE:HMC	4:B:754:H2S:S	2.49	0.52
1:C:629:HIS:HD2	5:C:1129:HOH:O	1.92	0.52
1:B:603:VAL:HG11	1:B:666:ILE:CD1	2.40	0.51
3:D:761[B]:HDE:HBCB	4:D:754:H2S:S	2.51	0.51
1:B:583:LYS:HZ3	1:B:583:LYS:H	1.57	0.51
1:B:578:ASP:HB3	1:B:582:LEU:O	2.10	0.51
1:C:359:LEU:H	1:C:507:HIS:CD2	2.29	0.51
1:D:359:LEU:HD21	5:D:2971:HOH:O	2.10	0.51
1:A:219:HIS:HB3	1:B:459:ASN:ND2	2.27	0.50
1:B:583:LYS:O	1:B:584:LYS:HB3	2.12	0.50
1:A:583:LYS:O	1:A:584:LYS:HB3	2.11	0.50
1:C:359:LEU:C	1:C:359:LEU:HD12	2.32	0.50
1:A:413:PHE:HB2	1:C:105:LEU:HD11	1.93	0.50
1:A:705:LYS:HE3	1:A:710:ILE:CG2	2.42	0.50
1:A:393:PRO:HD2	1:A:415:TYR:CG	2.47	0.49
1:A:725:ASP:H	1:A:728:PHE:HB3	1.77	0.49
1:B:157:ASN:HD22	1:B:157:ASN:C	2.15	0.49
1:D:713:GLN:O	1:D:713:GLN:HG2	2.11	0.49
1:C:440:TYR:HB3	5:C:3454:HOH:O	2.13	0.49
1:B:73:LYS:CD	5:D:3517:HOH:O	2.60	0.49
2:B:760[A]:HDD:CBB	2:B:760[A]:HDD:HMB1	2.43	0.49
1:B:165:ARG:HD3	3:B:761[B]:HDE:O2D	2.12	0.49
1:A:749:ASP:HB2	5:A:3511:HOH:O	2.11	0.49
1:B:201:ASN:ND2	2:B:760[A]:HDD:CMB	2.75	0.48
1:B:38:PRO:HG2	1:B:51:ALA:HB2	1.95	0.48
1:B:183:ARG:HG2	5:B:3407:HOH:O	2.13	0.48
1:B:274:CYS:SG	2:B:760[A]:HDD:HBB1	2.53	0.48
1:B:201:ASN:OD1	2:B:760[A]:HDD:HMB2	2.08	0.48
1:C:274:CYS:SG	2:C:760[A]:HDD:HBB1	2.54	0.48
1:C:459:ASN:ND2	1:D:219:HIS:HB3	2.29	0.48
1:D:157:ASN:ND2	5:D:2055:HOH:O	2.47	0.48
1:B:556:GLN:HG2	1:B:566:LEU:HD22	1.96	0.48
1:B:393:PRO:HD2	1:B:415:TYR:CG	2.49	0.47
1:D:535:VAL:O	1:D:537:PRO:HD3	2.14	0.47
1:B:629:HIS:HD2	5:B:1046:HOH:O	1.97	0.47
1:B:604:ALA:HB1	1:B:633:LEU:HD22	1.96	0.47
1:C:38:PRO:HG2	1:C:51:ALA:HB2	1.97	0.47
1:A:275:HIS:NE2	2:A:760[A]:HDD:HBB1	2.30	0.47
1:A:125:ARG:HB3	3:A:761[B]:HDE:HBA	1.97	0.47
1:B:214:PHE:CD2	2:B:760[A]:HDD:HMC2	2.50	0.47
1:A:751:ILE:O	1:A:751:ILE:CD1	2.58	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:31:PRO:HD2	1:D:36:HIS:HB3	1.98	0.46
1:A:451:MET:HE2	1:C:451:MET:HE1	1.97	0.46
1:A:610:GLU:HG2	5:A:2551:HOH:O	2.15	0.46
1:B:273:GLY:C	1:B:274:CYS:SG	2.93	0.46
1:D:341:ILE:HD11	1:D:360:ILE:HD13	1.96	0.46
1:B:52:PRO:HG3	5:D:1451:HOH:O	2.16	0.46
1:C:583:LYS:HE2	1:C:583:LYS:HB2	1.72	0.46
1:C:602[B]:VAL:HG13	1:C:662:VAL:HA	1.97	0.46
1:A:29:LEU:HB2	5:C:2405:HOH:O	2.15	0.46
1:C:594:PRO:HA	5:C:3460:HOH:O	2.16	0.46
1:B:319:ARG:HD3	1:C:227:TRP:O	2.16	0.46
1:B:274:CYS:HB3	2:B:760[A]:HDD:CBB	2.46	0.45
3:D:761[B]:HDE:CMB	3:D:761[B]:HDE:CBB	2.91	0.45
1:C:748:ILE:O	1:C:751:ILE:HG22	2.16	0.45
1:C:631:LYS:HG3	1:C:633:LEU:HD13	1.98	0.45
1:A:356:PRO:HG3	1:A:407:LEU:HB2	1.97	0.45
1:C:184:GLY:HA3	2:C:760[A]:HDD:HMA2	1.99	0.45
1:A:273:GLY:C	1:A:274:CYS:SG	2.94	0.45
1:A:36:HIS:CD2	1:A:36:HIS:H	2.34	0.45
1:A:275:HIS:CE1	2:A:760[A]:HDD:CBB	2.99	0.45
1:B:583:LYS:HZ2	1:B:583:LYS:H	1.62	0.45
1:A:65:LEU:HD21	1:A:135:HIS:CG	2.51	0.45
1:D:696:ALA:HB1	1:D:728:PHE:CZ	2.52	0.45
1:C:52:PRO:HG2	1:C:55:LEU:HD12	1.99	0.45
1:B:596:GLY:HA3	1:B:737:ALA:O	2.17	0.45
1:A:144:LEU:HD11	1:A:370:VAL:HG13	1.99	0.45
1:B:73:LYS:CE	5:D:3517:HOH:O	2.52	0.45
1:A:448:MET:HG3	1:A:449[B]:HIS:CD2	2.51	0.45
1:B:603:VAL:HG11	1:B:666:ILE:HD12	1.99	0.44
1:A:511:PHE:O	1:A:515:GLN:HG2	2.18	0.44
2:C:760[A]:HDD:CMC	2:C:760[A]:HDD:CBC	2.93	0.44
1:A:610:GLU:OE1	5:A:2394:HOH:O	2.21	0.44
1:C:207:PHE:O	1:C:249:THR:HA	2.17	0.44
1:B:669:ALA:HB1	5:B:3595:HOH:O	2.16	0.44
1:A:128:HIS:HA	1:A:168:THR:O	2.18	0.44
1:A:479:ARG:NH2	5:A:2607:HOH:O	2.45	0.44
1:A:207:PHE:O	1:A:249:THR:HA	2.18	0.44
1:B:369:ARG:HG2	5:B:1639:HOH:O	2.17	0.44
2:D:760[A]:HDD:CAB	4:D:754:H2S:S	3.02	0.44
1:A:37:ARG:HA	1:A:38:PRO:HD3	1.91	0.44
1:A:214:PHE:CD2	2:A:760[A]:HDD:HMC2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:761[B]:HDE:HMC	4:A:754:H2S:S	2.57	0.43
1:D:278:ARG:HH12	1:D:487:GLU:CD	2.22	0.43
1:B:682:ASN:HB3	1:B:707:THR:HG21	1.99	0.43
1:B:607:LEU:HD11	1:B:632:LEU:HB3	2.00	0.43
3:C:761[B]:HDE:HMAA	3:C:761[B]:HDE:HAAA	1.73	0.43
1:A:451:MET:HE1	1:C:451:MET:HE2	1.99	0.43
1:A:443:PHE:CZ	1:A:470:PRO:HD2	2.54	0.43
1:C:708:ILE:HG13	1:C:710:ILE:HG12	1.99	0.43
1:B:213:LYS:HE3	1:B:213:LYS:HB3	1.86	0.43
1:B:274:CYS:CB	2:B:760[A]:HDD:HBB1	2.48	0.43
1:D:448:MET:O	1:D:449[A]:HIS:HB2	2.18	0.43
1:C:73:LYS:HE3	1:C:73:LYS:HB3	1.86	0.43
1:D:38:PRO:HA	1:D:48:GLN:HE21	1.84	0.43
1:B:708:ILE:HG13	1:B:710:ILE:HG12	2.00	0.43
1:C:201:ASN:ND2	2:C:760[A]:HDD:CMB	2.77	0.42
1:A:274:CYS:CA	4:A:754:H2S:S	3.06	0.42
1:D:29:LEU:N	5:D:2467:HOH:O	2.38	0.42
1:C:393:PRO:HD2	1:C:415:TYR:CG	2.53	0.42
1:B:552:LEU:HD22	1:B:556:GLN:HG3	2.00	0.42
1:B:359:LEU:H	1:B:507:HIS:CD2	2.35	0.42
1:A:146:ASP:HB2	5:A:2592:HOH:O	2.19	0.42
1:B:449[B]:HIS:CE1	5:D:1789:HOH:O	2.64	0.42
1:D:359:LEU:H	1:D:507:HIS:HD2	1.66	0.42
1:A:393:PRO:HD2	1:A:415:TYR:CD2	2.54	0.42
1:A:61:ARG:HG2	1:A:61:ARG:HH11	1.83	0.42
1:B:451:MET:HE1	1:D:451:MET:HE2	2.01	0.42
1:C:61:ARG:HG3	5:C:2648:HOH:O	2.20	0.42
2:A:760[A]:HDD:HAB	4:A:754:H2S:S	2.59	0.42
3:B:761[B]:HDE:HMAA	3:B:761[B]:HDE:HAAA	1.79	0.42
1:B:39:ALA:HB1	1:B:41:GLU:HG2	2.01	0.42
1:A:156:PRO:HD2	5:A:3378:HOH:O	2.20	0.42
1:A:38:PRO:HG2	1:A:51:ALA:HB2	2.01	0.42
1:A:184:GLY:HA3	2:A:760[A]:HDD:HMA2	2.02	0.41
1:D:443:PHE:CZ	1:D:470:PRO:HD2	2.55	0.41
1:D:693:LYS:HA	1:D:694:PRO:HD3	1.96	0.41
1:B:507:HIS:HE1	5:B:888:HOH:O	2.02	0.41
1:B:128:HIS:HA	1:B:168:THR:O	2.20	0.41
1:C:461:GLU:HB2	1:C:462:PRO:HA	2.02	0.41
1:B:696:ALA:HB1	1:B:728:PHE:CZ	2.55	0.41
1:A:201:ASN:ND2	2:A:760[A]:HDD:CMB	2.78	0.41
1:B:128:HIS:CE1	1:B:169:VAL:HG22	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:596:GLY:HA3	1:D:737:ALA:O	2.20	0.41
1:A:634:TYR:O	1:A:653:THR:HA	2.20	0.41
3:C:761[B]:HDE:HBCB	4:C:754:H2S:S	2.56	0.41
1:A:578:ASP:OD1	1:A:583:LYS:NZ	2.53	0.41
1:B:344:GLU:CD	1:B:344:GLU:H	2.23	0.41
1:D:201:ASN:CB	2:D:760[A]:HDD:HMB2	2.50	0.41
1:A:451:MET:CE	1:C:451:MET:CE	2.97	0.41
1:B:509:ARG:HD2	1:B:576:PRO:HD2	2.03	0.41
1:B:751:ILE:HG23	1:B:751:ILE:O	2.21	0.41
1:A:319:ARG:HD3	1:D:227:TRP:O	2.20	0.41
1:A:299:LYS:HB2	1:A:299:LYS:HE3	1.90	0.41
1:D:260:ARG:HD3	1:D:590:LEU:HD21	2.03	0.41
1:A:275:HIS:CE1	2:A:760[A]:HDD:HBB2	2.56	0.41
1:C:748:ILE:O	1:C:751:ILE:CG2	2.69	0.41
1:A:211:ALA:HB3	1:A:410:GLY:HA3	2.03	0.41
1:C:710:ILE:HG23	1:C:715:GLU:HG2	2.02	0.41
1:A:509:ARG:HD2	1:A:576:PRO:HD2	2.03	0.41
1:D:313:ARG:HG3	1:D:660:LEU:HD12	2.03	0.41
1:D:211:ALA:CB	1:D:410:GLY:HA3	2.50	0.41
1:B:83:ASN:HB3	1:D:429:HIS:CG	2.56	0.41
1:D:404:ASN:O	1:D:405:ASP:C	2.59	0.41
1:A:214:PHE:CD1	2:A:760[A]:HDD:HAC	2.56	0.41
1:A:201:ASN:CG	3:A:761[B]:HDE:HAC	2.41	0.41
5:A:1788:HOH:O	1:C:449[A]:HIS:HE1	2.02	0.41
1:A:751:ILE:C	1:A:751:ILE:HD12	2.40	0.41
1:B:725:ASP:OD2	1:B:725:ASP:C	2.59	0.41
1:C:602[A]:VAL:HG21	5:C:2034:HOH:O	2.21	0.41
1:A:252:ASN:HA	1:A:252:ASN:HD22	1.71	0.41
1:C:252:ASN:HD22	1:C:252:ASN:HA	1.68	0.41
1:D:128:HIS:CE1	1:D:169:VAL:HG22	2.56	0.41
1:B:393:PRO:HD2	1:B:415:TYR:CD2	2.56	0.40
1:D:48:GLN:HB3	1:D:48:GLN:HE21	1.72	0.40
1:C:219:HIS:HB3	1:D:459:ASN:ND2	2.36	0.40
1:A:417:ASP:OD2	1:D:118:ASP:OD1	2.39	0.40
3:C:761[B]:HDE:CMB	3:C:761[B]:HDE:HBBA	2.46	0.40
1:D:207:PHE:O	1:D:249:THR:HA	2.21	0.40
1:C:686:MET:HB3	1:C:751:ILE:HD11	2.03	0.40
1:A:155:ASP:CG	5:A:3378:HOH:O	2.60	0.40
1:B:206:PHE:CG	1:B:207:PHE:N	2.90	0.40

All (5) 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:C:59:ASP:CB	5:B:3206:HOH:O[2_545]	1.99	0.21
1:C:584:LYS:NZ	5:A:1624:HOH:O[1_554]	2.06	0.14
5:D:2178:HOH:O	5:D:2976:HOH:O[1_655]	2.06	0.14
5:A:3348:HOH:O	5:B:2822:HOH:O[2_545]	2.10	0.10
5:A:3241:HOH:O	5:D:2457:HOH:O[2_646]	2.12	0.08

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	729/753 (97%)	708 (97%)	20 (3%)	1 (0%)	56	38
1	B	729/753 (97%)	709 (97%)	18 (2%)	2 (0%)	46	29
1	C	726/753 (96%)	703 (97%)	22 (3%)	1 (0%)	56	38
1	D	733/753 (97%)	712 (97%)	20 (3%)	1 (0%)	56	38
All	All	2917/3012 (97%)	2832 (97%)	80 (3%)	5 (0%)	52	35

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	725	ASP
1	C	75	SER
1	D	75	SER
1	A	75	SER
1	B	75	SER

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	A	614/634 (97%)	596 (97%)	18 (3%)	50	34
1	B	614/634 (97%)	586 (95%)	28 (5%)	33	15
1	C	611/634 (96%)	584 (96%)	27 (4%)	35	17
1	D	618/634 (98%)	593 (96%)	25 (4%)	38	20
All	All	2457/2536 (97%)	2359 (96%)	98 (4%)	39	20

All (98) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	SER
1	A	29	LEU
1	A	185	PHE
1	A	205	ILE
1	A	227	TRP
1	A	237	ASP
1	A	252	ASN
1	A	369	ARG
1	A	377	ARG
1	A	432	PRO
1	A	440	TYR
1	A	459	ASN
1	A	552	LEU
1	A	610	GLU
1	A	707	THR
1	A	713	GLN
1	A	732	LEU
1	A	751	ILE
1	B	140	PRO
1	B	157	ASN
1	B	158	LYS
1	B	185	PHE
1	B	205	ILE
1	B	227	TRP
1	B	237	ASP
1	B	252	ASN
1	B	274	CYS
1	B	344	GLU
1	B	370	VAL
1	B	432	PRO
1	B	440	TYR
1	B	459	ASN
1	B	552	LEU

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Mol	Chain	Res	Type
1	B	562	LEU
1	B	565	GLU
1	B	566	LEU
1	B	568	ASP
1	B	571	LEU
1	B	583	LYS
1	B	594	PRO
1	B	616	LEU
1	B	633	LEU
1	B	703	LYS
1	B	713	GLN
1	B	725	ASP
1	B	750	LYS
1	C	61	ARG
1	C	159	ILE
1	C	185	PHE
1	C	191	THR
1	C	205	ILE
1	C	227	TRP
1	C	252	ASN
1	C	274	CYS
1	C	285	LYS
1	C	377	ARG
1	C	440	TYR
1	C	459	ASN
1	C	488	ARG
1	C	552	LEU
1	C	571	LEU
1	C	584	LYS
1	C	606	LEU
1	C	616	LEU
1	C	617	LEU
1	C	626	LYS
1	C	636	ARG
1	C	639	GLU
1	C	648	LEU
1	C	725	ASP
1	C	732	LEU
1	C	733	LEU
1	C	750	LYS
1	D	32	GLU
1	D	48	GLN

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Mol	Chain	Res	Type
1	D	73[A]	LYS
1	D	73[B]	LYS
1	D	185	PHE
1	D	191	THR
1	D	205	ILE
1	D	227	TRP
1	D	237	ASP
1	D	252	ASN
1	D	416[A]	THR
1	D	416[B]	THR
1	D	440	TYR
1	D	459	ASN
1	D	490	GLU
1	D	552	LEU
1	D	574	THR
1	D	582	LEU
1	D	616	LEU
1	D	648	LEU
1	D	700	ASP
1	D	713	GLN
1	D	732	LEU
1	D	747	LYS
1	D	748	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	HIS
1	A	252	ASN
1	A	459	ASN
1	A	515	GLN
1	B	157	ASN
1	B	252	ASN
1	B	368	GLN
1	B	459	ASN
1	B	507	HIS
1	B	629	HIS
1	C	252	ASN
1	C	459	ASN
1	C	507	HIS
1	C	556	GLN
1	C	629	HIS

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Mol	Chain	Res	Type
1	C	671	ASN
1	D	48	GLN
1	D	157	ASN
1	D	252	ASN
1	D	459	ASN
1	D	507	HIS
1	D	549	HIS
1	D	556	GLN
1	D	629	HIS
1	D	671	ASN

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 4 are modelled with single atom - leaving 8 for Mogul analysis.

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	$\# Z > 2$
2	HDD	A	760[A]	1,5	30,52,52	2.58	10 (33%)	20,89,89	3.05	9 (45%)
3	HDE	A	761[B]	1,5	34,52,52	2.98	14 (41%)	27,89,89	2.65	15 (55%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HDD	B	760[A]	1,5	30,52,52	2.19	10 (33%)	20,89,89	3.38	10 (50%)
3	HDE	B	761[B]	1,5	34,52,52	3.03	13 (38%)	27,89,89	2.88	12 (44%)
2	HDD	C	760[A]	1,5	30,52,52	2.07	9 (30%)	20,89,89	4.03	12 (60%)
3	HDE	C	761[B]	1,5	34,52,52	3.03	13 (38%)	27,89,89	2.53	11 (40%)
2	HDD	D	760[A]	1,5	30,52,52	2.49	8 (26%)	20,89,89	3.25	11 (55%)
3	HDE	D	761[B]	1,5	34,52,52	2.62	12 (35%)	27,89,89	2.68	13 (48%)

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
2	HDD	A	760[A]	1,5	-	0/3/89/89	0/1/9/9
3	HDE	A	761[B]	1,5	-	1/7/89/89	0/1/9/9
2	HDD	B	760[A]	1,5	-	0/3/89/89	0/1/9/9
3	HDE	B	761[B]	1,5	-	2/7/89/89	0/1/9/9
2	HDD	C	760[A]	1,5	-	0/3/89/89	0/1/9/9
3	HDE	C	761[B]	1,5	-	2/7/89/89	0/1/9/9
2	HDD	D	760[A]	1,5	-	0/3/89/89	0/1/9/9
3	HDE	D	761[B]	1,5	-	1/7/89/89	0/1/9/9

All (89) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	760[A]	HDD	C3B-C2B	-6.88	1.31	1.40
2	D	760[A]	HDD	C3B-C2B	-5.95	1.32	1.40
2	A	760[A]	HDD	C3C-C2C	-5.80	1.32	1.40
2	B	760[A]	HDD	C3C-C2C	-5.47	1.33	1.40
2	A	760[A]	HDD	O1D-C3D	-5.27	1.37	1.46
2	C	760[A]	HDD	C3C-C2C	-4.49	1.34	1.40
2	C	760[A]	HDD	C3B-C2B	-3.78	1.35	1.40
2	D	760[A]	HDD	O1D-C3D	-3.78	1.40	1.46
2	B	760[A]	HDD	C3B-C2B	-3.64	1.35	1.40
2	D	760[A]	HDD	C3C-C2C	-3.54	1.35	1.40
2	B	760[A]	HDD	O1D-C3D	-3.32	1.41	1.46
2	C	760[A]	HDD	O1D-C3D	-2.70	1.42	1.46
3	B	761[B]	HDE	C1D-C2D	2.01	1.40	1.37
2	C	760[A]	HDD	CMA-C3A	2.03	1.55	1.51
2	A	760[A]	HDD	C4B-NB	2.06	1.39	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	761[B]	HDE	C1B-CHB	2.07	1.45	1.39
2	A	760[A]	HDD	C1B-NB	2.09	1.39	1.36
2	D	760[A]	HDD	CMC-C2C	2.13	1.56	1.51
2	C	760[A]	HDD	CMD-C2D	2.16	1.56	1.53
2	B	760[A]	HDD	C4D-ND	2.16	1.41	1.38
3	D	761[B]	HDE	C1B-CHB	2.16	1.45	1.39
2	C	760[A]	HDD	C1B-NB	2.24	1.39	1.36
2	C	760[A]	HDD	CAA-C2A	2.32	1.56	1.52
3	C	761[B]	HDE	C1A-NA	2.44	1.41	1.38
3	C	761[B]	HDE	C4D-CHA	2.46	1.46	1.39
2	B	760[A]	HDD	CMD-C2D	2.48	1.56	1.53
3	A	761[B]	HDE	C1D-ND	2.49	1.37	1.34
2	A	760[A]	HDD	CMC-C2C	2.55	1.56	1.51
2	B	760[A]	HDD	CMC-C2C	2.61	1.57	1.51
3	B	761[B]	HDE	C3D-C2D	2.64	1.45	1.37
2	A	760[A]	HDD	CAA-C2A	2.67	1.56	1.52
2	B	760[A]	HDD	CMA-C3A	2.82	1.57	1.51
3	A	761[B]	HDE	C4D-CHA	2.84	1.47	1.39
2	D	760[A]	HDD	OND-C2D	2.86	1.48	1.42
3	A	761[B]	HDE	C4A-NA	2.93	1.42	1.38
3	B	761[B]	HDE	C4D-CHA	3.06	1.48	1.39
2	A	760[A]	HDD	C3C-CAC	3.10	1.54	1.47
2	B	760[A]	HDD	C3C-CAC	3.11	1.54	1.47
2	A	760[A]	HDD	C3B-CAB	3.11	1.54	1.47
3	A	761[B]	HDE	C1B-CHB	3.13	1.48	1.39
2	C	760[A]	HDD	C3B-CAB	3.14	1.54	1.47
3	D	761[B]	HDE	C3C-C2C	3.16	1.47	1.37
3	D	761[B]	HDE	C1A-NA	3.18	1.42	1.38
3	D	761[B]	HDE	C3D-C2D	3.24	1.47	1.37
3	D	761[B]	HDE	C4D-CHA	3.29	1.48	1.39
3	C	761[B]	HDE	C3D-C2D	3.34	1.47	1.37
3	A	761[B]	HDE	C3C-C2C	3.34	1.47	1.37
3	B	761[B]	HDE	C1A-NA	3.37	1.43	1.38
3	B	761[B]	HDE	C3B-C2B	3.42	1.47	1.37
3	D	761[B]	HDE	C4A-NA	3.44	1.43	1.38
3	C	761[B]	HDE	C4A-NA	3.47	1.43	1.38
2	B	760[A]	HDD	C3B-CAB	3.50	1.55	1.47
3	C	761[B]	HDE	C1C-C2C	3.55	1.42	1.37
2	B	760[A]	HDD	FE-ND	3.56	2.09	1.95
3	A	761[B]	HDE	C1A-NA	3.56	1.43	1.38
3	A	761[B]	HDE	C1C-C2C	3.56	1.42	1.37
3	C	761[B]	HDE	C3C-C2C	3.59	1.48	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	761[B]	HDE	C1C-C2C	3.63	1.42	1.37
3	B	761[B]	HDE	C4A-NA	3.78	1.43	1.38
3	B	761[B]	HDE	C3C-C2C	3.79	1.48	1.37
3	C	761[B]	HDE	C3B-C2B	3.80	1.48	1.37
2	D	760[A]	HDD	C3C-CAC	3.89	1.56	1.47
3	A	761[B]	HDE	C3B-C2B	3.93	1.49	1.37
3	A	761[B]	HDE	C3D-C2D	3.98	1.49	1.37
2	D	760[A]	HDD	C3B-CAB	4.10	1.56	1.47
3	D	761[B]	HDE	C3B-C2B	4.11	1.49	1.37
3	A	761[B]	HDE	O1A-CGA	4.44	1.43	1.35
3	D	761[B]	HDE	O1A-CGA	4.50	1.43	1.35
3	D	761[B]	HDE	C4B-NB	4.83	1.40	1.34
3	C	761[B]	HDE	O1A-CGA	4.85	1.43	1.35
3	C	761[B]	HDE	C4B-NB	4.92	1.40	1.34
3	D	761[B]	HDE	C1C-NC	4.96	1.40	1.34
3	B	761[B]	HDE	C4B-NB	4.97	1.40	1.34
3	B	761[B]	HDE	O1A-CGA	4.98	1.44	1.35
2	A	760[A]	HDD	FE-ND	5.10	2.15	1.95
3	A	761[B]	HDE	C4B-NB	5.47	1.41	1.34
3	D	761[B]	HDE	C4C-NC	5.76	1.41	1.34
2	C	760[A]	HDD	FE-ND	5.82	2.18	1.95
3	B	761[B]	HDE	C4C-NC	6.01	1.42	1.34
3	C	761[B]	HDE	C4C-NC	6.33	1.42	1.34
3	A	761[B]	HDE	C1C-NC	6.44	1.42	1.34
3	D	761[B]	HDE	C4C-C3C	6.85	1.46	1.37
3	A	761[B]	HDE	C4C-NC	7.00	1.43	1.34
2	D	760[A]	HDD	FE-ND	7.24	2.24	1.95
3	C	761[B]	HDE	C1C-NC	7.37	1.43	1.34
3	A	761[B]	HDE	C4C-C3C	7.62	1.47	1.37
3	B	761[B]	HDE	C1C-NC	7.68	1.44	1.34
3	B	761[B]	HDE	C4C-C3C	8.35	1.48	1.37
3	C	761[B]	HDE	C4C-C3C	8.78	1.49	1.37

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	760[A]	HDD	C3C-CAC-CBC	-8.40	109.12	126.32
3	A	761[B]	HDE	CAD-CBD-CGD	-6.56	100.72	112.75
2	C	760[A]	HDD	OND-C2D-CMD	-6.10	98.40	109.41
2	C	760[A]	HDD	C3B-CAB-CBB	-5.80	114.45	126.32
2	A	760[A]	HDD	O1D-CGD-CBD	-5.78	103.42	110.20
2	A	760[A]	HDD	C3B-CAB-CBB	-5.67	114.72	126.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	760[A]	HDD	C3B-CAB-CBB	-5.60	114.87	126.32
3	C	761[B]	HDE	C1C-C2C-C3C	-5.57	100.56	105.67
3	B	761[B]	HDE	C4A-NA-C1A	-5.51	103.81	107.36
2	B	760[A]	HDD	C3C-CAC-CBC	-5.43	115.20	126.32
3	B	761[B]	HDE	CBC-CAC-C3C	-5.33	98.44	112.40
3	B	761[B]	HDE	C1C-C2C-C3C	-5.24	100.86	105.67
2	B	760[A]	HDD	O1D-CGD-CBD	-5.23	104.08	110.20
3	B	761[B]	HDE	CAD-CBD-CGD	-5.22	103.17	112.75
3	D	761[B]	HDE	CAD-CBD-CGD	-5.13	103.34	112.75
2	B	760[A]	HDD	CAA-CBA-CGA	-5.09	103.41	112.75
2	A	760[A]	HDD	CAA-CBA-CGA	-5.04	103.52	112.75
2	D	760[A]	HDD	C3C-CAC-CBC	-4.94	116.22	126.32
2	D	760[A]	HDD	CAA-CBA-CGA	-4.79	103.97	112.75
2	A	760[A]	HDD	CAD-CBD-CGD	-4.76	96.41	104.64
3	D	761[B]	HDE	CBC-CAC-C3C	-4.68	100.14	112.40
2	B	760[A]	HDD	C3B-CAB-CBB	-4.65	116.81	126.32
3	C	761[B]	HDE	CAD-CBD-CGD	-4.27	104.93	112.75
2	A	760[A]	HDD	C3C-CAC-CBC	-4.11	117.90	126.32
2	C	760[A]	HDD	O1D-CGD-CBD	-3.98	105.54	110.20
2	C	760[A]	HDD	CMA-C3A-C4A	-3.87	121.97	128.36
2	D	760[A]	HDD	O1D-CGD-CBD	-3.81	105.74	110.20
3	A	761[B]	HDE	C4A-NA-C1A	-3.77	104.93	107.36
3	D	761[B]	HDE	C4A-NA-C1A	-3.74	104.95	107.36
3	C	761[B]	HDE	C3A-C4A-CHB	-3.67	117.77	123.48
3	A	761[B]	HDE	CAB-C3B-C4B	-3.65	122.52	127.12
3	A	761[B]	HDE	C1C-C2C-C3C	-3.60	102.36	105.67
3	C	761[B]	HDE	CBC-CAC-C3C	-3.56	103.08	112.40
3	D	761[B]	HDE	C1C-C2C-C3C	-3.41	102.54	105.67
3	A	761[B]	HDE	CAC-C3C-C4C	-3.24	123.03	127.12
2	D	760[A]	HDD	OND-C2D-CMD	-3.22	103.60	109.41
3	D	761[B]	HDE	C3A-C4A-CHB	-3.20	118.50	123.48
3	D	761[B]	HDE	CBB-CAB-C3B	-3.17	104.10	112.40
3	B	761[B]	HDE	C3A-C4A-CHB	-3.16	118.56	123.48
2	B	760[A]	HDD	CAA-C2A-C1A	-3.10	123.64	127.01
2	C	760[A]	HDD	C3C-C4C-NC	-3.09	105.22	109.21
3	C	761[B]	HDE	C4A-NA-C1A	-3.09	105.37	107.36
2	A	760[A]	HDD	OND-C2D-CMD	-3.09	103.84	109.41
2	D	760[A]	HDD	CMA-C3A-C4A	-2.99	123.41	128.36
2	A	760[A]	HDD	C3B-C4B-NB	-2.98	105.31	110.94
3	D	761[B]	HDE	CMB-C2B-C1B	-2.98	123.44	128.36
2	B	760[A]	HDD	CMC-C2C-C1C	-2.94	123.50	128.36
3	B	761[B]	HDE	C1D-C2D-C3D	-2.57	103.31	105.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	761[B]	HDE	CBC-CAC-C3C	-2.55	105.73	112.40
3	A	761[B]	HDE	C1D-C2D-C3D	-2.47	103.40	105.67
2	A	760[A]	HDD	CMA-C3A-C4A	-2.41	124.38	128.36
2	D	760[A]	HDD	CMC-C2C-C1C	-2.40	124.40	128.36
2	B	760[A]	HDD	CAD-CBD-CGD	-2.36	100.57	104.64
2	D	760[A]	HDD	C3B-C4B-NB	-2.30	106.60	110.94
3	A	761[B]	HDE	CMD-C2D-C1D	-2.05	125.07	127.14
2	C	760[A]	HDD	CAA-CBA-CGA	-2.05	108.98	112.75
3	A	761[B]	HDE	CMC-C2C-C3C	2.04	129.50	125.24
3	B	761[B]	HDE	CAB-C3B-C2B	2.08	129.20	124.01
3	C	761[B]	HDE	CMC-C2C-C3C	2.15	129.73	125.24
3	A	761[B]	HDE	O1A-CGA-O2A	2.15	122.84	120.80
2	C	760[A]	HDD	CMB-C2B-C3B	2.17	129.33	125.09
3	A	761[B]	HDE	CMB-C2B-C3B	2.18	129.79	125.24
2	C	760[A]	HDD	CMA-C3A-C2A	2.23	129.90	125.24
3	B	761[B]	HDE	CAD-C3D-C4D	2.23	129.43	127.01
3	D	761[B]	HDE	CMC-C2C-C3C	2.26	129.97	125.24
3	C	761[B]	HDE	CMD-C2D-C3D	2.26	129.97	125.24
2	B	760[A]	HDD	CMC-C2C-C3C	2.29	129.57	125.09
3	D	761[B]	HDE	CAB-C3B-C2B	2.43	130.08	124.01
2	C	760[A]	HDD	C2D-C1D-CHD	2.52	127.40	123.48
3	C	761[B]	HDE	O1A-CGA-O2A	2.53	123.20	120.80
3	C	761[B]	HDE	CMC-C2C-C1C	2.53	129.69	127.14
2	D	760[A]	HDD	C2D-C1D-CHD	2.65	127.61	123.48
3	B	761[B]	HDE	CMD-C2D-C1D	2.68	129.85	127.14
3	D	761[B]	HDE	CAD-C3D-C4D	2.97	130.24	127.01
3	A	761[B]	HDE	CMD-C2D-C3D	3.00	131.50	125.24
3	A	761[B]	HDE	CAB-C3B-C2B	3.10	131.76	124.01
3	B	761[B]	HDE	C4B-CHC-C1C	3.37	119.42	112.50
3	D	761[B]	HDE	CMB-C2B-C3B	3.39	132.31	125.24
3	A	761[B]	HDE	C4C-CHD-C1D	3.58	119.84	112.50
3	B	761[B]	HDE	CMC-C2C-C1C	3.64	130.82	127.14
3	C	761[B]	HDE	C4B-CHC-C1C	3.82	120.34	112.50
3	A	761[B]	HDE	C4B-CHC-C1C	3.99	120.70	112.50
3	D	761[B]	HDE	C4B-CHC-C1C	4.14	121.00	112.50
2	A	760[A]	HDD	C4D-ND-C1D	4.31	110.14	107.36
3	D	761[B]	HDE	C4C-CHD-C1D	4.74	122.22	112.50
2	B	760[A]	HDD	C4D-ND-C1D	4.76	110.43	107.36
3	C	761[B]	HDE	C4C-CHD-C1D	5.02	122.80	112.50
2	C	760[A]	HDD	C4D-ND-C1D	5.03	110.60	107.36
2	D	760[A]	HDD	O1D-CGD-O2D	5.57	126.09	120.80
3	B	761[B]	HDE	C4C-CHD-C1D	5.87	124.54	112.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	760[A]	HDD	C4D-ND-C1D	6.51	111.56	107.36
2	B	760[A]	HDD	O1D-CGD-O2D	7.51	127.94	120.80
2	C	760[A]	HDD	O1D-CGD-O2D	9.18	129.53	120.80

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	761[B]	HDE	C2B-C3B-CAB-CBB
3	D	761[B]	HDE	C2B-C3B-CAB-CBB
3	A	761[B]	HDE	C2B-C3B-CAB-CBB
3	B	761[B]	HDE	C2C-C3C-CAC-CBC
3	C	761[B]	HDE	C2C-C3C-CAC-CBC
3	C	761[B]	HDE	C2B-C3B-CAB-CBB

There are no ring outliers.

8 monomers are involved in 102 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	760[A]	HDD	16	0
3	A	761[B]	HDE	8	0
2	B	760[A]	HDD	17	0
3	B	761[B]	HDE	12	0
2	C	760[A]	HDD	18	0
3	C	761[B]	HDE	13	0
2	D	760[A]	HDD	9	0
3	D	761[B]	HDE	9	0

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	726/753 (96%)	-0.76	4 (0%)	90 88	3, 10, 27, 44	2 (0%)
1	B	726/753 (96%)	-0.62	8 (1%)	82 80	4, 12, 32, 48	2 (0%)
1	C	726/753 (96%)	-0.65	7 (0%)	84 82	4, 12, 31, 47	2 (0%)
1	D	726/753 (96%)	-0.76	3 (0%)	93 91	4, 10, 28, 44	1 (0%)
All	All	2904/3012 (96%)	-0.70	22 (0%)	87 85	3, 11, 30, 48	7 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	726	GLY	4.4
1	B	713	GLN	3.7
1	C	594	PRO	3.2
1	B	28	SER	3.2
1	B	32	GLU	3.2
1	C	711	ALA	3.1
1	D	28	SER	3.0
1	C	726	GLY	2.9
1	D	749	ASP	2.6
1	D	711	ALA	2.6
1	C	750	LYS	2.6
1	A	713	GLN	2.5
1	A	28	SER	2.5
1	B	712	ASP	2.4
1	A	32	GLU	2.4
1	C	583	LYS	2.3
1	C	712	ASP	2.3
1	C	646	THR	2.3
1	B	711	ALA	2.3
1	A	594	PRO	2.2
1	B	647	VAL	2.2
1	B	725	ASP	2.2

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 carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	H2S	C	754	1/1	0.97	0.32	13.14	24,24,24,24	1
4	H2S	D	754	1/1	0.96	0.23	8.34	21,21,21,21	1
4	H2S	A	754	1/1	0.96	0.26	7.71	28,28,28,28	1
4	H2S	B	754	1/1	0.98	0.24	7.40	24,24,24,24	1
3	HDE	C	761[B]	44/44	0.98	0.07	0.78	3,11,14,15	44
2	HDD	C	760[A]	44/44	0.98	0.07	0.64	2,5,8,17	44
2	HDD	D	760[A]	44/44	0.98	0.07	0.49	2,4,9,14	44
3	HDE	D	761[B]	44/44	0.99	0.07	0.33	3,9,14,16	44
3	HDE	B	761[B]	44/44	0.98	0.07	0.15	3,11,13,16	44
2	HDD	B	760[A]	44/44	0.98	0.07	0.14	2,4,8,11	44
2	HDD	A	760[A]	44/44	0.99	0.06	0.02	2,3,9,10	44
3	HDE	A	761[B]	44/44	0.99	0.06	-0.10	2,8,11,12	44

6.5 Other polymers [i](#)

There are no such residues in this entry.