



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:35 AM GMT

PDB ID : 3P9S  
Title : Structure of I274A variant of E. coli KatE  
Authors : Loewen, P.C.; Jha, V.; Louis, S.; Chelikani, P.; Carpena, X.; Fita, I.  
Deposited on : 2010-10-18  
Resolution : 1.90 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](mailto: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.

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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

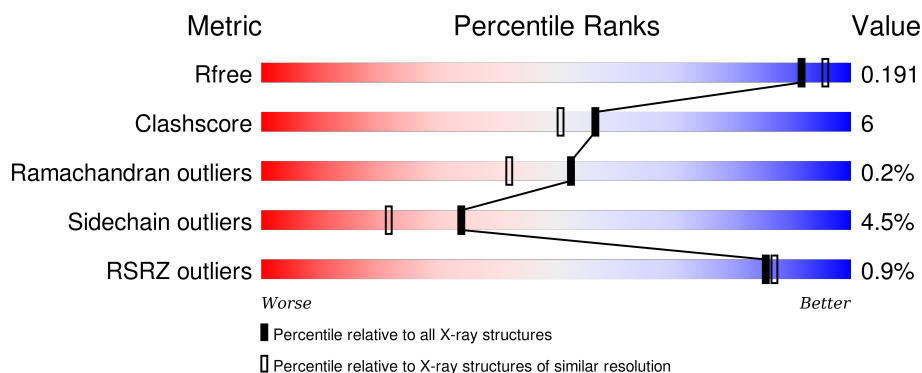
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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  $\geq 3$ , 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>86%</div> <div>9% . .</div> </div>
1	B	753	<div> <div>%</div> <div>83%</div> <div>12% . .</div> </div>
1	C	753	<div> <div>%</div> <div>83%</div> <div>12% . .</div> </div>
1	D	753	<div> <div>%</div> <div>86%</div> <div>9% . .</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
1	OCS	A	669	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 26530 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.

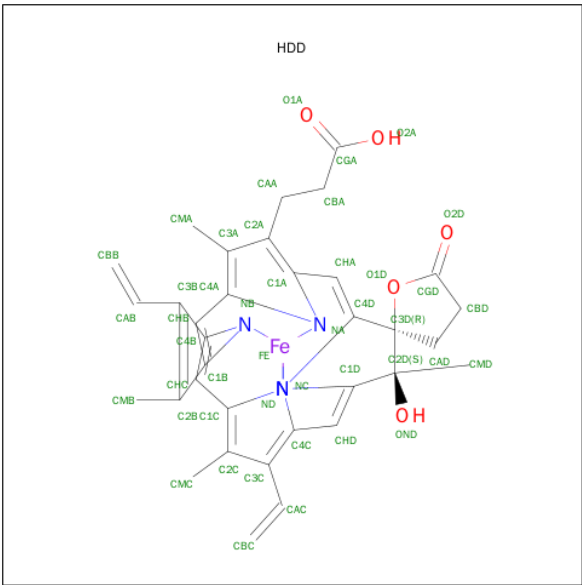
- Molecule 1 is a protein called Catalase HPIL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	726	Total	C	N	O	S	0	3	0
			5748	3644	1009	1083	12			
1	B	726	Total	C	N	O	S	0	2	0
			5749	3646	1007	1084	12			
1	C	726	Total	C	N	O	S	0	3	0
			5747	3644	1006	1085	12			
1	D	726	Total	C	N	O	S	0	2	0
			5751	3649	1007	1083	12			

There are 4 discrepancies between the modelled and reference sequences:

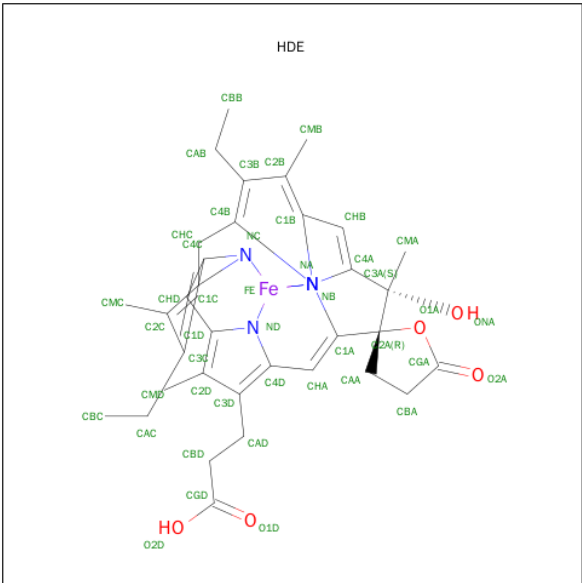
Chain	Residue	Modelled	Actual	Comment	Reference
A	274	ALA	ILE	ENGINEERED MUTATION	UNP P21179
B	274	ALA	ILE	ENGINEERED MUTATION	UNP P21179
C	274	ALA	ILE	ENGINEERED MUTATION	UNP P21179
D	274	ALA	ILE	ENGINEERED MUTATION	UNP P21179

- Molecule 2 is CIS-HEME D HYDROXYCHLORIN GAMMA-SPIROLACTONE (three-letter code: HDD) (formula:  $C_{34}H_{32}FeN_4O_5$ ).



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: C<sub>34</sub>H<sub>38</sub>FeN<sub>4</sub>O<sub>5</sub>).



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

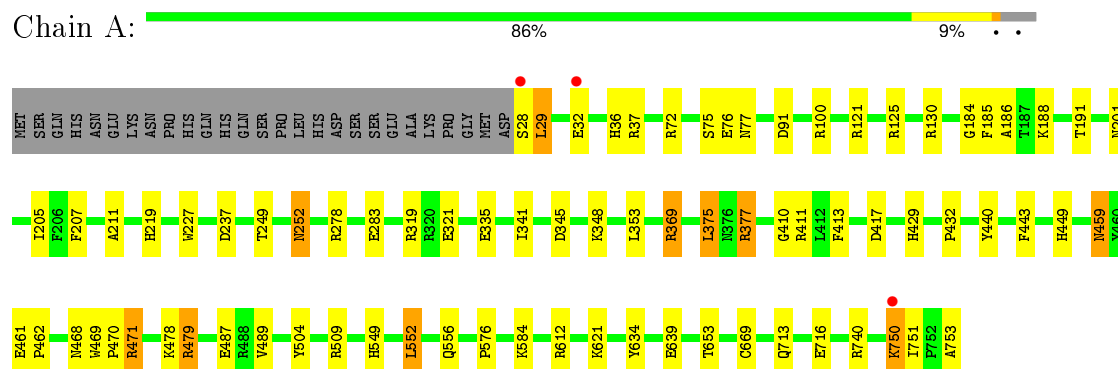
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	835	Total 835	O 835	0	0
4	B	751	Total 751	O 751	0	0
4	C	765	Total 765	O 765	0	0
4	D	832	Total 832	O 832	0	0

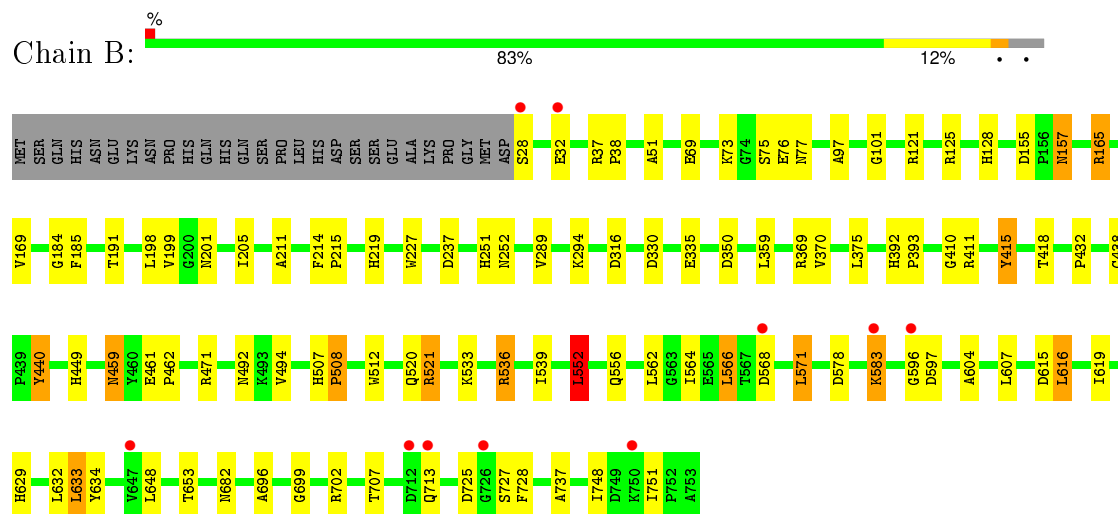
### 3 Residue-property plots

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.

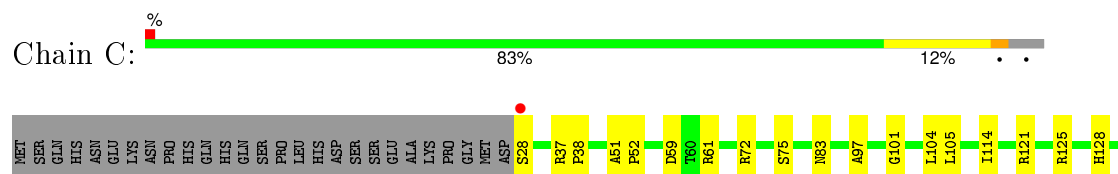
#### • Molecule 1: Catalase HP1I

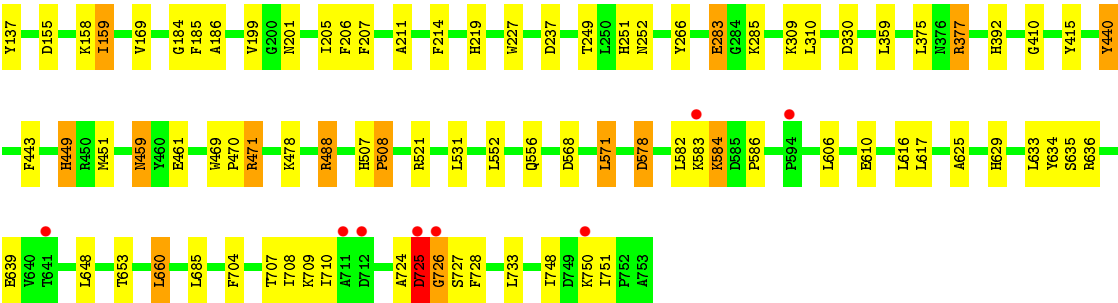


#### • Molecule 1: Catalase HP1I

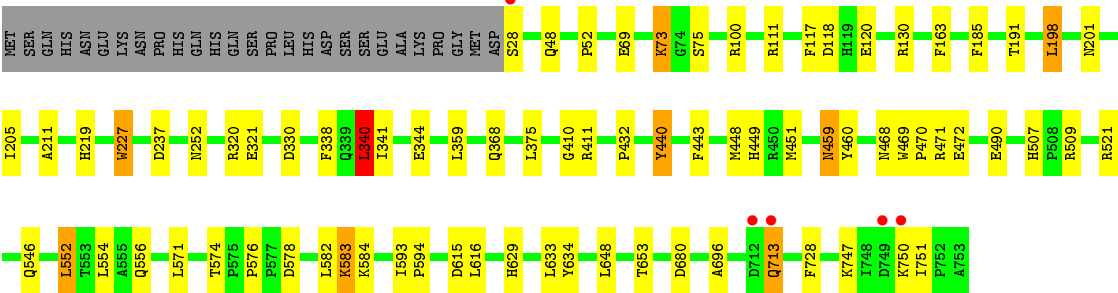
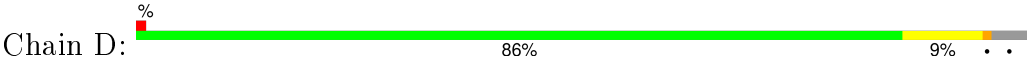


#### • Molecule 1: Catalase HP1I





● Molecule 1: Catalase HPII





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.56Å 133.17Å 122.81Å 90.00° 109.24° 90.00°	Depositor
Resolution (Å)	31.29 – 1.90 31.29 – 1.90	Depositor EDS
% Data completeness (in resolution range)	88.6 (31.29-1.90) 88.6 (31.29-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.13 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.137 , 0.191 0.138 , 0.191	Depositor DCC
$R_{free}$ test set	9959 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	11.8	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 42.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 197565 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	26530	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, OCS

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	1.13	4/5912 (0.1%)	0.94	11/8035 (0.1%)
1	B	1.11	9/5901 (0.2%)	0.92	8/8021 (0.1%)
1	C	1.09	3/5909 (0.1%)	0.91	10/8032 (0.1%)
1	D	1.13	6/5903 (0.1%)	0.93	7/8024 (0.1%)
All	All	1.12	22/23625 (0.1%)	0.93	36/32112 (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 (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	460	TYR	CD1-CE1	7.67	1.50	1.39
1	B	494	VAL	CB-CG2	7.62	1.68	1.52
1	D	321	GLU	CD-OE1	6.20	1.32	1.25
1	B	69	GLU	CB-CG	6.08	1.63	1.52
1	B	438	CYS	CB-SG	5.96	1.92	1.82
1	B	440	TYR	CE1-CZ	5.82	1.46	1.38
1	A	489	VAL	CB-CG1	5.67	1.64	1.52
1	B	157	ASN	CB-CG	5.66	1.64	1.51
1	D	69	GLU	CG-CD	5.57	1.60	1.51
1	A	186	ALA	CA-CB	5.51	1.64	1.52
1	C	266	TYR	CD1-CE1	5.50	1.47	1.39
1	B	289	VAL	CB-CG1	5.38	1.64	1.52
1	A	321	GLU	CD-OE1	5.34	1.31	1.25
1	D	163	PHE	CE1-CZ	5.29	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	69	GLU	CG-CD	5.25	1.59	1.51
1	D	163	PHE	CG-CD2	5.20	1.46	1.38
1	C	283	GLU	CB-CG	-5.19	1.42	1.52
1	D	344	GLU	CD-OE2	5.05	1.31	1.25
1	B	415	TYR	CD1-CE1	5.04	1.47	1.39
1	A	504	TYR	CD2-CE2	-5.04	1.31	1.39
1	B	335	GLU	CB-CG	-5.02	1.42	1.52
1	C	186	ALA	CA-CB	5.01	1.62	1.52

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	72	ARG	NE-CZ-NH2	-8.41	116.10	120.30
1	D	340	LEU	CB-CG-CD1	8.06	124.70	111.00
1	C	37	ARG	NE-CZ-NH2	-7.24	116.68	120.30
1	A	121	ARG	NE-CZ-NH2	-7.13	116.73	120.30
1	B	552	LEU	CA-CB-CG	6.92	131.21	115.30
1	A	509	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	D	615	ASP	CB-CG-OD2	6.31	123.98	118.30
1	D	130	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	B	536	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	D	680	ASP	CB-CG-OD2	6.15	123.84	118.30
1	A	740	ARG	NE-CZ-NH1	6.15	123.37	120.30
1	A	471	ARG	NE-CZ-NH1	-6.00	117.30	120.30
1	C	72	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	D	320	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	A	130	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	B	536	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	C	471	ARG	NE-CZ-NH2	-5.63	117.49	120.30
1	C	725	ASP	CB-CA-C	-5.55	99.31	110.40
1	C	121	ARG	NE-CZ-NH2	-5.47	117.57	120.30
1	C	59[A]	ASP	CB-CG-OD1	5.45	123.21	118.30
1	C	59[B]	ASP	CB-CG-OD1	5.45	123.21	118.30
1	B	471	ARG	NE-CZ-NH2	-5.45	117.58	120.30
1	D	111	ARG	NE-CZ-NH2	5.43	123.02	120.30
1	A	552	LEU	CB-CG-CD2	5.32	120.04	111.00
1	B	350	ASP	CB-CG-OD1	-5.29	113.54	118.30
1	A	375	LEU	CB-CG-CD2	5.26	119.94	111.00
1	A	100	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	B	121	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	B	316	ASP	CB-CG-OD2	-5.20	113.62	118.30
1	D	198	LEU	CA-CB-CG	5.12	127.09	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	479	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	C	578	ASP	CB-CG-OD1	-5.06	113.74	118.30
1	B	165	ARG	NE-CZ-NH2	-5.05	117.77	120.30
1	C	59[A]	ASP	CB-CG-OD2	-5.01	113.79	118.30
1	C	59[B]	ASP	CB-CG-OD2	-5.01	113.79	118.30
1	A	377	ARG	NE-CZ-NH2	-5.01	117.80	120.30

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 [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	5748	0	5572	55	0
1	B	5749	0	5573	72	0
1	C	5747	0	5571	76	0
1	D	5751	0	5579	52	0
2	A	44	0	31	10	0
2	B	44	0	31	10	0
2	C	44	0	31	9	0
2	D	44	0	31	4	0
3	A	44	0	37	7	0
3	B	44	0	37	10	0
3	C	44	0	37	3	0
3	D	44	0	37	7	0
4	A	835	0	0	15	0
4	B	751	0	0	19	0
4	C	765	0	0	25	0
4	D	832	0	0	25	1
All	All	26530	0	22567	277	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 6.

All (277) 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:D:449[B]:HIS:CE1	4:D:3341:HOH:O	1.73	1.31
4:B:2705:HOH:O	1:D:73:LYS:HD3	1.35	1.27
1:A:449[A]:HIS:CE1	4:A:3335:HOH:O	1.74	1.26
1:B:392:HIS:CE1	1:B:415:TYR:HB2	1.71	1.24
1:C:451:MET:SD	4:C:3338:HOH:O	1.95	1.21
1:C:392:HIS:CE1	1:C:415:TYR:HB2	1.75	1.21
1:D:449[B]:HIS:NE2	4:D:3341:HOH:O	1.62	1.19
1:C:449[B]:HIS:CE1	4:C:3336:HOH:O	1.96	1.16
1:B:392:HIS:ND1	1:B:415:TYR:HB2	0.80	1.12
1:A:369:ARG:HH21	1:A:369:ARG:HG3	1.10	1.11
1:B:583:LYS:HD2	1:B:583:LYS:H	1.05	1.11
1:D:546:GLN:HG3	4:D:2742:HOH:O	0.95	1.11
1:A:716:GLU:HG2	4:A:3090:HOH:O	1.51	1.10
1:C:392:HIS:ND1	1:C:415:TYR:HB2	0.77	1.09
1:C:578:ASP:HB3	4:C:2919:HOH:O	1.53	1.09
3:D:761[B]:HDE:HBC	4:D:3348:HOH:O	0.82	0.98
1:B:583:LYS:CD	1:B:583:LYS:H	1.73	0.98
3:B:761[B]:HDE:HBBB	3:B:761[B]:HDE:HMB	1.50	0.93
1:C:392:HIS:CG	1:C:415:TYR:HB2	2.03	0.92
3:A:761[B]:HDE:HBC	4:A:3345:HOH:O	0.72	0.89
3:B:761[B]:HDE:HBCB	3:B:761[B]:HDE:HMC	1.53	0.88
1:D:451:MET:SD	4:D:3342:HOH:O	2.30	0.88
1:A:639:GLU:HG3	4:A:2414:HOH:O	1.74	0.88
1:D:201:ASN:CG	2:D:760[A]:HDD:HMB2	1.95	0.87
1:B:521:ARG:HH21	1:B:521:ARG:HG2	1.37	0.87
1:D:201:ASN:ND2	2:D:760[A]:HDD:HMB2	1.88	0.87
1:B:521:ARG:HH21	1:B:521:ARG:CG	1.91	0.83
1:C:28:SER:HB2	4:C:3319:HOH:O	1.81	0.81
1:B:583:LYS:N	1:B:583:LYS:HD2	1.91	0.80
3:A:761[B]:HDE:HBCB	3:A:761[B]:HDE:HMC	1.63	0.79
1:C:704:PHE:O	1:C:707:THR:HG22	1.83	0.78
1:C:201:ASN:CG	2:C:760[A]:HDD:HMB2	2.02	0.78
1:B:748:ILE:O	1:B:751:ILE:HG22	1.86	0.75
2:B:760[A]:HDD:HBD2	2:B:760[A]:HDD:HMD1	1.68	0.75
1:A:29:LEU:HD23	4:C:3144:HOH:O	1.85	0.75
1:D:368:GLN:HG2	4:D:3287:HOH:O	1.87	0.75
1:C:449[B]:HIS:NE2	4:C:3336:HOH:O	2.11	0.74
1:A:369:ARG:HH21	1:A:369:ARG:CG	1.96	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:552:LEU:HD13	1:C:556:GLN:HE21	1.54	0.73
1:C:201:ASN:ND2	2:C:760[A]:HDD:HMB2	2.03	0.73
1:B:449[B]:HIS:HD2	4:B:3343:HOH:O	1.71	0.72
1:A:29:LEU:CB	4:C:2405:HOH:O	2.36	0.72
3:D:761[B]:HDE:HMB	3:D:761[B]:HDE:CBB	2.20	0.72
1:A:751:ILE:HD12	1:A:751:ILE:O	1.88	0.72
1:C:552:LEU:HD23	4:C:3225:HOH:O	1.88	0.71
1:C:137:TYR:HB2	1:C:159:ILE:CD1	2.19	0.71
1:B:392:HIS:ND1	1:B:415:TYR:HB3	2.00	0.71
1:A:201:ASN:CG	2:A:760[A]:HDD:HMB2	2.10	0.71
2:C:760[A]:HDD:HMB3	4:C:3347:HOH:O	1.91	0.71
3:B:761[B]:HDE:CBC	3:B:761[B]:HDE:HMC	2.20	0.71
1:C:725:ASP:H	1:C:728:PHE:HB3	1.55	0.70
1:C:629:HIS:HD2	4:C:1129:HOH:O	1.74	0.70
1:C:392:HIS:ND1	1:C:415:TYR:CG	2.59	0.70
1:C:552:LEU:CD1	1:C:556:GLN:HE21	2.05	0.69
2:B:760[A]:HDD:HMB3	4:B:3346:HOH:O	1.92	0.69
1:A:29:LEU:HB3	4:C:2405:HOH:O	1.90	0.69
1:B:552:LEU:HD22	1:B:556:GLN:HG3	1.73	0.69
1:C:725:ASP:HB2	1:C:728:PHE:HB2	1.74	0.69
1:B:201:ASN:ND2	2:B:760[A]:HDD:HMB2	2.08	0.69
1:A:369:ARG:NH2	1:A:369:ARG:HG3	1.90	0.69
1:C:469:TRP:CE3	1:C:471:ARG:HG3	2.29	0.68
2:B:760[A]:HDD:HMC1	2:B:760[A]:HDD:HBC1	1.73	0.68
1:C:708:ILE:HG13	1:C:710:ILE:HG12	1.74	0.68
2:B:760[A]:HDD:CBC	2:B:760[A]:HDD:HMC1	2.25	0.67
1:A:612[A]:ARG:HH21	1:A:669:OCS:CB	2.07	0.67
1:C:725:ASP:HB2	1:C:728:PHE:CB	2.24	0.67
1:C:552:LEU:HD21	1:C:571:LEU:HD12	1.78	0.66
4:A:2649:HOH:O	1:C:28:SER:HA	1.93	0.66
1:B:578:ASP:OD2	4:B:3117:HOH:O	2.12	0.66
1:A:479:ARG:NH2	4:A:2607:HOH:O	2.03	0.65
1:B:411:ARG:HG3	3:B:761[B]:HDE:HBBA	1.79	0.65
1:D:552[B]:LEU:CD2	4:D:1705:HOH:O	2.44	0.65
1:C:449[A]:HIS:HD2	4:C:3337:HOH:O	1.79	0.65
3:D:761[B]:HDE:HBBB	3:D:761[B]:HDE:HMB	1.79	0.65
2:A:760[A]:HDD:HMD1	2:A:760[A]:HDD:HBD2	1.80	0.64
1:C:552:LEU:HD11	1:C:556:GLN:NE2	2.13	0.64
1:D:341:ILE:HD12	4:D:3022:HOH:O	1.96	0.64
1:C:125:ARG:HB3	2:C:760[A]:HDD:HBD1	1.80	0.64
1:A:201:ASN:ND2	2:A:760[A]:HDD:HMB2	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:201:ASN:CG	2:B:760[A]:HDD:HMB2	2.19	0.63
1:D:629:HIS:HD2	4:D:1554:HOH:O	1.80	0.63
1:C:137:TYR:HB2	1:C:159:ILE:HD11	1.81	0.63
3:C:761[B]:HDE:HBBB	3:C:761[B]:HDE:HMB	1.81	0.63
1:A:28:SER:OG	1:A:28:SER:O	2.13	0.63
1:C:488:ARG:HD2	4:C:2379:HOH:O	1.99	0.62
1:C:552:LEU:CD1	1:C:556:GLN:NE2	2.63	0.62
1:B:696:ALA:HB1	1:B:728:PHE:CZ	2.35	0.62
3:D:761[B]:HDE:HMC	3:D:761[B]:HDE:HBCB	1.81	0.61
2:A:760[A]:HDD:HMB3	4:A:3345:HOH:O	1.99	0.61
1:A:29:LEU:HD22	4:C:2405:HOH:O	2.00	0.61
1:B:682:ASN:HB3	1:B:707:THR:HG21	1.82	0.60
1:B:28:SER:HA	4:B:2571:HOH:O	2.02	0.59
2:A:760[A]:HDD:CBB	2:A:760[A]:HDD:HMB1	2.31	0.59
1:A:612[A]:ARG:NH2	1:A:669:OCS:OD3	2.35	0.59
1:B:492:ASN:CG	4:B:2605:HOH:O	2.40	0.59
1:D:552[B]:LEU:HD22	4:D:1705:HOH:O	2.02	0.59
1:D:341:ILE:CD1	4:D:3022:HOH:O	2.51	0.59
1:B:330:ASP:OD1	1:B:629:HIS:HE1	1.86	0.58
1:D:469:TRP:CE3	1:D:471:ARG:HG3	2.38	0.58
1:D:330:ASP:OD1	1:D:629:HIS:HE1	1.85	0.58
1:C:214:PHE:CD2	2:C:760[A]:HDD:HMC2	2.38	0.58
1:B:634:TYR:O	1:B:653:THR:HA	2.04	0.58
1:D:556:GLN:NE2	4:D:2773:HOH:O	2.36	0.58
1:D:368:GLN:CG	4:D:3287:HOH:O	2.49	0.58
1:A:278:ARG:HH12	1:A:487:GLU:CD	2.08	0.58
1:B:533:LYS:CE	4:B:2623:HOH:O	2.51	0.57
1:D:449[A]:HIS:HD2	4:D:3340:HOH:O	1.87	0.57
1:A:556:GLN:NE2	4:A:2369:HOH:O	2.37	0.57
1:B:294:LYS:HB2	4:B:1097:HOH:O	2.05	0.57
3:B:761[B]:HDE:CMB	3:B:761[B]:HDE:HBBB	2.32	0.57
1:C:251:HIS:HA	1:C:508:PRO:HG3	1.87	0.57
1:D:341:ILE:CG1	4:D:3022:HOH:O	2.52	0.57
3:C:761[B]:HDE:HBCB	3:C:761[B]:HDE:HMC	1.85	0.57
1:A:29:LEU:CD2	4:C:2405:HOH:O	2.53	0.56
1:D:341:ILE:HG13	4:D:3022:HOH:O	2.03	0.56
1:C:392:HIS:CG	1:C:415:TYR:CB	2.77	0.56
1:C:443:PHE:CZ	1:C:470:PRO:HD2	2.40	0.56
1:A:36:HIS:CD2	1:A:36:HIS:H	2.24	0.56
1:B:556:GLN:HG2	1:B:566:LEU:CD2	2.36	0.55
1:D:552[B]:LEU:HD23	4:D:1705:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:760[A]:HDD:HMC1	2:A:760[A]:HDD:CBC	2.38	0.54
1:C:726:GLY:O	4:C:2714:HOH:O	2.19	0.54
1:B:556:GLN:HG2	1:B:566:LEU:HD22	1.90	0.53
1:A:469:TRP:CE3	1:A:471:ARG:HG3	2.43	0.53
1:A:478:LYS:HG2	4:A:1955:HOH:O	2.08	0.53
1:B:564:ILE:O	4:B:2603:HOH:O	2.19	0.53
1:A:345:ASP:HA	1:A:348:LYS:HD2	1.90	0.53
1:A:750:LYS:NZ	1:A:750:LYS:HB3	2.24	0.53
3:D:761[B]:HDE:HBBA	3:D:761[B]:HDE:HMB	1.90	0.53
1:C:578:ASP:HB2	1:C:582:LEU:O	2.09	0.52
3:A:761[B]:HDE:CBB	3:A:761[B]:HDE:HMB	2.39	0.52
1:C:359:LEU:H	1:C:507:HIS:CD2	2.27	0.52
1:D:448:MET:O	1:D:449[A]:HIS:HB2	2.10	0.52
1:D:449[A]:HIS:HE1	4:D:1789:HOH:O	1.93	0.52
1:D:713:GLN:O	1:D:713:GLN:HG2	2.10	0.52
1:B:125:ARG:HB3	3:B:761[B]:HDE:HBA	1.92	0.52
1:D:521:ARG:HD2	4:D:2917:HOH:O	2.08	0.52
1:C:634:TYR:O	1:C:653:THR:HA	2.10	0.52
1:D:359:LEU:H	1:D:507:HIS:HD2	1.58	0.52
1:A:37:ARG:HD2	4:A:3181:HOH:O	2.09	0.51
1:A:219:HIS:HB3	1:B:459:ASN:ND2	2.26	0.51
1:A:335:GLU:OE1	1:A:369:ARG:HG2	2.11	0.51
1:A:468:ASN:O	1:A:471:ARG:HG2	2.11	0.51
1:B:597:ASP:OD1	4:B:3327:HOH:O	2.19	0.51
1:B:521:ARG:NH2	1:B:521:ARG:CG	2.61	0.51
2:B:760[A]:HDD:CMB	4:B:3346:HOH:O	2.57	0.51
1:B:38:PRO:HG2	1:B:51:ALA:HB2	1.93	0.51
1:A:751:ILE:HD13	1:A:753:ALA:HB3	1.92	0.51
1:D:201:ASN:CG	3:D:761[B]:HDE:HAC	2.32	0.50
1:B:521:ARG:CB	1:B:521:ARG:HH21	2.24	0.50
1:D:552[A]:LEU:HD11	1:D:571:LEU:HD23	1.93	0.50
1:C:125:ARG:CB	2:C:760[A]:HDD:HBD1	2.40	0.50
3:A:761[B]:HDE:HBBB	3:A:761[B]:HDE:HMB	1.94	0.50
1:B:512:TRP:CH2	1:B:520:GLN:HB3	2.47	0.50
1:B:449[B]:HIS:HE1	4:D:1789:HOH:O	1.93	0.50
1:B:629:HIS:HD2	4:B:1062:HOH:O	1.95	0.50
1:B:73:LYS:HE3	1:D:440:TYR:CE1	2.47	0.50
2:D:760[A]:HDD:HMB1	2:D:760[A]:HDD:CBB	2.42	0.49
1:C:459:ASN:ND2	1:D:219:HIS:HB3	2.27	0.49
1:B:521:ARG:CB	1:B:521:ARG:NH2	2.75	0.49
1:C:309:LYS:NZ	4:C:1061:HOH:O	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:310:LEU:HD13	1:C:660:LEU:HB3	1.95	0.49
2:B:760[A]:HDD:HBC1	2:B:760[A]:HDD:CMC	2.43	0.49
1:A:36:HIS:HE1	4:A:1872:HOH:O	1.95	0.49
1:A:634:TYR:O	1:A:653:THR:HA	2.13	0.49
2:A:760[A]:HDD:CMB	4:A:3345:HOH:O	2.58	0.49
1:B:533:LYS:HE3	4:B:2623:HOH:O	2.12	0.48
1:C:751:ILE:HB	4:C:2367:HOH:O	2.14	0.48
1:C:330:ASP:OD1	1:C:629:HIS:HE1	1.97	0.48
1:B:583:LYS:N	1:B:583:LYS:CD	2.52	0.48
1:D:201:ASN:ND2	2:D:760[A]:HDD:CMB	2.71	0.48
1:B:128:HIS:CE1	1:B:169:VAL:HG22	2.49	0.48
1:D:578:ASP:OD1	1:D:583:LYS:HE3	2.14	0.48
1:D:490:GLU:OE1	4:D:2308:HOH:O	2.20	0.48
1:A:449[B]:HIS:HD2	4:A:3339:HOH:O	1.97	0.48
1:D:546:GLN:CG	4:D:2742:HOH:O	1.83	0.48
1:C:206:PHE:CG	2:C:760[A]:HDD:HAB	2.49	0.48
1:A:612[A]:ARG:HH21	1:A:669:OCS:HB3	1.76	0.48
1:D:472:GLU:CD	4:D:1829:HOH:O	2.51	0.48
1:C:128:HIS:CE1	1:C:169:VAL:HG22	2.49	0.47
1:A:211:ALA:CB	1:A:410:GLY:HA3	2.45	0.47
1:C:38:PRO:HG2	1:C:51:ALA:HB2	1.97	0.47
1:C:184:GLY:HA3	2:C:760[A]:HDD:HMA2	1.96	0.47
1:B:28:SER:HB2	4:D:2425:HOH:O	2.14	0.47
1:A:413:PHE:HB2	1:C:105:LEU:HD11	1.95	0.47
1:A:417:ASP:OD2	1:D:118:ASP:OD1	2.32	0.47
1:A:207:PHE:O	1:A:249:THR:HA	2.15	0.47
1:B:699:GLY:HA2	1:B:702:ARG:NH2	2.29	0.47
1:C:211:ALA:CB	1:C:410:GLY:HA3	2.45	0.47
1:B:604:ALA:HB1	1:B:633:LEU:HD22	1.96	0.47
1:C:137:TYR:CD1	1:C:159:ILE:HD13	2.50	0.46
1:C:440:TYR:HD1	4:C:1917:HOH:O	1.98	0.46
1:C:636:ARG:NH2	1:C:639:GLU:O	2.49	0.46
1:B:536:ARG:HB2	1:B:539:ILE:HD12	1.98	0.46
1:D:211:ALA:CB	1:D:410:GLY:HA3	2.46	0.46
1:C:359:LEU:H	1:C:507:HIS:HD2	1.61	0.46
1:A:125:ARG:HB3	3:A:761[B]:HDE:HBA	1.97	0.46
1:D:411:ARG:HG2	3:D:761[B]:HDE:C3B	2.46	0.46
4:A:2649:HOH:O	1:C:28:SER:CA	2.57	0.46
1:B:393:PRO:HD2	1:B:415:TYR:CG	2.51	0.45
1:B:552:LEU:HD21	1:B:571:LEU:HD12	1.98	0.45
1:B:184:GLY:HA3	2:B:760[A]:HDD:HMA2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:468:ASN:O	1:D:471:ARG:HG2	2.17	0.45
1:B:392:HIS:ND1	1:B:415:TYR:CA	2.68	0.45
1:B:607:LEU:HD11	1:B:632:LEU:HB3	1.99	0.45
2:A:760[A]:HDD:CBC	2:A:760[A]:HDD:CMC	2.94	0.45
1:C:748:ILE:O	1:C:751:ILE:HG22	2.16	0.45
1:C:51:ALA:HB1	1:C:52:PRO:HD2	1.98	0.45
1:C:207:PHE:O	1:C:249:THR:HA	2.15	0.45
1:B:211:ALA:CB	1:B:410:GLY:HA3	2.47	0.45
1:C:219:HIS:HB3	1:D:459:ASN:ND2	2.32	0.45
1:C:748:ILE:O	1:C:751:ILE:CG2	2.65	0.45
1:B:359:LEU:H	1:B:507:HIS:HD2	1.64	0.45
1:A:411:ARG:HG2	3:A:761[B]:HDE:C3B	2.47	0.45
1:B:165:ARG:HD3	3:B:761[B]:HDE:O2D	2.17	0.44
1:B:596:GLY:HA3	1:B:737:ALA:O	2.17	0.44
1:D:696:ALA:HB1	1:D:728:PHE:CZ	2.52	0.44
1:C:309:LYS:HE3	4:C:1232:HOH:O	2.16	0.44
1:B:37:ARG:HD3	4:B:2886:HOH:O	2.17	0.44
1:A:459:ASN:ND2	1:B:219:HIS:HB3	2.33	0.44
1:C:583:LYS:O	1:C:584:LYS:HB3	2.17	0.44
1:A:341:ILE:HD12	1:A:353:LEU:HD21	1.99	0.44
1:B:615:ASP:O	1:B:619:ILE:HG13	2.17	0.44
1:C:725:ASP:HB2	1:C:728:PHE:HB3	2.00	0.44
1:A:91:ASP:OD1	1:C:461:GLU:OE1	2.35	0.44
1:B:157:ASN:HB2	4:B:3138:HOH:O	2.16	0.44
1:C:199:VAL:HG12	3:C:761[B]:HDE:HHDA	1.99	0.43
1:B:459:ASN:H	1:B:459:ASN:HD22	1.65	0.43
4:A:1016:HOH:O	1:C:104:LEU:HB3	2.17	0.43
1:C:625:ALA:HA	4:C:3234:HOH:O	2.18	0.43
1:A:211:ALA:HA	3:A:761[B]:HDE:HBB	2.00	0.43
1:C:727:SER:HA	4:C:2714:HOH:O	2.17	0.43
1:A:549:HIS:O	1:A:576:PRO:HD3	2.18	0.43
1:B:199:VAL:HG12	3:B:761[B]:HDE:HHDA	2.01	0.43
1:B:507:HIS:HE1	4:B:901:HOH:O	2.01	0.43
1:A:429:HIS:CG	1:C:83:ASN:HB3	2.54	0.43
1:A:76:GLU:O	1:A:77:ASN:HB2	2.18	0.43
4:B:991:HOH:O	1:D:52:PRO:HG3	2.19	0.43
2:C:760[A]:HDD:CMB	4:C:3347:HOH:O	2.60	0.43
1:B:461:GLU:HA	1:B:462:PRO:C	2.39	0.43
1:B:214:PHE:HB3	1:B:215:PRO:HD3	2.01	0.42
1:D:338:PHE:HB3	1:D:340:LEU:HD13	2.00	0.42
1:D:583:LYS:O	1:D:584:LYS:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:LYS:HE2	1:A:188:LYS:HB2	1.84	0.42
1:A:369:ARG:NH2	1:A:369:ARG:CG	2.65	0.42
1:D:509:ARG:HD2	1:D:576:PRO:HD2	2.02	0.42
1:D:593:ILE:HA	1:D:594:PRO:HD2	1.78	0.42
1:A:461:GLU:HA	1:A:462:PRO:C	2.39	0.42
1:B:492:ASN:CB	4:B:2605:HOH:O	2.68	0.42
1:A:443:PHE:CZ	1:A:470:PRO:HD2	2.55	0.42
1:B:214:PHE:CD2	3:B:761[B]:HDE:HAB	2.55	0.42
3:B:761[B]:HDE:CMC	3:B:761[B]:HDE:CBC	2.91	0.42
1:B:251:HIS:HA	1:B:508:PRO:HG3	2.00	0.42
1:B:76:GLU:O	1:B:77:ASN:HB2	2.20	0.42
1:A:319:ARG:HD3	1:D:227:TRP:O	2.19	0.41
1:D:117:PHE:HA	1:D:120:GLU:HG3	2.03	0.41
1:B:616:LEU:CD1	1:B:648:LEU:HD22	2.50	0.41
1:B:699:GLY:HA2	1:B:702:ARG:HH21	1.85	0.41
1:D:634:TYR:O	1:D:653:THR:HA	2.20	0.41
1:C:155:ASP:HB3	1:C:158:LYS:HB2	2.03	0.41
1:A:612[A]:ARG:HE	1:A:669:OCS:HB2	1.85	0.41
2:A:760[A]:HDD:HBC1	2:A:760[A]:HDD:CMC	2.51	0.41
1:B:418:THR:HG21	2:B:760[A]:HDD:CGD	2.51	0.41
1:C:309:LYS:CE	4:C:1232:HOH:O	2.68	0.40
1:B:393:PRO:HD2	1:B:415:TYR:CD2	2.56	0.40
1:C:377:ARG:HH11	1:C:377:ARG:HD3	1.77	0.40
1:D:443:PHE:CZ	1:D:470:PRO:HD2	2.57	0.40
1:C:586:PRO:HG2	4:C:2930:HOH:O	2.20	0.40
1:C:97:ALA:O	1:C:101:GLY:HA3	2.22	0.40
1:A:184:GLY:HA3	2:A:760[A]:HDD:HMA2	2.03	0.40
1:D:359:LEU:H	1:D:507:HIS:CD2	2.37	0.40
1:A:252:ASN:HD22	1:A:252:ASN:HA	1.75	0.40
1:D:100:ARG:HG3	4:D:1533:HOH:O	2.21	0.40
1:C:748:ILE:HA	1:C:751:ILE:HG22	2.02	0.40
1:B:97:ALA:O	1:B:101:GLY:HA3	2.21	0.40
1:B:533:LYS:CD	4:B:2623:HOH:O	2.69	0.40
1:C:114:ILE:HD12	1:C:114:ILE:HG23	1.76	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:2178:HOH:O	4:D:2976:HOH:O[1_655]	2.09	0.11

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	726/753 (96%)	705 (97%)	20 (3%)	1 (0%)	56	46
1	B	725/753 (96%)	700 (97%)	23 (3%)	2 (0%)	46	35
1	C	726/753 (96%)	704 (97%)	20 (3%)	2 (0%)	46	35
1	D	725/753 (96%)	704 (97%)	20 (3%)	1 (0%)	56	46
All	All	2902/3012 (96%)	2813 (97%)	83 (3%)	6 (0%)	52	42

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	725	ASP
1	C	726	GLY
1	B	75	SER
1	D	75	SER
1	A	75	SER
1	C	75	SER

### 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	612/634 (96%)	592 (97%)	20 (3%)	45	34
1	B	611/634 (96%)	584 (96%)	27 (4%)	35	22
1	C	612/634 (96%)	576 (94%)	36 (6%)	24	12
1	D	611/634 (96%)	583 (95%)	28 (5%)	33	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2446/2536 (96%)	2335 (96%)	111 (4%)	34 21

All (111) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	LEU
1	A	32	GLU
1	A	185	PHE
1	A	191	THR
1	A	205	ILE
1	A	227	TRP
1	A	237	ASP
1	A	252	ASN
1	A	283	GLU
1	A	369	ARG
1	A	375	LEU
1	A	377	ARG
1	A	432	PRO
1	A	440	TYR
1	A	459	ASN
1	A	552	LEU
1	A	584	LYS
1	A	621	LYS
1	A	713	GLN
1	A	750	LYS
1	B	32	GLU
1	B	155	ASP
1	B	185	PHE
1	B	191	THR
1	B	198	LEU
1	B	205	ILE
1	B	227	TRP
1	B	237	ASP
1	B	252	ASN
1	B	369	ARG
1	B	370	VAL
1	B	375	LEU
1	B	432	PRO
1	B	440	TYR
1	B	459	ASN
1	B	508	PRO
1	B	521	ARG

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Mol	Chain	Res	Type
1	B	552	LEU
1	B	562	LEU
1	B	566	LEU
1	B	568	ASP
1	B	571	LEU
1	B	583	LYS
1	B	616	LEU
1	B	633	LEU
1	B	713	GLN
1	B	727	SER
1	C	61	ARG
1	C	159	ILE
1	C	185	PHE
1	C	205	ILE
1	C	227	TRP
1	C	237	ASP
1	C	252	ASN
1	C	283	GLU
1	C	285	LYS
1	C	375	LEU
1	C	377	ARG
1	C	440	TYR
1	C	449[A]	HIS
1	C	449[B]	HIS
1	C	459	ASN
1	C	478	LYS
1	C	488	ARG
1	C	508	PRO
1	C	521	ARG
1	C	531	LEU
1	C	568	ASP
1	C	571	LEU
1	C	584	LYS
1	C	606	LEU
1	C	610	GLU
1	C	616	LEU
1	C	617	LEU
1	C	633	LEU
1	C	635	SER
1	C	648	LEU
1	C	660	LEU
1	C	685	LEU

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Mol	Chain	Res	Type
1	C	709	LYS
1	C	725	ASP
1	C	733	LEU
1	C	750	LYS
1	D	28	SER
1	D	48	GLN
1	D	73	LYS
1	D	185	PHE
1	D	191	THR
1	D	198	LEU
1	D	205	ILE
1	D	227	TRP
1	D	237	ASP
1	D	252	ASN
1	D	340	LEU
1	D	375	LEU
1	D	432	PRO
1	D	440	TYR
1	D	459	ASN
1	D	552[A]	LEU
1	D	552[B]	LEU
1	D	554	LEU
1	D	574	THR
1	D	582	LEU
1	D	583	LYS
1	D	616	LEU
1	D	633	LEU
1	D	648	LEU
1	D	713	GLN
1	D	747	LYS
1	D	750	LYS
1	D	751	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	368	GLN
1	A	459	ASN
1	A	515	GLN
1	A	556	GLN

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Mol	Chain	Res	Type
1	B	252	ASN
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
1	C	671	ASN
1	C	713	GLN
1	D	48	GLN
1	D	157	ASN
1	D	252	ASN
1	D	459	ASN
1	D	507	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 ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
1	OCS	A	669	1	7,8,9	1.27	1 (14%)	7,11,13	1.17	1 (14%)
1	OCS	B	669	1	7,8,9	1.16	1 (14%)	7,11,13	2.10	1 (14%)
1	OCS	C	669	1	7,8,9	1.03	0	7,11,13	2.23	2 (28%)
1	OCS	D	669	1	7,8,9	1.36	1 (14%)	7,11,13	1.63	2 (28%)



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
1	OCS	A	669	1	-	1/4/7/9	0/0/0/0
1	OCS	B	669	1	-	1/4/7/9	0/0/0/0
1	OCS	C	669	1	-	1/4/7/9	0/0/0/0
1	OCS	D	669	1	-	1/4/7/9	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	669	OCS	CB-SG	2.48	1.81	1.77
1	B	669	OCS	CB-SG	2.65	1.81	1.77
1	D	669	OCS	CB-SG	2.71	1.82	1.77

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	669	OCS	OD1-SG-CB	-3.56	103.94	106.94
1	D	669	OCS	OD1-SG-CB	-2.78	104.60	106.94
1	D	669	OCS	OD3-SG-CB	-2.68	104.68	106.94
1	A	669	OCS	OD3-SG-CB	-2.13	105.14	106.94
1	C	669	OCS	OD3-SG-CB	4.17	110.46	106.94
1	B	669	OCS	OD1-SG-CB	4.85	111.03	106.94

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	669	OCS	SG-CB-CA-N
1	A	669	OCS	SG-CB-CA-N
1	B	669	OCS	SG-CB-CA-N
1	D	669	OCS	SG-CB-CA-N

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	669	OCS	4	0

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	HDD	A	760[A]	1,4	30,52,52	2.41	10 (33%)	20,89,89	2.88	9 (45%)
3	HDE	A	761[B]	1,4	34,52,52	2.85	13 (38%)	27,89,89	2.90	12 (44%)
2	HDD	B	760[A]	4	30,52,52	2.25	8 (26%)	20,89,89	3.30	8 (40%)
3	HDE	B	761[B]	1,4	34,52,52	2.56	12 (35%)	27,89,89	3.03	11 (40%)
2	HDD	C	760[A]	1	30,52,52	2.26	6 (20%)	20,89,89	3.11	11 (55%)
3	HDE	C	761[B]	1,4	34,52,52	2.64	12 (35%)	27,89,89	2.76	14 (51%)
2	HDD	D	760[A]	1	30,52,52	2.51	9 (30%)	20,89,89	2.87	11 (55%)
3	HDE	D	761[B]	1,4	34,52,52	2.51	13 (38%)	27,89,89	3.13	16 (59%)

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]	1,4	-	0/3/89/89	0/1/9/9
3	HDE	A	761[B]	1,4	-	1/7/89/89	0/1/9/9
2	HDD	B	760[A]	4	-	0/3/89/89	0/1/9/9
3	HDE	B	761[B]	1,4	-	0/7/89/89	0/1/9/9
2	HDD	C	760[A]	1	-	0/3/89/89	0/1/9/9
3	HDE	C	761[B]	1,4	-	0/7/89/89	0/1/9/9
2	HDD	D	760[A]	1	-	0/3/89/89	0/1/9/9
3	HDE	D	761[B]	1,4	-	1/7/89/89	0/1/9/9

All (83) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	760[A]	HDD	C3C-C2C	-5.75	1.32	1.40
2	A	760[A]	HDD	O1D-C3D	-5.68	1.37	1.46
2	A	760[A]	HDD	C3B-C2B	-5.67	1.32	1.40
2	D	760[A]	HDD	C3C-C2C	-5.58	1.33	1.40
2	C	760[A]	HDD	C3B-C2B	-5.41	1.33	1.40
2	B	760[A]	HDD	C3C-C2C	-5.38	1.33	1.40
2	D	760[A]	HDD	C3B-C2B	-5.12	1.33	1.40
2	B	760[A]	HDD	C3B-C2B	-4.97	1.33	1.40
2	C	760[A]	HDD	C3C-C2C	-4.86	1.33	1.40
2	D	760[A]	HDD	O1D-C3D	-4.59	1.38	1.46
2	C	760[A]	HDD	O1D-C3D	-4.47	1.39	1.46
2	B	760[A]	HDD	O1D-C3D	-3.65	1.40	1.46
2	B	760[A]	HDD	C4D-ND	2.10	1.41	1.38
2	D	760[A]	HDD	CMC-C2C	2.13	1.56	1.51
2	A	760[A]	HDD	C1B-NB	2.14	1.39	1.36
2	D	760[A]	HDD	CMD-C2D	2.16	1.56	1.53
2	A	760[A]	HDD	CMC-C2C	2.18	1.56	1.51
2	D	760[A]	HDD	OND-C2D	2.18	1.47	1.42
2	A	760[A]	HDD	CMB-C2B	2.21	1.56	1.51
3	D	761[B]	HDE	CMA-C3A	2.23	1.56	1.53
2	A	760[A]	HDD	CAA-C2A	2.28	1.55	1.52
3	D	761[B]	HDE	C4B-NB	2.33	1.37	1.34
3	C	761[B]	HDE	C1B-CHB	2.35	1.46	1.39
3	C	761[B]	HDE	C1C-C2C	2.40	1.41	1.37
3	D	761[B]	HDE	C4D-CHA	2.41	1.46	1.39
3	B	761[B]	HDE	C1B-CHB	2.46	1.46	1.39
3	D	761[B]	HDE	C1B-CHB	2.48	1.46	1.39
2	B	760[A]	HDD	CMD-C2D	2.51	1.56	1.53
3	B	761[B]	HDE	C4A-NA	2.58	1.42	1.38
3	A	761[B]	HDE	C1A-NA	2.60	1.42	1.38
3	B	761[B]	HDE	C3D-C2D	2.65	1.45	1.37
2	A	760[A]	HDD	C3C-CAC	2.71	1.53	1.47
3	A	761[B]	HDE	C1B-CHB	2.73	1.47	1.39
3	A	761[B]	HDE	C4D-CHA	2.89	1.47	1.39
2	A	760[A]	HDD	C3B-CAB	2.90	1.53	1.47
3	C	761[B]	HDE	C4D-CHA	3.01	1.48	1.39
2	C	760[A]	HDD	C3C-CAC	3.06	1.54	1.47
3	A	761[B]	HDE	C3C-C2C	3.12	1.46	1.37
3	D	761[B]	HDE	C3B-C2B	3.18	1.47	1.37
3	C	761[B]	HDE	C4A-NA	3.19	1.42	1.38
2	C	760[A]	HDD	C3B-CAB	3.21	1.54	1.47
3	B	761[B]	HDE	C4D-CHA	3.21	1.48	1.39
3	D	761[B]	HDE	C1A-NA	3.27	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	761[B]	HDE	C3D-C2D	3.30	1.47	1.37
3	D	761[B]	HDE	C4A-NA	3.34	1.43	1.38
3	B	761[B]	HDE	C3C-C2C	3.35	1.47	1.37
2	B	760[A]	HDD	C3C-CAC	3.36	1.54	1.47
3	A	761[B]	HDE	C3D-C2D	3.41	1.47	1.37
3	B	761[B]	HDE	C3B-C2B	3.41	1.47	1.37
3	A	761[B]	HDE	C4B-NB	3.41	1.39	1.34
3	B	761[B]	HDE	C1C-C2C	3.44	1.42	1.37
3	A	761[B]	HDE	C4A-NA	3.50	1.43	1.38
3	D	761[B]	HDE	C3C-C2C	3.51	1.48	1.37
2	B	760[A]	HDD	C3B-CAB	3.54	1.55	1.47
3	C	761[B]	HDE	C3C-C2C	3.55	1.48	1.37
3	A	761[B]	HDE	C3B-C2B	3.58	1.48	1.37
3	A	761[B]	HDE	O1A-CGA	3.67	1.41	1.35
3	D	761[B]	HDE	C3D-C2D	3.73	1.48	1.37
2	D	760[A]	HDD	C3B-CAB	3.77	1.55	1.47
2	D	760[A]	HDD	C3C-CAC	3.78	1.55	1.47
3	B	761[B]	HDE	C4B-NB	3.90	1.39	1.34
3	C	761[B]	HDE	C3B-C2B	3.90	1.49	1.37
3	C	761[B]	HDE	O1A-CGA	4.00	1.42	1.35
3	D	761[B]	HDE	O1A-CGA	4.00	1.42	1.35
3	C	761[B]	HDE	C4C-NC	4.05	1.39	1.34
3	B	761[B]	HDE	O1A-CGA	4.07	1.42	1.35
3	C	761[B]	HDE	C4B-NB	4.17	1.39	1.34
3	A	761[B]	HDE	C1C-C2C	4.22	1.43	1.37
3	B	761[B]	HDE	C1A-NA	4.53	1.44	1.38
3	D	761[B]	HDE	C4C-NC	5.07	1.41	1.34
2	A	760[A]	HDD	FE-ND	5.31	2.16	1.95
2	B	760[A]	HDD	FE-ND	5.48	2.17	1.95
3	D	761[B]	HDE	C1C-NC	5.92	1.42	1.34
3	A	761[B]	HDE	C4C-NC	6.04	1.42	1.34
3	B	761[B]	HDE	C1C-NC	6.15	1.42	1.34
2	C	760[A]	HDD	FE-ND	6.38	2.20	1.95
3	D	761[B]	HDE	C4C-C3C	6.61	1.46	1.37
3	A	761[B]	HDE	C1C-NC	6.85	1.43	1.34
3	C	761[B]	HDE	C1C-NC	6.92	1.43	1.34
2	D	760[A]	HDD	FE-ND	6.98	2.23	1.95
3	B	761[B]	HDE	C4C-C3C	7.20	1.47	1.37
3	C	761[B]	HDE	C4C-C3C	7.51	1.47	1.37
3	A	761[B]	HDE	C4C-C3C	8.35	1.48	1.37

All (92) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	761[B]	HDE	C4A-NA-C1A	-7.85	102.30	107.36
3	B	761[B]	HDE	C1C-C2C-C3C	-7.02	99.23	105.67
3	C	761[B]	HDE	CAD-CBD-CGD	-5.44	102.77	112.75
2	B	760[A]	HDD	CAA-CBA-CGA	-5.43	102.79	112.75
2	A	760[A]	HDD	C3C-CAC-CBC	-5.42	115.22	126.32
3	D	761[B]	HDE	CAD-CBD-CGD	-5.38	102.88	112.75
3	A	761[B]	HDE	C4A-NA-C1A	-5.19	104.01	107.36
3	C	761[B]	HDE	C1C-C2C-C3C	-5.16	100.94	105.67
3	B	761[B]	HDE	CAD-CBD-CGD	-5.02	103.55	112.75
3	D	761[B]	HDE	CAC-C3C-C4C	-4.77	121.10	127.12
3	B	761[B]	HDE	CAC-C3C-C4C	-4.73	121.14	127.12
3	A	761[B]	HDE	CAD-CBD-CGD	-4.61	104.30	112.75
3	B	761[B]	HDE	C4A-NA-C1A	-4.49	104.46	107.36
3	A	761[B]	HDE	CAB-C3B-C4B	-4.35	121.62	127.12
3	D	761[B]	HDE	ONA-C3A-CMA	-4.34	101.58	109.41
3	C	761[B]	HDE	CAC-C3C-C4C	-4.30	121.69	127.12
2	D	760[A]	HDD	CAA-CBA-CGA	-4.20	105.05	112.75
3	C	761[B]	HDE	C4A-NA-C1A	-4.19	104.66	107.36
2	C	760[A]	HDD	C3B-CAB-CBB	-4.05	118.03	126.32
2	A	760[A]	HDD	O1D-CGD-CBD	-4.04	105.47	110.20
2	C	760[A]	HDD	C3C-CAC-CBC	-3.98	118.17	126.32
2	B	760[A]	HDD	C3B-CAB-CBB	-3.95	118.24	126.32
3	A	761[B]	HDE	C1C-C2C-C3C	-3.79	102.19	105.67
2	D	760[A]	HDD	O1D-CGD-CBD	-3.72	105.84	110.20
2	A	760[A]	HDD	C3B-CAB-CBB	-3.67	118.81	126.32
3	C	761[B]	HDE	CAB-C3B-C4B	-3.66	122.50	127.12
3	D	761[B]	HDE	CAB-C3B-C4B	-3.41	122.81	127.12
2	C	760[A]	HDD	O1D-CGD-CBD	-3.40	106.22	110.20
3	B	761[B]	HDE	C1D-C2D-C3D	-3.38	102.57	105.67
2	B	760[A]	HDD	O1D-CGD-CBD	-3.29	106.34	110.20
2	B	760[A]	HDD	C3C-CAC-CBC	-3.06	120.06	126.32
3	D	761[B]	HDE	C1C-C2C-C3C	-3.02	102.89	105.67
2	A	760[A]	HDD	CAD-CBD-CGD	-2.94	99.55	104.64
3	A	761[B]	HDE	CAC-C3C-C4C	-2.92	123.43	127.12
2	D	760[A]	HDD	C3C-C4C-NC	-2.83	105.55	109.21
2	D	760[A]	HDD	C3B-CAB-CBB	-2.79	120.61	126.32
2	A	760[A]	HDD	CAA-CBA-CGA	-2.73	107.75	112.75
2	C	760[A]	HDD	CBA-CAA-C2A	-2.71	107.67	112.53
2	B	760[A]	HDD	CAD-CBD-CGD	-2.56	100.22	104.64
2	C	760[A]	HDD	CAA-CBA-CGA	-2.52	108.12	112.75
2	D	760[A]	HDD	C3C-CAC-CBC	-2.47	121.26	126.32
3	A	761[B]	HDE	C3A-C4A-CHB	-2.46	119.65	123.48
3	C	761[B]	HDE	C3A-C4A-CHB	-2.44	119.69	123.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	760[A]	HDD	C3C-C4C-NC	-2.32	106.21	109.21
2	D	760[A]	HDD	CMC-C2C-C1C	-2.32	124.53	128.36
2	C	760[A]	HDD	CMA-C3A-C4A	-2.32	124.53	128.36
2	C	760[A]	HDD	CMC-C2C-C1C	-2.24	124.65	128.36
2	D	760[A]	HDD	CMA-C3A-C4A	-2.24	124.66	128.36
3	D	761[B]	HDE	O1A-CGA-CBA	-2.21	107.61	110.20
2	C	760[A]	HDD	OND-C2D-CMD	-2.17	105.49	109.41
2	D	760[A]	HDD	C3B-C4B-NB	-2.14	106.91	110.94
3	D	761[B]	HDE	C1D-C2D-C3D	-2.12	103.72	105.67
2	A	760[A]	HDD	C3B-C4B-NB	-2.05	107.08	110.94
3	C	761[B]	HDE	ONA-C3A-CMA	-2.03	105.74	109.41
3	C	761[B]	HDE	CMD-C2D-C3D	2.15	129.74	125.24
3	C	761[B]	HDE	CAC-C3C-C2C	2.18	129.45	124.01
2	B	760[A]	HDD	C2D-C1D-CHD	2.20	126.90	123.48
3	A	761[B]	HDE	CMB-C2B-C3B	2.21	129.86	125.24
3	C	761[B]	HDE	CAD-C3D-C4D	2.23	129.43	127.01
3	B	761[B]	HDE	CMC-C2C-C3C	2.37	130.19	125.24
3	D	761[B]	HDE	CMD-C2D-C3D	2.41	130.28	125.24
3	D	761[B]	HDE	CAB-C3B-C2B	2.44	130.12	124.01
3	D	761[B]	HDE	O1A-CGA-O2A	2.49	123.17	120.80
3	B	761[B]	HDE	CAD-C3D-C4D	2.70	129.94	127.01
3	D	761[B]	HDE	CMC-C2C-C3C	2.83	131.15	125.24
2	C	760[A]	HDD	C2D-C1D-CHD	2.88	127.97	123.48
3	C	761[B]	HDE	CMC-C2C-C3C	3.01	131.52	125.24
3	D	761[B]	HDE	CAD-C3D-C4D	3.02	130.29	127.01
3	B	761[B]	HDE	O1A-CGA-O2A	3.10	123.74	120.80
3	D	761[B]	HDE	CAC-C3C-C2C	3.12	131.82	124.01
3	B	761[B]	HDE	CMC-C2C-C1C	3.33	130.50	127.14
2	D	760[A]	HDD	C2D-C1D-CHD	3.39	128.76	123.48
2	A	760[A]	HDD	O1D-CGD-O2D	3.41	124.04	120.80
3	A	761[B]	HDE	CAB-C3B-C2B	3.47	132.67	124.01
3	C	761[B]	HDE	CAB-C3B-C2B	3.69	133.23	124.01
3	C	761[B]	HDE	C4B-CHC-C1C	4.11	120.93	112.50
3	A	761[B]	HDE	CMC-C2C-C1C	4.42	131.60	127.14
3	D	761[B]	HDE	C4B-CHC-C1C	4.78	122.31	112.50
3	A	761[B]	HDE	C4C-CHD-C1D	4.80	122.36	112.50
3	A	761[B]	HDE	O1A-CGA-O2A	5.00	125.56	120.80
3	C	761[B]	HDE	C4C-CHD-C1D	5.11	122.99	112.50
3	A	761[B]	HDE	C4B-CHC-C1C	5.20	123.18	112.50
2	D	760[A]	HDD	O1D-CGD-O2D	5.27	125.81	120.80
3	D	761[B]	HDE	C4C-CHD-C1D	5.27	123.33	112.50
3	B	761[B]	HDE	C4B-CHC-C1C	5.29	123.35	112.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	761[B]	HDE	C4C-CHD-C1D	6.15	125.13	112.50
2	C	760[A]	HDD	O1D-CGD-O2D	6.32	126.81	120.80
2	B	760[A]	HDD	C4D-ND-C1D	6.76	111.72	107.36
2	D	760[A]	HDD	C4D-ND-C1D	6.88	111.80	107.36
2	A	760[A]	HDD	C4D-ND-C1D	7.44	112.16	107.36
2	C	760[A]	HDD	C4D-ND-C1D	7.69	112.32	107.36
2	B	760[A]	HDD	O1D-CGD-O2D	8.66	129.04	120.80

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	761[B]	HDE	C2B-C3B-CAB-CBB
3	D	761[B]	HDE	C2B-C3B-CAB-CBB

There are no ring outliers.

8 monomers are involved in 60 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	760[A]	HDD	10	0
3	A	761[B]	HDE	7	0
2	B	760[A]	HDD	10	0
3	B	761[B]	HDE	10	0
2	C	760[A]	HDD	9	0
3	C	761[B]	HDE	3	0
2	D	760[A]	HDD	4	0
3	D	761[B]	HDE	7	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	725/753 (96%)	-0.75	3 (0%) 93 93	3, 10, 29, 50	0
1	B	725/753 (96%)	-0.65	10 (1%) 78 80	3, 12, 34, 52	0
1	C	725/753 (96%)	-0.65	9 (1%) 81 83	4, 12, 34, 53	0
1	D	725/753 (96%)	-0.72	5 (0%) 89 90	3, 11, 30, 50	0
All	All	2900/3012 (96%)	-0.69	27 (0%) 85 87	3, 12, 32, 53	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	28	SER	3.7
1	B	28	SER	3.5
1	C	750	LYS	3.2
1	C	28	SER	3.1
1	B	32	GLU	3.0
1	B	726	GLY	3.0
1	B	568	ASP	2.9
1	D	28	SER	2.9
1	A	32	GLU	2.9
1	B	583	LYS	2.6
1	B	713	GLN	2.6
1	B	712	ASP	2.5
1	C	726	GLY	2.5
1	C	725	ASP	2.5
1	C	711	ALA	2.4
1	D	750	LYS	2.3
1	A	750	LYS	2.3
1	D	749	ASP	2.3
1	D	712	ASP	2.2
1	B	750	LYS	2.2
1	D	713	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	594	PRO	2.2
1	C	712	ASP	2.1
1	B	596	GLY	2.0
1	C	583	LYS	2.0
1	C	641	THR	2.0
1	B	647	VAL	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	OCS	D	669	9/10	0.98	0.08	-	25,26,30,31	0
1	OCS	C	669	9/10	0.97	0.09	-	29,29,33,35	0
1	OCS	B	669	9/10	0.96	0.11	-	29,30,35,36	0
1	OCS	A	669	9/10	0.97	0.07	-	20,22,26,28	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	HDD	B	760[A]	44/44	0.99	0.07	0.67	2,3,4,6	44
2	HDD	C	760[A]	44/44	0.99	0.07	0.60	2,3,5,6	44
2	HDD	D	760[A]	44/44	0.99	0.06	0.43	2,2,5,9	44
3	HDE	B	761[B]	44/44	0.99	0.07	0.40	4,9,13,15	44
2	HDD	A	760[A]	44/44	0.99	0.06	0.18	2,3,6,10	44

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	HDE	C	761[B]	44/44	0.99	0.07	0.10	2,9,12,14	44
3	HDE	D	761[B]	44/44	0.99	0.06	0.08	2,9,12,14	44
3	HDE	A	761[B]	44/44	0.99	0.06	-0.10	2,7,9,12	44

## 6.5 Other polymers

There are no such residues in this entry.