



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:50 AM GMT

PDB ID : 2BFG
Title : crystal structure of beta-xylosidase (fam GH39) in complex with dinitrophenyl-beta-xyloside and covalently bound xyloside
Authors : Czjzek, M.; Bravman, T.; Henrissat, B.; Shoham, Y.
Deposited on : 2004-12-07
Resolution : 2.40 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

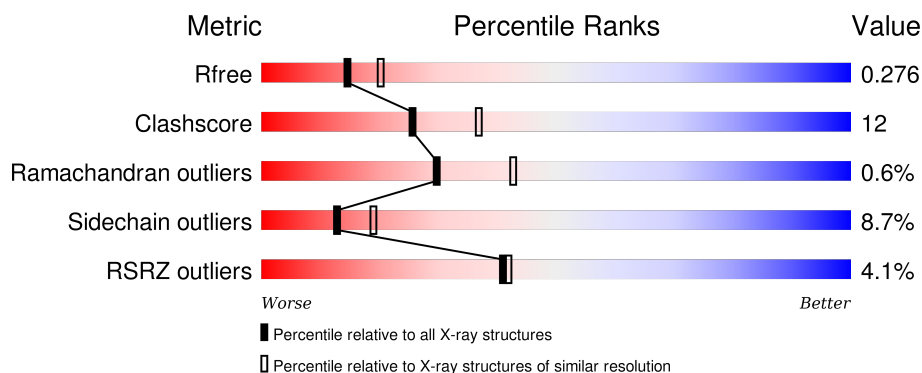
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	503	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>25%</div> <div>.</div> </div> </div>
1	B	503	<div> <div>6%</div> <div> <div></div> <div>68%</div> <div>27%</div> <div>.</div> </div> </div>
1	C	503	<div> <div>5%</div> <div> <div></div> <div>68%</div> <div>28%</div> <div>.</div> </div> </div>
1	D	503	<div> <div>4%</div> <div> <div></div> <div>70%</div> <div>26%</div> <div>.</div> </div> </div>
1	E	503	<div> <div>2%</div> <div> <div></div> <div>71%</div> <div>26%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	503	
1	G	503	
1	H	503	

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
2	NA	A	1503	-	-	-	X
2	NA	E	1503	-	-	-	X
2	NA	F	1503	-	-	-	X
3	ANX	A	1504	-	-	-	X
3	ANX	D	1504	-	-	-	X
4	XYP	D	1505	X	-	-	-
6	XYS	C	1504	-	-	-	X
6	XYS	E	1504	-	-	-	X
6	XYS	F	1504	-	-	-	X
6	XYS	G	1504	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 34237 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 BETA-XYLOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	501	Total	C	N	O	S	0	0	0
			4087	2641	693	742	11			
1	B	501	Total	C	N	O	S	0	0	0
			4087	2641	693	742	11			
1	C	501	Total	C	N	O	S	0	0	0
			4084	2640	693	740	11			
1	D	501	Total	C	N	O	S	0	0	0
			4087	2641	693	742	11			
1	E	501	Total	C	N	O	S	0	0	0
			4087	2641	693	742	11			
1	F	501	Total	C	N	O	S	0	0	0
			4087	2641	693	742	11			
1	G	501	Total	C	N	O	S	0	0	0
			4087	2641	693	742	11			
1	H	501	Total	C	N	O	S	0	0	0
			4087	2641	693	742	11			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	.	-	LEU	DELETION	UNP Q9ZFM2
A	.	-	GLU	DELETION	UNP Q9ZFM2
A	406	GLU	PHE	CONFLICT	UNP Q9ZFM2
A	445	ARG	PRO	CONFLICT	UNP Q9ZFM2
A	446	GLN	-	INSERTION	UNP Q9ZFM2
A	447	VAL	SER	CONFLICT	UNP Q9ZFM2
B	.	-	LEU	DELETION	UNP Q9ZFM2
B	.	-	GLU	DELETION	UNP Q9ZFM2
B	406	GLU	PHE	CONFLICT	UNP Q9ZFM2
B	445	ARG	PRO	CONFLICT	UNP Q9ZFM2
B	446	GLN	-	INSERTION	UNP Q9ZFM2
B	447	VAL	SER	CONFLICT	UNP Q9ZFM2
C	.	-	LEU	DELETION	UNP Q9ZFM2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	.	-	GLU	DELETION	UNP Q9ZFM2
C	406	GLU	PHE	CONFLICT	UNP Q9ZFM2
C	445	ARG	PRO	CONFLICT	UNP Q9ZFM2
C	446	GLN	-	INSERTION	UNP Q9ZFM2
C	447	VAL	SER	CONFLICT	UNP Q9ZFM2
D	.	-	LEU	DELETION	UNP Q9ZFM2
D	.	-	GLU	DELETION	UNP Q9ZFM2
D	406	GLU	PHE	CONFLICT	UNP Q9ZFM2
D	445	ARG	PRO	CONFLICT	UNP Q9ZFM2
D	446	GLN	-	INSERTION	UNP Q9ZFM2
D	447	VAL	SER	CONFLICT	UNP Q9ZFM2
E	.	-	LEU	DELETION	UNP Q9ZFM2
E	.	-	GLU	DELETION	UNP Q9ZFM2
E	406	GLU	PHE	CONFLICT	UNP Q9ZFM2
E	445	ARG	PRO	CONFLICT	UNP Q9ZFM2
E	446	GLN	-	INSERTION	UNP Q9ZFM2
E	447	VAL	SER	CONFLICT	UNP Q9ZFM2
F	.	-	LEU	DELETION	UNP Q9ZFM2
F	.	-	GLU	DELETION	UNP Q9ZFM2
F	406	GLU	PHE	CONFLICT	UNP Q9ZFM2
F	445	ARG	PRO	CONFLICT	UNP Q9ZFM2
F	446	GLN	-	INSERTION	UNP Q9ZFM2
F	447	VAL	SER	CONFLICT	UNP Q9ZFM2
G	.	-	LEU	DELETION	UNP Q9ZFM2
G	.	-	GLU	DELETION	UNP Q9ZFM2
G	406	GLU	PHE	CONFLICT	UNP Q9ZFM2
G	445	ARG	PRO	CONFLICT	UNP Q9ZFM2
G	446	GLN	-	INSERTION	UNP Q9ZFM2
G	447	VAL	SER	CONFLICT	UNP Q9ZFM2
H	.	-	LEU	DELETION	UNP Q9ZFM2
H	.	-	GLU	DELETION	UNP Q9ZFM2
H	406	GLU	PHE	CONFLICT	UNP Q9ZFM2
H	445	ARG	PRO	CONFLICT	UNP Q9ZFM2
H	446	GLN	-	INSERTION	UNP Q9ZFM2
H	447	VAL	SER	CONFLICT	UNP Q9ZFM2

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

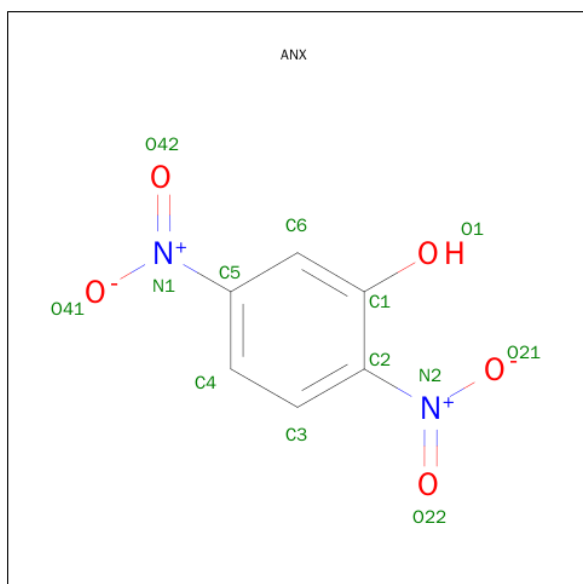
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Na 1 1	0	0
2	D	1	Total Na 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	1	Total	Na	0	0
			1	1		
2	H	1	Total	Na	0	0
			1	1		
2	B	1	Total	Na	0	0
			1	1		
2	C	1	Total	Na	0	0
			1	1		
2	A	1	Total	Na	0	0
			1	1		
2	F	1	Total	Na	0	0
			1	1		

- Molecule 3 is 2,5-DINITROPHENOL (three-letter code: ANX) (formula: C₆H₄N₂O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			13	6	2	5		
3	D	1	Total	C	N	O	0	0
			13	6	2	5		

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	2	Total	C	O	0	0
			18	10	8		

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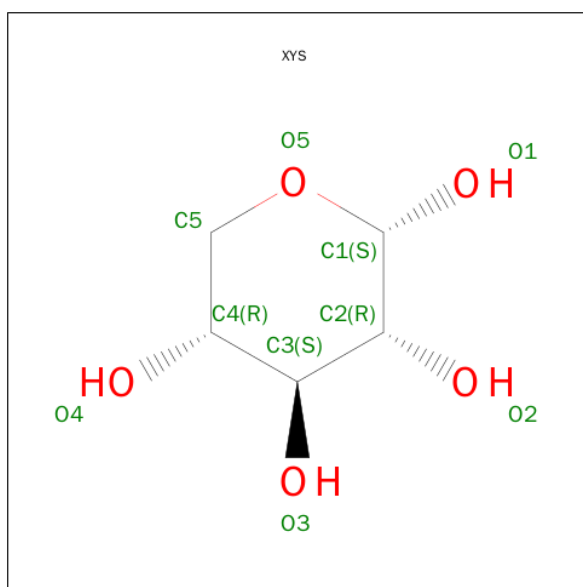
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	2	Total	C	O	0	0
			18	10	8		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is SUGAR (XYLOPYRANOSE) (three-letter code: XYS) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			9	5	4		
6	C	1	Total	C	O	0	0
			9	5	4		
6	E	1	Total	C	O	0	0
			9	5	4		
6	F	1	Total	C	O	0	0
			9	5	4		
6	G	1	Total	C	O	0	0
			9	5	4		
6	H	1	Total	C	O	0	0
			9	5	4		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	172	Total	O	0	0
			172	172		
7	B	167	Total	O	0	0
			167	167		
7	C	179	Total	O	0	0
			179	179		
7	D	160	Total	O	0	0
			160	160		
7	E	187	Total	O	0	0
			187	187		
7	F	144	Total	O	0	0
			144	144		

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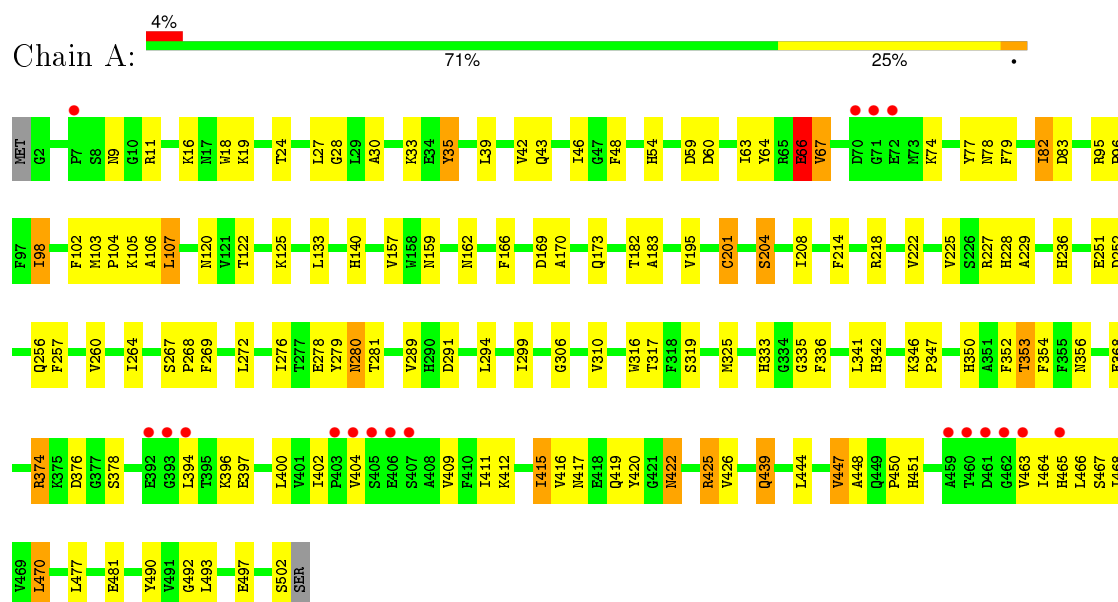
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	G	178	Total 178	O 178	0	0
7	H	193	Total 193	O 193	0	0

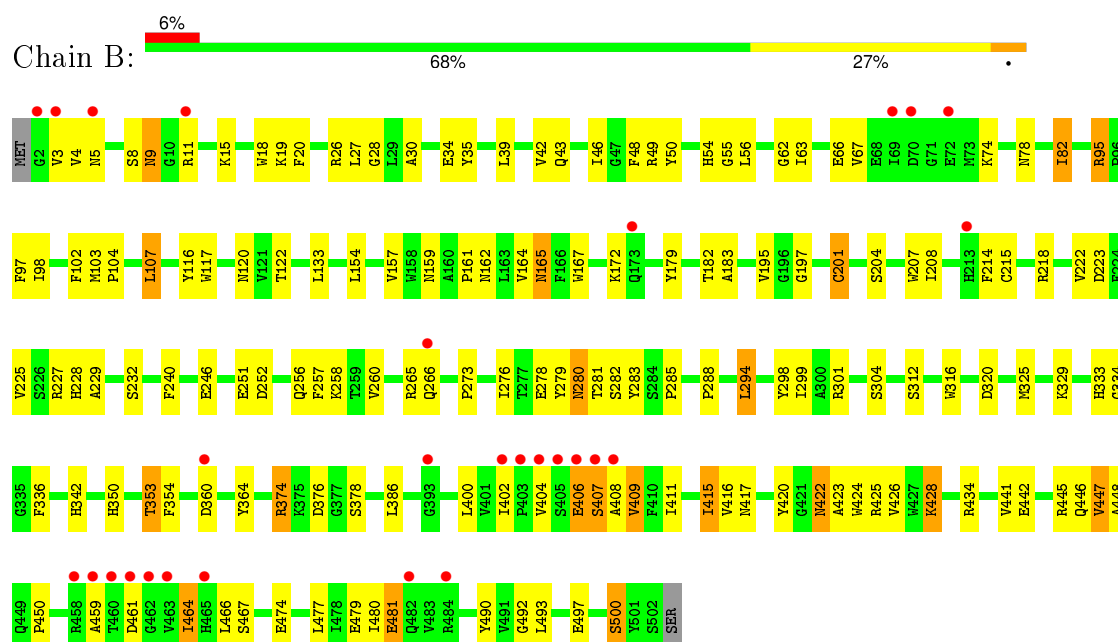
3 Residue-property plots

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.

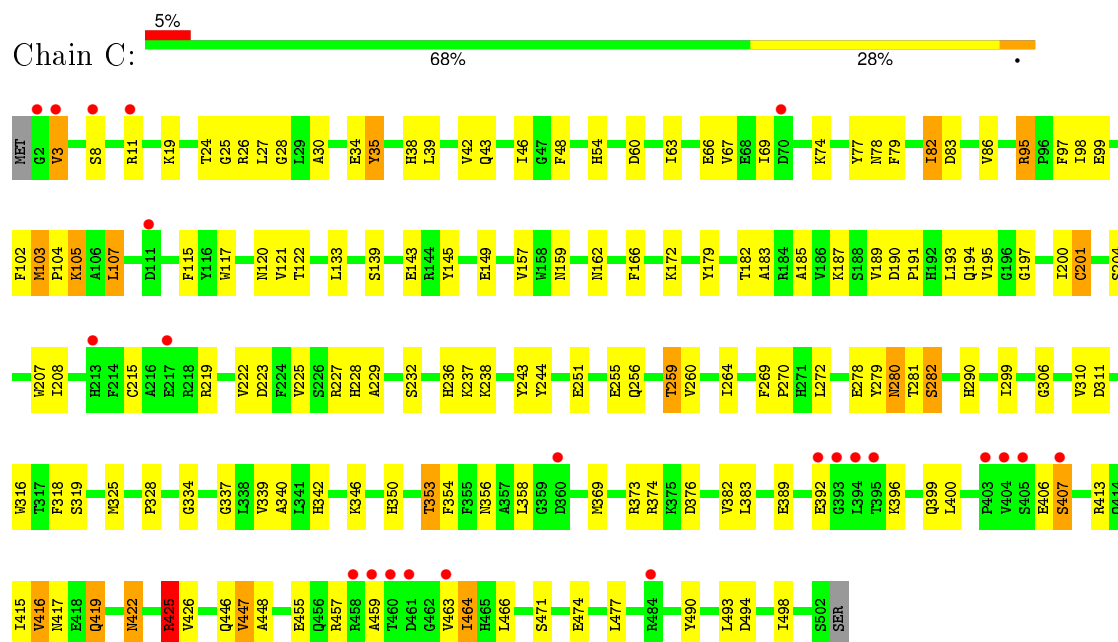
• Molecule 1: BETA-XYLOSIDASE



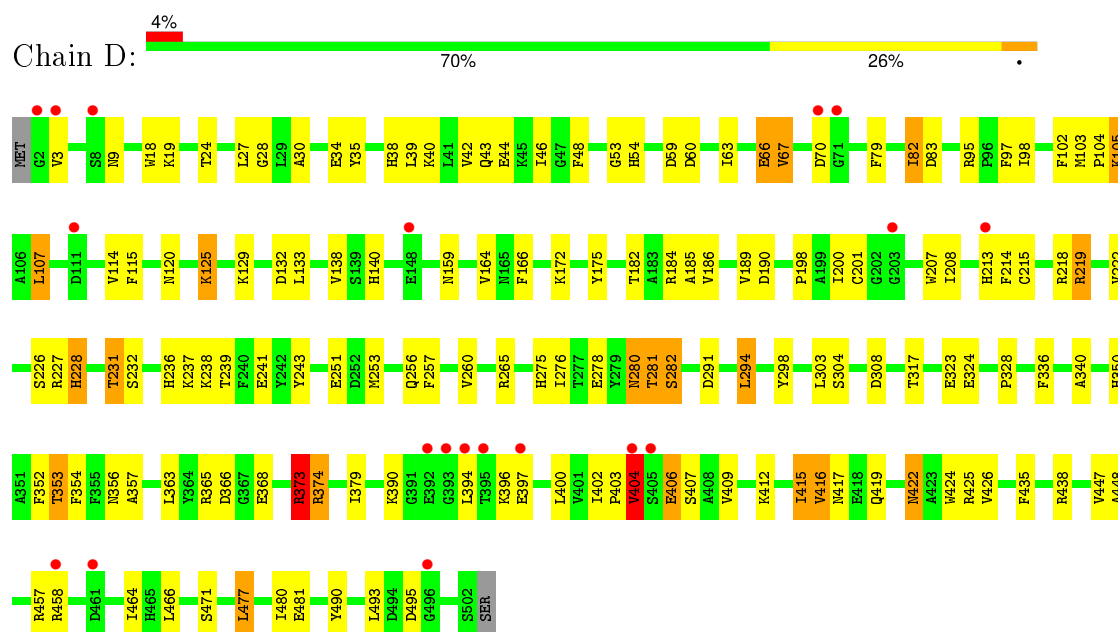
• Molecule 1: BETA-XYLOSIDASE



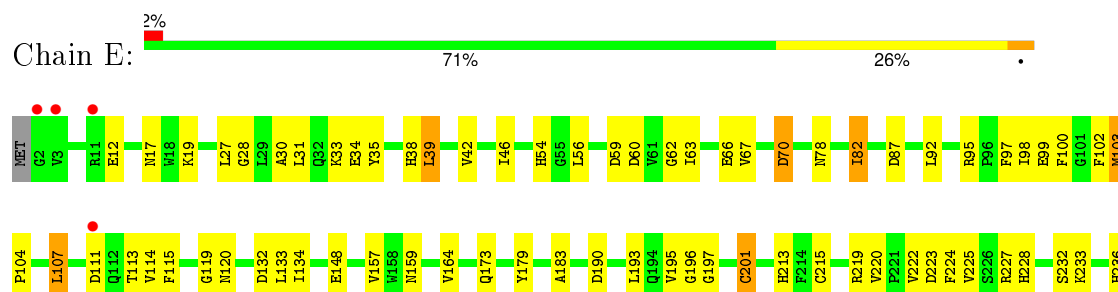
- Molecule 1: BETA-XYLOSIDASE

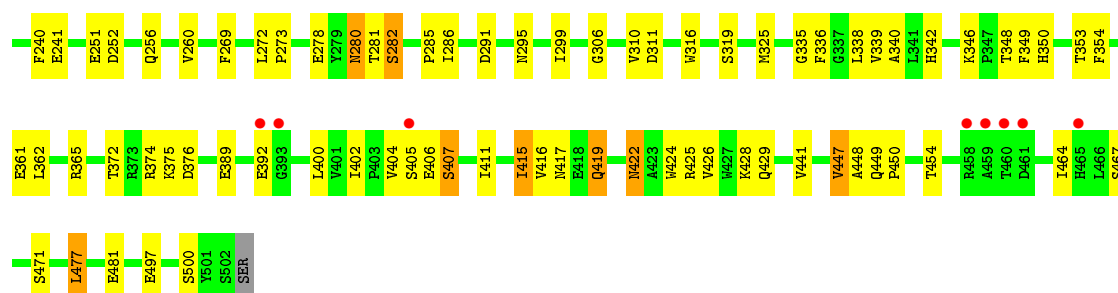


- Molecule 1: BETA-XYLOSIDASE

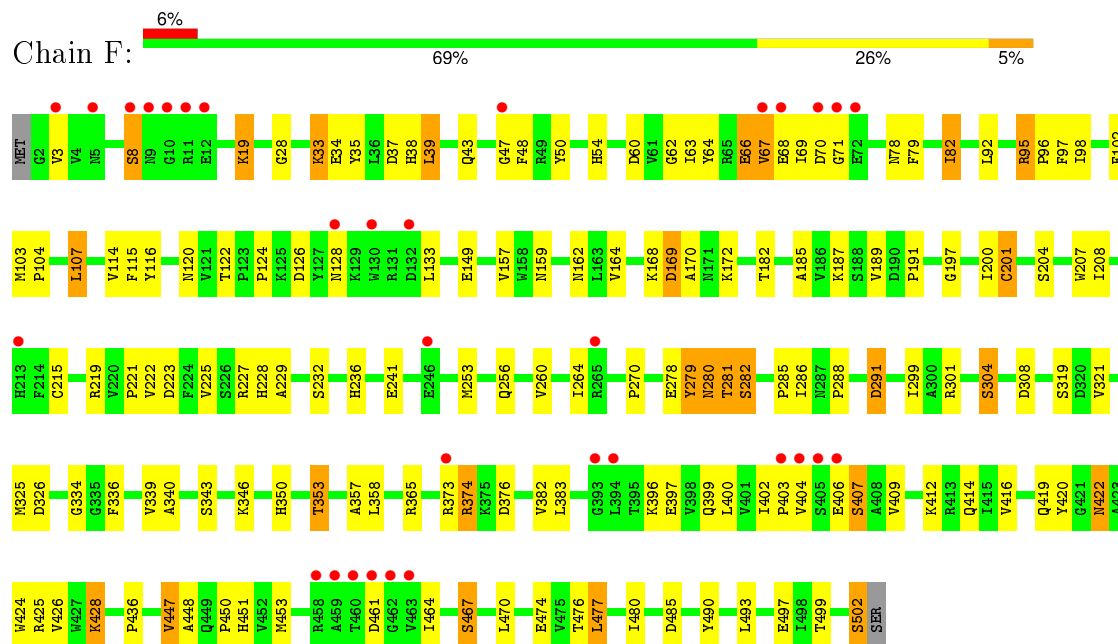


- Molecule 1: BETA-XYLOSIDASE

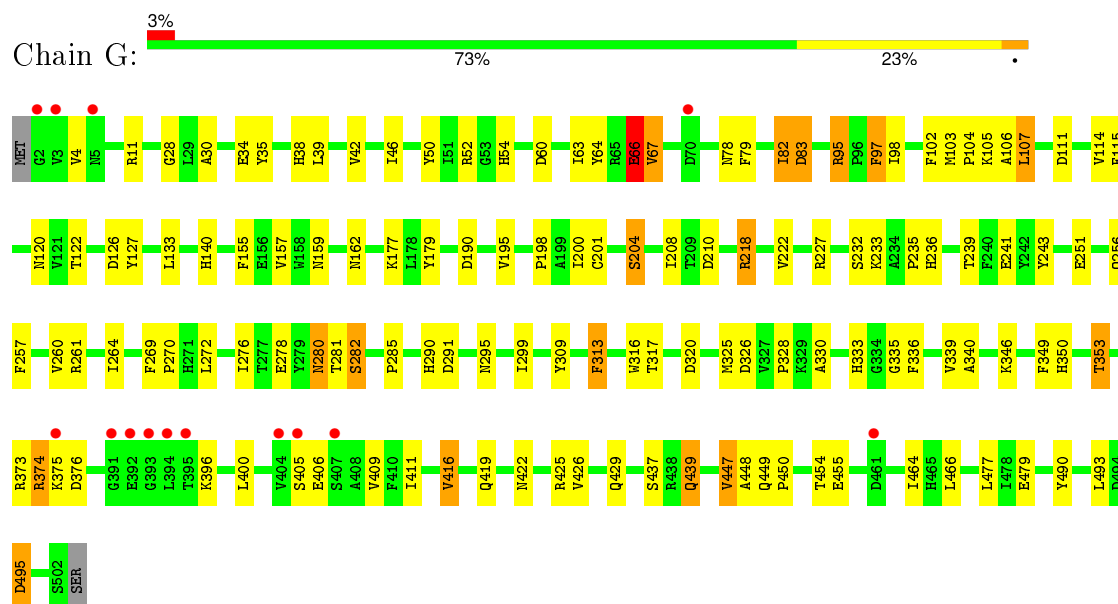




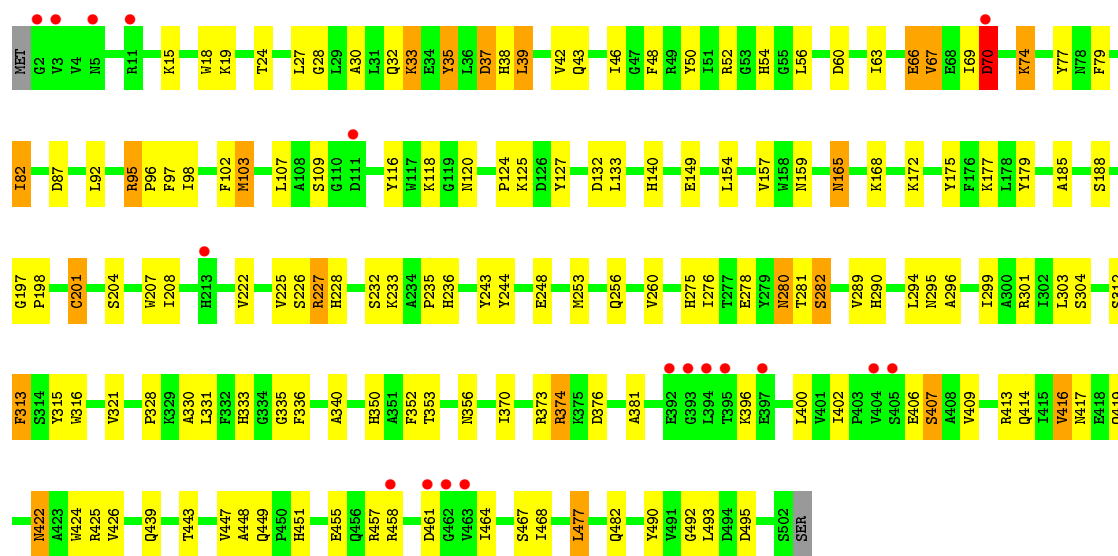
• Molecule 1: BETA-XYLOSIDASE



• Molecule 1: BETA-XYLOSIDASE



• Molecule 1: BETA-XYLOSIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.95Å 162.16Å 308.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.11 – 2.40 39.62 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.11-2.40) 99.6 (39.62-2.40)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.194 , 0.270 0.207 , 0.276	Depositor DCC
R_{free} test set	8689 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	18.3	Xtriage
Anisotropy	0.617	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	3 of 173787 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	34237	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.35 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.1498e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: XYP, NA, XYS, ANX, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.75	0/4202	0.86	5/5705 (0.1%)
1	B	0.75	1/4202 (0.0%)	0.85	7/5705 (0.1%)
1	C	0.73	1/4199 (0.0%)	0.85	4/5701 (0.1%)
1	D	0.70	0/4202	0.86	10/5705 (0.2%)
1	E	0.75	1/4202 (0.0%)	0.88	10/5705 (0.2%)
1	F	0.70	1/4202 (0.0%)	0.84	8/5705 (0.1%)
1	G	0.74	0/4202	0.87	8/5705 (0.1%)
1	H	0.77	1/4202 (0.0%)	0.88	6/5705 (0.1%)
All	All	0.74	5/33613 (0.0%)	0.86	58/45636 (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	E	0	1
1	F	0	1
1	G	0	1
4	D	1	0
All	All	1	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	103	MET	SD-CE	-5.55	1.46	1.77
1	H	103	MET	SD-CE	-5.48	1.47	1.77
1	F	447	VAL	CB-CG1	-5.14	1.42	1.52
1	C	425	ARG	CG-CD	5.03	1.64	1.51
1	B	246	GLU	CD-OE1	5.02	1.31	1.25

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	376	ASP	CB-CG-OD2	7.72	125.25	118.30
1	A	376	ASP	CB-CG-OD2	7.55	125.10	118.30
1	D	291	ASP	CB-CG-OD2	7.30	124.87	118.30
1	G	210	ASP	CB-CG-OD2	7.14	124.72	118.30
1	D	83	ASP	CB-CG-OD2	7.02	124.61	118.30
1	H	37	ASP	CB-CG-OD2	6.88	124.49	118.30
1	E	252	ASP	CB-CG-OD2	6.86	124.47	118.30
1	A	59	ASP	CB-CG-OD2	6.73	124.36	118.30
1	F	374	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	E	66	GLU	C-N-CA	6.58	138.15	121.70
1	H	132	ASP	CB-CG-OD2	6.56	124.20	118.30
1	H	461	ASP	CB-CG-OD2	6.41	124.06	118.30
1	F	485	ASP	CB-CG-OD2	6.36	124.02	118.30
1	C	376	ASP	CB-CG-OD2	6.34	124.01	118.30
1	G	376	ASP	CB-CG-OD2	6.26	123.94	118.30
1	F	291	ASP	CB-CG-OD2	6.23	123.90	118.30
1	F	169	ASP	CB-CG-OD2	6.21	123.89	118.30
1	F	376	ASP	CB-CG-OD2	6.16	123.84	118.30
1	C	83	ASP	CB-CG-OD2	6.11	123.80	118.30
1	E	59	ASP	CB-CG-OD2	6.08	123.77	118.30
1	H	66	GLU	C-N-CA	6.06	136.84	121.70
1	B	66	GLU	C-N-CA	5.95	136.58	121.70
1	E	111	ASP	CB-CG-OD2	5.94	123.64	118.30
1	D	190	ASP	CB-CG-OD2	5.90	123.61	118.30
1	E	87	ASP	CB-CG-OD2	5.86	123.58	118.30
1	A	291	ASP	CB-CG-OD2	5.85	123.57	118.30
1	C	311	ASP	CB-CG-OD2	5.85	123.56	118.30
1	G	83	ASP	CB-CG-OD2	5.79	123.51	118.30
1	G	190	ASP	CB-CG-OD2	5.69	123.42	118.30
1	D	495	ASP	CB-CG-OD2	5.66	123.39	118.30
1	D	373	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	E	66	GLU	CA-C-N	5.63	129.58	117.20
1	B	252	ASP	CB-CG-OD2	5.62	123.36	118.30
1	E	223	ASP	CB-CG-OD2	5.60	123.34	118.30
1	D	132	ASP	CB-CG-OD2	5.56	123.31	118.30
1	C	494	ASP	CB-CG-OD2	5.55	123.30	118.30
1	G	261	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	F	70	ASP	CB-CG-OD2	5.38	123.15	118.30
1	B	46	ILE	C-N-CA	-5.34	111.08	122.30
1	A	252	ASP	CB-CG-OD2	5.34	123.11	118.30
1	F	326	ASP	CB-CG-OD1	5.34	123.11	118.30
1	F	461	ASP	CB-CG-OD2	5.33	123.09	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	GLU	CA-C-N	5.32	128.90	117.20
1	H	87	ASP	CB-CG-OD2	5.30	123.07	118.30
1	B	360	ASP	CB-CG-OD2	5.29	123.06	118.30
1	D	308	ASP	CB-CG-OD2	5.29	123.06	118.30
1	G	495	ASP	CB-CG-OD2	5.29	123.06	118.30
1	E	132	ASP	CB-CG-OD2	5.29	123.06	118.30
1	D	374	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	E	376	ASP	CB-CG-OD2	5.24	123.02	118.30
1	D	366	ASP	CB-CG-OD2	5.23	123.01	118.30
1	G	111	ASP	CB-CG-OD2	5.19	122.97	118.30
1	B	461	ASP	CB-CG-OD2	5.15	122.93	118.30
1	B	376	ASP	CB-CG-OD2	5.14	122.93	118.30
1	G	126	ASP	CB-CG-OD2	5.12	122.91	118.30
1	E	70	ASP	CB-CG-OD2	5.11	122.90	118.30
1	A	66	GLU	C-N-CA	5.03	134.27	121.70
1	D	59	ASP	CB-CG-OD2	5.01	122.81	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	D	1505	XYP	C1B

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	405	SER	Peptide
1	F	66	GLU	Peptide
1	G	66	GLU	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	4087	0	4000	94	0
1	B	4087	0	4000	109	0
1	C	4084	0	3998	99	0
1	D	4087	0	3999	108	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	4087	0	4000	96	1
1	F	4087	0	4000	114	1
1	G	4087	0	4000	99	0
1	H	4087	0	4000	114	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	13	0	3	1	0
3	D	13	0	3	0	0
4	A	18	0	6	3	0
4	D	18	0	6	5	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
5	E	5	0	0	0	0
5	F	5	0	0	0	0
5	G	5	0	0	1	0
5	H	5	0	0	1	0
6	B	9	0	8	1	0
6	C	9	0	8	1	0
6	E	9	0	8	0	0
6	F	9	0	8	0	0
6	G	9	0	8	1	0
6	H	9	0	8	2	0
7	A	172	0	0	7	0
7	B	167	0	0	13	0
7	C	179	0	0	6	0
7	D	160	0	0	8	0
7	E	187	0	0	13	0
7	F	144	0	0	14	0
7	G	178	0	0	11	0
7	H	193	0	0	18	0
All	All	34237	0	32063	809	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 12.

All (809) 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:B:350:HIS:CE1	7:B:2120:HOH:O	1.89	1.20
1:A:201:CYS:SG	3:A:1504:ANX:O21	1.99	1.20
1:E:103:MET:SD	7:E:2061:HOH:O	2.10	1.10
1:F:426:VAL:HG21	1:F:447:VAL:HG11	1.34	1.07
1:B:280:ASN:HD22	1:B:281:THR:H	1.06	1.02
1:A:228:HIS:ND1	1:A:278:GLU:HB2	1.74	1.01
1:D:213:HIS:HB3	7:D:2081:HOH:O	1.61	1.00
1:E:280:ASN:HD22	1:E:281:THR:H	1.10	0.99
1:H:280:ASN:HD22	1:H:281:THR:H	1.13	0.94
1:H:168:LYS:HE2	7:H:2024:HOH:O	1.69	0.93
1:D:227:ARG:HH12	1:D:256:GLN:HE21	1.11	0.93
1:E:38:HIS:ND1	7:E:2018:HOH:O	2.00	0.92
1:G:63:ILE:HD11	1:G:82:ILE:HG12	1.51	0.92
1:F:103:MET:HG3	1:F:122:THR:O	1.71	0.90
1:A:227:ARG:HH12	1:A:256:GLN:HE21	1.14	0.89
1:E:227:ARG:HH12	1:E:256:GLN:HE21	1.23	0.87
1:B:227:ARG:HH12	1:B:256:GLN:HE21	1.19	0.87
1:E:103:MET:HE3	1:E:107:LEU:HB3	1.58	0.86
1:H:426:VAL:HG21	1:H:447:VAL:HG11	1.54	0.86
1:C:280:ASN:HD22	1:C:281:THR:H	1.23	0.86
1:D:280:ASN:HD22	1:D:281:THR:H	1.23	0.86
1:A:280:ASN:HD22	1:A:281:THR:H	1.21	0.86
1:C:227:ARG:HH12	1:C:256:GLN:HE21	1.20	0.85
1:A:103:MET:HG3	1:A:122:THR:O	1.78	0.83
1:E:34:GLU:O	1:E:38:HIS:HD2	1.59	0.82
1:E:406:GLU:O	7:E:2147:HOH:O	1.97	0.81
1:D:63:ILE:HD11	1:D:82:ILE:HG12	1.62	0.80
1:E:38:HIS:CG	7:E:2018:HOH:O	2.33	0.80
1:C:103:MET:HG2	1:C:122:THR:O	1.81	0.80
1:G:227:ARG:HH12	1:G:256:GLN:HE21	1.30	0.79
1:E:406:GLU:O	1:E:407:SER:HB3	1.82	0.79
1:G:353:THR:HG21	7:G:2122:HOH:O	1.84	0.77
1:D:227:ARG:NH1	1:D:256:GLN:HE21	1.82	0.77
1:C:238:LYS:HE2	1:C:243:TYR:CE2	2.21	0.76
1:E:103:MET:CE	1:E:107:LEU:HB3	2.16	0.76
1:F:280:ASN:HD22	1:F:281:THR:H	1.32	0.76
1:F:422:ASN:HD21	1:F:424:TRP:HB3	1.51	0.75
1:G:439:GLN:HE21	1:G:439:GLN:H	1.34	0.75
1:H:227:ARG:HH12	1:H:256:GLN:HE21	1.34	0.75
1:E:350:HIS:ND1	1:E:450:PRO:HG3	2.03	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:353:THR:HG21	7:F:2104:HOH:O	1.87	0.74
1:B:280:ASN:HD22	1:B:281:THR:N	1.84	0.73
1:F:227:ARG:HH12	1:F:256:GLN:HE21	1.34	0.73
1:E:103:MET:HE1	1:E:107:LEU:HD13	1.71	0.73
1:C:103:MET:CE	1:C:107:LEU:HB3	2.19	0.73
1:A:439:GLN:HE21	1:A:439:GLN:H	1.36	0.73
1:G:455:GLU:OE2	7:G:2159:HOH:O	2.07	0.72
1:B:165:ASN:H	1:B:165:ASN:HD22	1.36	0.72
1:B:103:MET:HG3	1:B:122:THR:O	1.88	0.72
1:F:404:VAL:HA	7:F:2106:HOH:O	1.88	0.72
1:F:426:VAL:CG2	1:F:447:VAL:HG11	2.14	0.72
1:E:38:HIS:HE1	1:E:340:ALA:O	1.72	0.72
1:G:103:MET:HG3	1:G:122:THR:O	1.91	0.71
1:B:227:ARG:NH1	1:B:256:GLN:HE21	1.89	0.71
1:E:454:THR:OG1	1:G:429:GLN:NE2	2.24	0.71
1:H:455:GLU:OE2	7:H:2173:HOH:O	2.09	0.71
1:A:96:PRO:HB2	1:A:98:ILE:HD12	1.72	0.71
1:E:38:HIS:CE1	7:E:2018:HOH:O	2.43	0.70
1:F:34:GLU:O	1:F:38:HIS:HD2	1.72	0.70
1:D:42:VAL:O	1:D:46:ILE:O	2.10	0.70
1:G:11:ARG:NE	7:G:2003:HOH:O	2.22	0.70
1:F:497:GLU:OE1	1:H:236:HIS:HE1	1.73	0.70
1:D:125:LYS:HZ1	1:D:129:LYS:HZ2	1.39	0.70
1:B:500:SER:HB3	1:D:294:LEU:HD13	1.72	0.69
1:D:422:ASN:HD21	1:D:424:TRP:HB3	1.57	0.69
1:D:125:LYS:NZ	1:D:129:LYS:NZ	2.39	0.69
1:A:63:ILE:HD11	1:A:82:ILE:HG12	1.73	0.69
1:B:280:ASN:ND2	1:B:281:THR:H	1.87	0.69
1:E:406:GLU:O	1:E:407:SER:CB	2.38	0.69
1:G:280:ASN:HD22	1:G:281:THR:H	1.39	0.69
1:G:34:GLU:O	1:G:38:HIS:CD2	2.46	0.68
1:A:415:ILE:C	1:A:415:ILE:HD12	2.13	0.68
1:E:34:GLU:O	1:E:38:HIS:CD2	2.44	0.68
1:C:28:GLY:HA3	1:C:60:ASP:OD2	1.94	0.68
1:H:208:ILE:HD13	1:H:260:VAL:HG13	1.74	0.68
1:C:238:LYS:HE2	1:C:243:TYR:CZ	2.28	0.68
1:F:34:GLU:O	1:F:38:HIS:CD2	2.47	0.68
1:E:497:GLU:OE1	1:G:236:HIS:NE2	2.24	0.68
1:E:280:ASN:HD22	1:E:281:THR:N	1.88	0.67
1:D:350:HIS:NE2	1:D:448:ALA:O	2.27	0.67
1:G:103:MET:CE	1:G:107:LEU:HB3	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:79:PHE:HD2	1:C:82:ILE:HD11	1.58	0.67
1:B:215:CYS:SG	1:B:222:VAL:CG2	2.82	0.67
1:A:201:CYS:HA	1:A:228:HIS:HB2	1.77	0.67
1:E:280:ASN:ND2	1:E:281:THR:H	1.90	0.67
1:F:227:ARG:NH1	1:F:256:GLN:HE21	1.92	0.67
1:C:227:ARG:HD2	1:C:260:VAL:HG21	1.76	0.67
1:B:411:ILE:HD13	1:B:466:LEU:HD21	1.77	0.67
1:B:415:ILE:C	1:B:415:ILE:HD12	2.16	0.66
1:G:426:VAL:HG21	1:G:447:VAL:HG11	1.77	0.66
1:A:28:GLY:HA3	1:A:60:ASP:OD2	1.96	0.66
1:H:19:LYS:NZ	1:H:356:ASN:HD21	1.94	0.66
1:D:353:THR:HG21	7:D:2118:HOH:O	1.97	0.65
1:B:422:ASN:HD21	1:B:424:TRP:HB3	1.62	0.65
1:B:434:ARG:HD2	7:D:2155:HOH:O	1.97	0.65
1:D:184:ARG:HG2	7:D:2075:HOH:O	1.97	0.65
1:G:411:ILE:HD13	1:G:466:LEU:HD21	1.78	0.65
1:A:439:GLN:NE2	1:A:439:GLN:H	1.95	0.64
1:H:236:HIS:HD2	7:H:2098:HOH:O	1.79	0.64
1:G:34:GLU:O	1:G:38:HIS:HD2	1.80	0.64
1:G:54:HIS:HE1	1:G:159:ASN:CG	1.99	0.64
1:G:162:ASN:HD22	1:G:204:SER:HB3	1.62	0.64
1:C:63:ILE:HD11	1:C:82:ILE:HG12	1.80	0.64
1:B:415:ILE:HD11	1:B:420:TYR:HB2	1.80	0.64
1:G:162:ASN:HD22	1:G:204:SER:CB	2.10	0.64
1:D:28:GLY:HA3	1:D:60:ASP:OD2	1.98	0.64
1:A:353:THR:HG21	7:A:2131:HOH:O	1.97	0.64
1:G:350:HIS:ND1	1:G:450:PRO:HG3	2.12	0.64
1:H:426:VAL:CG2	1:H:447:VAL:HG11	2.27	0.64
1:G:375:LYS:CE	7:G:2124:HOH:O	2.45	0.64
1:B:350:HIS:ND1	7:B:2120:HOH:O	2.04	0.64
1:C:3:VAL:HG12	7:C:2001:HOH:O	1.97	0.64
1:F:470:LEU:HD21	1:F:476:THR:HG22	1.79	0.63
1:F:54:HIS:HE1	1:F:159:ASN:CG	2.02	0.63
1:G:38:HIS:HE1	1:G:340:ALA:O	1.82	0.63
1:H:63:ILE:HD11	1:H:82:ILE:HG12	1.80	0.63
1:G:30:ALA:HA	1:G:35:TYR:CG	2.34	0.63
1:F:8:SER:O	7:F:2001:HOH:O	2.16	0.62
1:E:232:SER:HB3	1:E:282:SER:HA	1.81	0.62
1:G:350:HIS:CE1	1:G:450:PRO:HD3	2.33	0.62
1:D:105:LYS:NZ	1:D:120:ASN:HD22	1.97	0.62
1:C:236:HIS:HD2	7:C:2092:HOH:O	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:CYS:SG	1:B:222:VAL:HG22	2.39	0.62
1:A:333:HIS:HE1	7:A:2116:HOH:O	1.81	0.62
1:A:426:VAL:HG21	1:A:447:VAL:HG11	1.82	0.62
1:C:54:HIS:HE1	1:C:159:ASN:CG	2.03	0.62
1:H:280:ASN:HD22	1:H:281:THR:N	1.92	0.62
1:D:19:LYS:NZ	1:D:356:ASN:HD21	1.97	0.62
1:A:227:ARG:NH1	1:A:256:GLN:HE21	1.92	0.62
1:H:201:CYS:HA	1:H:228:HIS:HB2	1.81	0.62
1:D:214:PHE:CE1	1:D:218:ARG:HD3	2.34	0.62
1:F:103:MET:CG	1:F:122:THR:O	2.45	0.62
1:E:99:GLU:OE1	7:E:2046:HOH:O	2.16	0.62
1:D:125:LYS:NZ	1:D:129:LYS:HZ2	1.98	0.61
1:F:497:GLU:OE1	1:H:236:HIS:CE1	2.53	0.61
1:H:426:VAL:HG21	1:H:447:VAL:CG1	2.27	0.61
1:E:415:ILE:HD11	1:E:417:ASN:ND2	2.16	0.61
1:B:103:MET:CE	1:B:107:LEU:HB3	2.30	0.61
1:H:422:ASN:HD21	1:H:424:TRP:HB3	1.66	0.61
1:G:375:LYS:HE2	7:G:2124:HOH:O	1.99	0.61
1:E:415:ILE:HD11	1:E:417:ASN:CG	2.21	0.61
1:C:201:CYS:HA	1:C:228:HIS:HB2	1.82	0.61
1:E:103:MET:CE	1:E:107:LEU:HD13	2.31	0.61
1:D:227:ARG:HH12	1:D:256:GLN:NE2	1.92	0.61
1:C:215:CYS:SG	1:C:222:VAL:HG21	2.41	0.61
1:H:42:VAL:O	1:H:46:ILE:O	2.19	0.61
1:C:30:ALA:HA	1:C:35:TYR:CG	2.36	0.61
1:D:125:LYS:HZ3	1:D:129:LYS:NZ	1.99	0.60
1:G:426:VAL:CG2	1:G:447:VAL:HG11	2.31	0.60
1:B:400:LEU:HD23	1:B:402:ILE:HD11	1.82	0.60
1:C:99:GLU:OE1	7:C:2061:HOH:O	2.15	0.60
1:H:79:PHE:HA	1:H:82:ILE:HD11	1.83	0.60
1:F:33:LYS:NZ	1:F:37:ASP:OD1	2.33	0.60
1:B:415:ILE:HD13	1:B:417:ASN:ND2	2.16	0.60
1:H:54:HIS:HE1	1:H:159:ASN:CG	2.05	0.60
1:A:411:ILE:HD13	1:A:466:LEU:HD21	1.84	0.60
1:B:350:HIS:CG	7:B:2120:HOH:O	2.46	0.60
1:H:280:ASN:ND2	1:H:281:THR:H	1.93	0.60
1:F:187:LYS:NZ	1:F:223:ASP:OD2	2.34	0.60
1:D:125:LYS:HZ3	1:D:129:LYS:HZ3	1.49	0.59
1:E:415:ILE:CD1	1:E:417:ASN:ND2	2.65	0.59
1:H:227:ARG:NH1	1:H:256:GLN:HE21	2.00	0.59
1:B:63:ILE:HD11	1:B:82:ILE:HG12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:PHE:CD2	1:C:69:ILE:HD11	2.37	0.59
1:C:358:LEU:HD21	1:C:382:VAL:HG23	1.85	0.59
1:A:103:MET:CE	1:A:107:LEU:HB3	2.33	0.59
1:A:350:HIS:CG	1:A:416:VAL:HG11	2.38	0.59
1:G:66:GLU:HG3	1:G:106:ALA:HB1	1.84	0.59
1:F:406:GLU:O	1:F:407:SER:HB3	2.02	0.59
1:D:103:MET:CE	1:D:107:LEU:HB3	2.32	0.59
1:D:490:TYR:HB3	1:D:493:LEU:HB2	1.85	0.59
1:E:63:ILE:HA	1:E:78:ASN:O	2.03	0.59
1:B:350:HIS:CB	1:B:416:VAL:HG11	2.33	0.59
1:C:426:VAL:HG21	1:C:447:VAL:HG11	1.85	0.58
1:E:426:VAL:HG21	1:E:447:VAL:HG11	1.86	0.58
1:E:256:GLN:O	1:E:260:VAL:HG23	2.04	0.58
1:F:227:ARG:HH12	1:F:256:GLN:NE2	2.00	0.58
1:B:201:CYS:HA	1:B:228:HIS:HB2	1.85	0.58
1:D:238:LYS:HE2	1:D:243:TYR:CE2	2.38	0.58
1:A:412:LYS:HZ1	1:C:446:GLN:NE2	2.01	0.58
1:G:232:SER:HB3	1:G:282:SER:HA	1.86	0.58
1:H:449:GLN:HG3	7:H:2166:HOH:O	2.04	0.58
1:C:43:GLN:HE22	1:C:48:PHE:HB2	1.69	0.58
1:C:255:GLU:O	1:C:259:THR:HB	2.03	0.58
1:A:350:HIS:CD2	1:A:416:VAL:HG11	2.39	0.58
1:H:118:LYS:HE3	7:H:2071:HOH:O	2.03	0.58
1:C:413:ARG:NH2	1:C:474:GLU:OE2	2.37	0.58
1:D:40:LYS:NZ	1:D:44:GLU:OE2	2.34	0.58
1:G:54:HIS:HE1	1:G:159:ASN:ND2	2.02	0.57
1:H:54:HIS:HE1	1:H:159:ASN:ND2	2.02	0.57
1:B:350:HIS:ND1	1:B:450:PRO:HG3	2.19	0.57
1:H:43:GLN:HE22	1:H:48:PHE:H	1.52	0.57
1:H:419:GLN:HG2	7:H:2152:HOH:O	2.05	0.57
1:A:103:MET:HE1	1:A:107:LEU:HD13	1.87	0.57
1:C:103:MET:CE	1:C:107:LEU:HD13	2.34	0.57
1:A:402:ILE:HB	1:A:464:ILE:HG22	1.85	0.57
1:H:449:GLN:CG	7:H:2166:HOH:O	2.51	0.57
1:A:374:ARG:HD3	1:A:378:SER:OG	2.05	0.57
1:G:64:TYR:HB3	1:G:104:PRO:HB3	1.87	0.56
1:F:201:CYS:HA	1:F:228:HIS:HB2	1.87	0.56
1:A:350:HIS:CE1	1:A:450:PRO:HD3	2.40	0.56
1:B:353:THR:HG21	7:B:2121:HOH:O	2.05	0.56
1:G:256:GLN:NE2	7:G:2090:HOH:O	2.38	0.56
1:G:439:GLN:NE2	1:G:439:GLN:H	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:228:HIS:CE1	1:B:278:GLU:OE2	2.59	0.56
1:D:30:ALA:HA	1:D:35:TYR:CG	2.40	0.56
1:H:373:ARG:NE	7:H:2139:HOH:O	2.38	0.56
1:E:353:THR:HG21	7:E:2139:HOH:O	2.06	0.56
1:B:43:GLN:HE22	1:B:48:PHE:H	1.53	0.56
1:D:38:HIS:CE1	1:D:340:ALA:O	2.59	0.56
1:E:54:HIS:HE1	1:E:159:ASN:CG	2.09	0.56
1:F:38:HIS:HE1	1:F:340:ALA:O	1.89	0.55
1:H:353:THR:HG21	7:H:2137:HOH:O	2.05	0.55
1:F:162:ASN:HD22	1:F:204:SER:HB3	1.71	0.55
1:B:350:HIS:CG	1:B:416:VAL:HG11	2.41	0.55
1:E:42:VAL:O	1:E:46:ILE:O	2.24	0.55
1:B:481:GLU:OE2	7:B:2155:HOH:O	2.18	0.55
1:H:103:MET:CE	1:H:107:LEU:HB3	2.36	0.55
1:A:43:GLN:HE22	1:A:48:PHE:HB2	1.72	0.55
1:E:228:HIS:ND1	1:E:278:GLU:HB2	2.21	0.55
1:A:54:HIS:HE1	1:A:159:ASN:CG	2.09	0.55
1:H:103:MET:HE2	1:H:107:LEU:HB3	1.88	0.55
1:C:373:ARG:HD2	7:C:2002:HOH:O	2.07	0.55
1:B:283:TYR:O	6:B:1504:XY5:H51	2.06	0.55
1:F:62:GLY:O	1:F:78:ASN:HB3	2.07	0.55
1:C:215:CYS:SG	1:C:222:VAL:CG2	2.95	0.55
1:E:63:ILE:HD11	1:E:82:ILE:HG12	1.87	0.55
1:B:183:ALA:HA	1:B:195:VAL:HG21	1.89	0.55
1:A:79:PHE:HD2	1:A:82:ILE:HD11	1.71	0.54
1:F:502:SER:C	7:F:2144:HOH:O	2.45	0.54
1:C:422:ASN:C	1:C:422:ASN:HD22	2.11	0.54
1:A:54:HIS:NE2	4:A:1505:XYP:O3B	2.37	0.54
1:D:236:HIS:HD2	7:D:2083:HOH:O	1.90	0.54
1:D:426:VAL:HG21	1:D:447:VAL:HG11	1.90	0.54
1:D:227:ARG:HD2	1:D:260:VAL:HG21	1.89	0.54
1:C:42:VAL:O	1:C:46:ILE:O	2.25	0.54
1:H:227:ARG:O	1:H:276:ILE:HA	2.08	0.54
1:D:103:MET:HE2	1:D:107:LEU:HB3	1.90	0.54
1:D:172:LYS:HA	1:D:207:TRP:CH2	2.42	0.54
1:B:350:HIS:NE2	7:B:2120:HOH:O	2.20	0.54
1:D:419:GLN:NE2	7:D:2130:HOH:O	2.40	0.54
1:B:30:ALA:HA	1:B:35:TYR:CG	2.43	0.54
1:A:236:HIS:HD2	7:A:2086:HOH:O	1.90	0.54
1:F:107:LEU:HD22	1:F:124:PRO:HB3	1.89	0.54
1:E:291:ASP:HA	1:E:346:LYS:HD3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:233:LYS:NZ	1:H:248:GLU:OE2	2.41	0.54
1:H:413:ARG:NH1	1:H:468:ILE:HG23	2.23	0.54
1:G:278:GLU:HG2	1:G:316:TRP:CD2	2.43	0.54
1:D:103:MET:HE3	1:D:104:PRO:HD2	1.90	0.54
1:F:197:GLY:O	1:F:225:VAL:HA	2.07	0.53
1:E:269:PHE:HB3	1:E:272:LEU:HG	1.90	0.53
1:E:227:ARG:NH1	1:E:256:GLN:HE21	1.99	0.53
1:B:20:PHE:HB3	1:B:312:SER:HB2	1.88	0.53
1:F:103:MET:CE	1:F:107:LEU:HB3	2.37	0.53
1:C:63:ILE:O	1:C:77:TYR:HA	2.08	0.53
1:H:330:ALA:O	1:H:333:HIS:HB3	2.08	0.53
1:G:449:GLN:NE2	7:G:2153:HOH:O	2.28	0.53
1:B:8:SER:C	1:B:9:ASN:HD22	2.12	0.53
1:H:109:SER:HA	1:H:125:LYS:HG2	1.91	0.53
1:A:280:ASN:ND2	1:A:281:THR:H	2.00	0.53
1:F:399:GLN:NE2	1:F:467:SER:OG	2.42	0.53
1:H:172:LYS:HA	1:H:207:TRP:CH2	2.43	0.53
1:D:43:GLN:HE22	1:D:48:PHE:H	1.56	0.53
1:E:38:HIS:ND1	1:E:339:VAL:CG1	2.72	0.53
1:C:208:ILE:HD13	1:C:260:VAL:HG13	1.91	0.53
1:F:50:TYR:CD2	1:F:95:ARG:HB2	2.43	0.53
1:E:236:HIS:HD2	7:E:2093:HOH:O	1.91	0.53
1:G:63:ILE:HD11	1:G:82:ILE:CG1	2.34	0.53
1:C:264:ILE:O	1:C:270:PRO:HA	2.07	0.53
1:F:28:GLY:HA3	1:F:60:ASP:OD2	2.09	0.53
1:A:19:LYS:NZ	1:A:356:ASN:ND2	2.57	0.53
1:D:227:ARG:O	1:D:276:ILE:HA	2.08	0.53
1:B:422:ASN:HD22	1:B:422:ASN:C	2.12	0.53
1:E:62:GLY:O	1:E:78:ASN:HB3	2.09	0.53
1:F:264:ILE:O	1:F:270:PRO:HA	2.09	0.53
1:G:350:HIS:HB2	1:G:416:VAL:HG11	1.91	0.53
1:G:30:ALA:HA	1:G:35:TYR:CD2	2.44	0.53
1:D:66:GLU:HA	1:D:67:VAL:HB	1.89	0.53
1:G:316:TRP:O	1:G:336:PHE:HB3	2.09	0.52
1:D:231:THR:HG21	1:D:298:TYR:OH	2.09	0.52
1:D:215:CYS:SG	1:D:222:VAL:CG2	2.97	0.52
1:A:66:GLU:HA	1:A:67:VAL:HB	1.90	0.52
1:E:28:GLY:HA3	1:E:60:ASP:OD2	2.09	0.52
1:E:426:VAL:HG21	1:E:447:VAL:HG21	1.91	0.52
1:B:490:TYR:HB3	1:B:493:LEU:HB2	1.92	0.52
1:F:229:ALA:O	1:F:279:TYR:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:33:LYS:HD3	1:H:37:ASP:OD2	2.10	0.52
1:H:69:ILE:O	1:H:70:ASP:HB2	2.09	0.52
1:B:165:ASN:H	1:B:165:ASN:ND2	2.04	0.52
1:D:34:GLU:O	1:D:38:HIS:CD2	2.62	0.52
1:F:350:HIS:ND1	1:F:450:PRO:HG3	2.25	0.52
1:E:103:MET:HE3	1:E:104:PRO:HD2	1.92	0.52
1:E:183:ALA:HA	1:E:195:VAL:HG21	1.92	0.52
1:F:426:VAL:HG21	1:F:447:VAL:CG1	2.24	0.52
1:C:280:ASN:HD22	1:C:281:THR:N	2.00	0.52
1:H:253:MET:O	1:H:256:GLN:HB2	2.09	0.52
1:C:422:ASN:ND2	1:C:425:ARG:H	2.08	0.52
1:C:103:MET:HE1	1:C:107:LEU:HD13	1.92	0.52
1:H:413:ARG:HA	1:H:477:LEU:O	2.10	0.52
1:A:183:ALA:HA	1:A:195:VAL:HG21	1.92	0.52
1:F:422:ASN:ND2	1:F:424:TRP:HB3	2.23	0.52
1:B:288:PRO:HA	1:B:334:GLY:HA2	1.92	0.51
1:E:213:HIS:CD2	7:E:2090:HOH:O	2.62	0.51
1:D:18:TRP:CE3	1:D:19:LYS:HB3	2.45	0.51
1:C:278:GLU:HG2	1:C:316:TRP:CE3	2.45	0.51
1:A:502:SER:C	7:A:2167:HOH:O	2.48	0.51
1:C:236:HIS:CD2	7:C:2092:HOH:O	2.58	0.51
1:A:280:ASN:HD22	1:A:281:THR:N	1.99	0.51
1:D:38:HIS:HE1	1:D:340:ALA:O	1.93	0.51
1:A:18:TRP:CE3	1:A:19:LYS:HB3	2.46	0.51
1:C:54:HIS:HE1	1:C:159:ASN:ND2	2.07	0.51
1:H:373:ARG:HD2	7:H:2139:HOH:O	2.10	0.51
1:F:79:PHE:HA	1:F:82:ILE:HD11	1.93	0.51
1:H:490:TYR:HB3	1:H:493:LEU:HB2	1.93	0.51
1:D:219:ARG:HG3	1:F:191:PRO:CG	2.41	0.51
1:G:114:VAL:O	1:G:115:PHE:HB2	2.10	0.51
1:E:342:HIS:CE1	1:E:441:VAL:HG21	2.46	0.51
1:A:78:ASN:O	7:A:2038:HOH:O	2.18	0.51
1:A:426:VAL:CG2	1:A:447:VAL:HG11	2.40	0.51
1:H:103:MET:HB3	1:H:120:ASN:HB3	1.93	0.51
1:C:95:ARG:HD2	1:C:149:GLU:OE2	2.10	0.51
1:D:350:HIS:CB	1:D:416:VAL:HG11	2.41	0.51
1:D:19:LYS:HZ3	1:D:356:ASN:HD21	1.57	0.51
1:D:368:GLU:OE1	1:D:396:LYS:HD3	2.11	0.51
1:H:333:HIS:NE2	7:H:2132:HOH:O	2.33	0.50
1:B:426:VAL:HG21	1:B:447:VAL:HG11	1.92	0.50
1:F:285:PRO:HB3	1:F:336:PHE:CE1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:232:SER:HB3	1:F:282:SER:HA	1.92	0.50
1:C:38:HIS:CE1	1:C:340:ALA:O	2.64	0.50
1:F:383:LEU:N	1:F:383:LEU:HD12	2.26	0.50
1:H:303:LEU:HD21	1:H:352:PHE:CZ	2.46	0.50
1:F:422:ASN:HD22	1:F:422:ASN:C	2.15	0.50
1:F:227:ARG:HD2	1:F:260:VAL:HG21	1.93	0.50
1:G:103:MET:HE1	1:G:107:LEU:HB3	1.91	0.50
1:D:125:LYS:NZ	1:D:129:LYS:HZ3	2.06	0.50
1:D:238:LYS:CE	1:D:243:TYR:CE2	2.95	0.50
1:H:96:PRO:HB2	1:H:98:ILE:HG13	1.93	0.50
1:H:38:HIS:CE1	1:H:340:ALA:O	2.64	0.50
1:D:280:ASN:HD22	1:D:281:THR:N	2.01	0.50
1:A:43:GLN:HE22	1:A:48:PHE:H	1.59	0.50
1:E:228:HIS:CE1	1:E:278:GLU:HB2	2.46	0.50
1:A:257:PHE:CE1	1:A:276:ILE:HG13	2.47	0.50
1:B:34:GLU:OE1	7:B:2020:HOH:O	2.19	0.50
1:H:232:SER:HB3	1:H:282:SER:HA	1.92	0.50
1:B:374:ARG:HD3	1:B:378:SER:OG	2.11	0.50
1:B:257:PHE:CE1	1:B:276:ILE:HG13	2.46	0.50
1:F:412:LYS:NZ	1:H:443:THR:OG1	2.26	0.50
1:A:42:VAL:HG12	1:A:43:GLN:HE21	1.76	0.50
1:B:342:HIS:ND1	1:B:441:VAL:HG21	2.27	0.50
1:G:419:GLN:HG2	7:G:2136:HOH:O	2.10	0.50
1:F:350:HIS:CE1	1:F:450:PRO:HD3	2.47	0.50
1:H:35:TYR:O	1:H:38:HIS:HB2	2.12	0.50
1:A:27:LEU:O	1:A:30:ALA:HB3	2.12	0.50
1:B:227:ARG:O	1:B:276:ILE:HA	2.11	0.50
1:H:19:LYS:HZ3	1:H:356:ASN:HD21	1.58	0.50
1:C:69:ILE:HB	1:C:74:LYS:HD2	1.92	0.50
1:C:38:HIS:CE1	1:C:339:VAL:HG12	2.46	0.50
1:H:289:VAL:O	1:H:295:ASN:HB2	2.12	0.49
1:D:379:ILE:HG13	1:D:402:ILE:HG21	1.94	0.49
1:F:420:TYR:CE2	1:F:451:HIS:HD2	2.30	0.49
1:B:214:PHE:CE1	1:B:218:ARG:HD3	2.47	0.49
1:A:103:MET:HE3	1:A:107:LEU:HB3	1.93	0.49
1:G:281:THR:OG1	1:G:295:ASN:ND2	2.43	0.49
1:E:114:VAL:O	1:E:115:PHE:HB2	2.12	0.49
1:E:419:GLN:HB3	7:E:2153:HOH:O	2.12	0.49
1:F:79:PHE:HD2	1:F:82:ILE:HD11	1.77	0.49
1:H:350:HIS:CB	1:H:416:VAL:HG11	2.42	0.49
1:H:350:HIS:NE2	1:H:448:ALA:O	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:42:VAL:O	1:G:46:ILE:O	2.29	0.49
1:D:357:ALA:CB	1:D:477:LEU:HD11	2.42	0.49
1:G:50:TYR:HA	1:G:95:ARG:O	2.13	0.49
1:B:165:ASN:N	1:B:165:ASN:ND2	2.60	0.49
1:C:63:ILE:HD11	1:C:82:ILE:CG1	2.42	0.49
1:B:43:GLN:HE22	1:B:48:PHE:HB2	1.77	0.49
1:G:28:GLY:HA3	1:G:60:ASP:OD2	2.13	0.49
1:H:185:ALA:O	1:H:188:SER:OG	2.22	0.49
1:B:497:GLU:OE1	1:D:236:HIS:HE1	1.95	0.49
1:E:17:ASN:ND2	1:E:310:VAL:O	2.43	0.49
1:A:225:VAL:HG21	1:A:264:ILE:HG12	1.95	0.49
1:G:269:PHE:HB3	1:G:272:LEU:HG	1.95	0.49
1:D:166:PHE:CZ	4:D:1505:XYP:H2B	2.47	0.49
1:G:374:ARG:HA	5:G:1505:SO4:O4	2.11	0.49
1:F:64:TYR:HB3	1:F:104:PRO:HB3	1.95	0.49
1:G:66:GLU:HA	1:G:67:VAL:HB	1.95	0.49
1:H:103:MET:HE1	1:H:124:PRO:HB3	1.94	0.49
1:F:103:MET:HE3	1:F:104:PRO:HD2	1.95	0.49
1:H:235:PRO:HG3	1:H:243:TYR:CD1	2.47	0.49
1:C:290:HIS:HD2	1:C:334:GLY:O	1.96	0.49
1:B:103:MET:HE1	1:B:107:LEU:HB3	1.95	0.49
1:D:422:ASN:C	1:D:422:ASN:HD22	2.16	0.49
1:B:55:GLY:O	1:B:56:LEU:C	2.50	0.49
1:C:190:ASP:HB3	1:C:193:LEU:HG	1.95	0.49
1:D:79:PHE:HD2	1:D:82:ILE:HD11	1.78	0.49
1:F:95:ARG:NE	1:F:149:GLU:OE2	2.45	0.49
1:H:175:TYR:OH	1:H:198:PRO:HA	2.13	0.49
1:H:299:ILE:HG12	1:H:315:TYR:CE1	2.48	0.49
1:F:280:ASN:ND2	1:F:281:THR:H	2.07	0.48
1:H:102:PHE:HB3	1:H:120:ASN:O	2.12	0.48
1:H:103:MET:CE	1:H:107:LEU:CB	2.90	0.48
1:A:422:ASN:ND2	1:A:425:ARG:H	2.11	0.48
1:H:406:GLU:HB3	1:H:482:GLN:HG3	1.95	0.48
1:F:66:GLU:HA	1:F:67:VAL:HB	1.94	0.48
1:A:278:GLU:OE2	4:A:1507:XYS:O2	2.31	0.48
1:E:227:ARG:HD2	1:E:260:VAL:HG21	1.95	0.48
1:B:353:THR:HG22	1:B:354:PHE:CD2	2.48	0.48
1:E:201:CYS:HA	1:E:228:HIS:HB2	1.95	0.48
1:D:409:VAL:HG13	1:D:480:ILE:HG23	1.94	0.48
1:G:373:ARG:HD2	7:G:2001:HOH:O	2.12	0.48
1:B:165:ASN:N	1:B:165:ASN:HD22	2.09	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:19:LYS:NZ	1:H:356:ASN:ND2	2.61	0.48
1:D:253:MET:O	1:D:256:GLN:HB2	2.14	0.48
6:H:1504:XYX:H2	7:H:2193:HOH:O	2.12	0.48
1:B:492:GLY:O	1:D:237:LYS:NZ	2.46	0.48
1:G:52:ARG:HB2	1:G:97:PHE:HB3	1.95	0.48
1:A:102:PHE:HB3	1:A:120:ASN:O	2.12	0.48
1:C:459:ALA:HA	1:C:464:ILE:HD12	1.95	0.48
1:D:303:LEU:HD21	1:D:352:PHE:CE2	2.48	0.48
1:D:175:TYR:O	1:D:175:TYR:CG	2.67	0.48
1:A:227:ARG:HD3	1:A:228:HIS:O	2.14	0.48
1:E:350:HIS:CE1	1:E:448:ALA:O	2.67	0.48
1:D:353:THR:HG22	1:D:354:PHE:CD2	2.48	0.48
1:A:166:PHE:CZ	4:A:1505:XYP:H2B	2.49	0.48
1:D:403:PRO:O	1:D:404:VAL:HG13	2.12	0.48
1:F:236:HIS:HD2	7:F:2064:HOH:O	1.96	0.48
1:D:226:SER:HA	1:D:275:HIS:O	2.13	0.48
1:H:227:ARG:HH12	1:H:256:GLN:NE2	2.08	0.48
1:H:24:THR:OG1	1:H:35:TYR:OH	2.31	0.48
1:C:162:ASN:HD22	1:C:204:SER:HB3	1.79	0.48
1:G:198:PRO:HG2	1:G:200:ILE:HG23	1.95	0.48
1:D:30:ALA:HA	1:D:35:TYR:CD2	2.49	0.48
1:C:197:GLY:O	1:C:225:VAL:HA	2.13	0.48
1:C:269:PHE:HB3	1:C:272:LEU:HG	1.94	0.48
1:C:102:PHE:HB3	1:C:120:ASN:O	2.13	0.48
1:A:269:PHE:HB3	1:A:272:LEU:HG	1.95	0.48
1:F:470:LEU:HD23	1:F:474:GLU:HG2	1.96	0.48
1:F:373:ARG:HD2	7:F:2001:HOH:O	2.13	0.48
1:B:172:LYS:HA	1:B:207:TRP:CH2	2.49	0.48
1:G:490:TYR:HB3	1:G:493:LEU:HB2	1.96	0.48
1:B:42:VAL:HG12	1:B:43:GLN:HE21	1.79	0.47
1:C:105:LYS:NZ	1:C:120:ASN:HD22	2.12	0.47
1:D:24:THR:HG23	1:D:53:GLY:HA3	1.96	0.47
1:F:68:GLU:HG2	7:F:2025:HOH:O	2.13	0.47
1:C:187:LYS:NZ	1:C:223:ASP:OD2	2.45	0.47
1:E:38:HIS:CE1	1:E:340:ALA:O	2.60	0.47
1:H:330:ALA:O	1:H:331:LEU:C	2.51	0.47
1:A:227:ARG:HH12	1:A:256:GLN:NE2	1.96	0.47
1:G:38:HIS:CE1	1:G:340:ALA:O	2.66	0.47
1:B:350:HIS:CD2	7:B:2120:HOH:O	2.55	0.47
1:E:215:CYS:HA	1:E:220:VAL:HB	1.97	0.47
1:G:200:ILE:HD11	1:G:208:ILE:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:GLU:OE1	1:A:396:LYS:NZ	2.37	0.47
1:C:103:MET:HE3	1:C:107:LEU:HB3	1.95	0.47
1:H:56:LEU:CD1	1:H:82:ILE:HG21	2.44	0.47
1:B:240:PHE:CD2	1:C:69:ILE:CD1	2.98	0.47
1:A:350:HIS:CE1	1:A:450:PRO:HG3	2.50	0.47
1:E:426:VAL:CG2	1:E:447:VAL:HG11	2.44	0.47
1:E:102:PHE:HB3	1:E:120:ASN:O	2.13	0.47
1:C:417:ASN:ND2	1:C:471:SER:OG	2.42	0.47
1:H:197:GLY:O	1:H:225:VAL:HA	2.15	0.47
1:F:208:ILE:HD13	1:F:260:VAL:HG13	1.97	0.47
1:G:350:HIS:HE1	1:G:450:PRO:HD3	1.77	0.47
1:F:436:PRO:HA	7:F:2118:HOH:O	2.13	0.47
1:C:19:LYS:NZ	1:C:356:ASN:HD21	2.13	0.47
1:G:218:ARG:HB3	1:G:218:ARG:HE	1.52	0.47
1:B:208:ILE:HD13	1:B:260:VAL:HG13	1.96	0.47
1:D:19:LYS:NZ	1:D:356:ASN:ND2	2.63	0.47
1:E:417:ASN:ND2	1:E:471:SER:OG	2.48	0.47
1:C:406:GLU:O	1:C:407:SER:CB	2.63	0.47
1:A:306:GLY:O	1:A:310:VAL:HG22	2.15	0.47
1:A:415:ILE:HD13	1:A:417:ASN:ND2	2.30	0.47
1:C:63:ILE:HA	1:C:78:ASN:O	2.14	0.47
1:F:232:SER:CB	1:F:282:SER:HA	2.45	0.47
1:H:226:SER:HA	1:H:275:HIS:O	2.15	0.47
1:F:428:LYS:HE2	1:H:495:ASP:OD2	2.14	0.47
1:F:96:PRO:HB2	1:F:98:ILE:HG13	1.96	0.47
1:A:63:ILE:O	1:A:77:TYR:HA	2.15	0.46
1:H:103:MET:HE2	1:H:107:LEU:CB	2.46	0.46
1:D:54:HIS:NE2	4:D:1505:XYP:O3B	2.44	0.46
1:G:235:PRO:HG3	1:G:243:TYR:CD1	2.50	0.46
1:F:169:ASP:O	1:F:170:ALA:C	2.52	0.46
1:F:288:PRO:HA	1:F:334:GLY:HA2	1.98	0.46
1:D:422:ASN:ND2	1:D:424:TRP:HB3	2.27	0.46
1:B:28:GLY:O	7:B:2012:HOH:O	2.21	0.46
1:E:273:PRO:HA	1:E:311:ASP:OD2	2.15	0.46
1:F:157:VAL:HG22	1:F:182:THR:HG21	1.96	0.46
1:D:400:LEU:HD23	1:D:402:ILE:HD11	1.97	0.46
1:G:285:PRO:O	1:G:335:GLY:HA2	2.15	0.46
1:F:241:GLU:O	1:F:286:ILE:HB	2.16	0.46
1:D:232:SER:HB3	1:D:282:SER:HA	1.98	0.46
1:F:304:SER:OG	1:F:365:ARG:HD2	2.15	0.46
1:B:459:ALA:HB2	1:B:464:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:CYS:SG	1:B:222:VAL:HG21	2.56	0.46
1:F:35:TYR:HB2	1:F:321:VAL:HG11	1.96	0.46
1:B:227:ARG:HH12	1:B:256:GLN:NE2	1.99	0.46
1:B:103:MET:CG	1:B:122:THR:O	2.62	0.46
1:C:194:GLN:OE1	1:C:223:ASP:HB3	2.16	0.46
1:D:185:ALA:O	1:D:189:VAL:HG23	2.15	0.46
1:D:239:THR:C	1:D:241:GLU:H	2.18	0.46
1:B:227:ARG:HD2	1:B:260:VAL:HG21	1.98	0.46
1:H:140:HIS:HE1	7:H:2049:HOH:O	1.97	0.46
1:A:347:PRO:O	1:A:350:HIS:HB2	2.15	0.46
1:D:357:ALA:HB3	1:D:477:LEU:HD11	1.97	0.46
1:H:232:SER:CB	1:H:282:SER:HA	2.45	0.46
1:F:308:ASP:OD2	1:F:365:ARG:NH2	2.49	0.46
1:C:172:LYS:HA	1:C:207:TRP:CH2	2.50	0.46
1:A:24:THR:HG1	1:A:35:TYR:HH	1.63	0.46
1:H:39:LEU:HB3	1:H:92:LEU:HD13	1.96	0.46
1:G:426:VAL:HG21	1:G:447:VAL:CG1	2.45	0.46
1:B:285:PRO:HB3	1:B:336:PHE:CE1	2.51	0.46
1:B:162:ASN:HA	1:B:207:TRP:CZ2	2.50	0.46
1:E:241:GLU:O	1:E:286:ILE:HB	2.15	0.46
1:B:425:ARG:O	1:B:428:LYS:HB2	2.15	0.46
1:B:26:ARG:HD3	1:B:117:TRP:CD2	2.51	0.46
1:E:346:LYS:O	1:E:349:PHE:HB3	2.16	0.45
1:E:415:ILE:CD1	1:E:417:ASN:CG	2.84	0.45
1:A:229:ALA:O	1:A:279:TYR:HA	2.15	0.45
1:E:148:GLU:OE1	7:E:2074:HOH:O	2.20	0.45
1:B:103:MET:HE1	1:B:107:LEU:HD13	1.97	0.45
1:B:103:MET:HE3	1:B:107:LEU:HB3	1.97	0.45
1:A:214:PHE:CE1	1:A:218:ARG:HD3	2.51	0.45
1:B:157:VAL:HG11	1:B:179:TYR:HA	1.97	0.45
1:C:185:ALA:O	1:C:189:VAL:HG23	2.16	0.45
1:F:64:TYR:HB3	1:F:104:PRO:CB	2.45	0.45
1:B:30:ALA:HA	1:B:35:TYR:CD2	2.50	0.45
1:D:278:GLU:OE2	4:D:1505:XYP:O2B	2.34	0.45
1:A:420:TYR:CE2	1:A:451:HIS:HD2	2.34	0.45
1:C:227:ARG:CD	1:C:260:VAL:HG21	2.46	0.45
1:B:157:VAL:HG22	1:B:182:THR:HG21	1.99	0.45
1:E:39:LEU:HB3	1:E:92:LEU:HD13	1.98	0.45
1:A:162:ASN:HD22	1:A:204:SER:HB3	1.82	0.45
1:E:113:THR:HA	1:E:119:GLY:O	2.16	0.45
1:F:493:LEU:HD23	1:F:493:LEU:C	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:31:LEU:HB3	1:H:32:GLN:HG2	1.99	0.45
1:G:239:THR:C	1:G:241:GLU:H	2.20	0.45
1:C:103:MET:HE2	1:C:107:LEU:HD13	1.98	0.45
1:F:38:HIS:ND1	1:F:339:VAL:CG1	2.79	0.45
1:F:409:VAL:HG13	1:F:480:ILE:HG23	1.97	0.45
1:B:49:ARG:HG3	7:B:2025:HOH:O	2.16	0.45
1:A:278:GLU:HG2	1:A:316:TRP:CD2	2.52	0.45
1:E:346:LYS:O	1:E:350:HIS:HD2	1.99	0.45
1:H:54:HIS:CE1	1:H:159:ASN:ND2	2.83	0.45
1:A:422:ASN:HD22	1:A:425:ARG:H	1.65	0.45
1:A:341:LEU:O	1:A:342:HIS:HB2	2.17	0.45
1:C:337:GLY:O	1:C:346:LYS:HD2	2.17	0.45
1:A:490:TYR:HB3	1:A:493:LEU:HB2	1.98	0.45
1:H:66:GLU:HA	1:H:74:LYS:O	2.17	0.45
1:D:63:ILE:HD11	1:D:82:ILE:CG1	2.41	0.45
1:F:172:LYS:HA	1:F:207:TRP:CH2	2.51	0.45
1:F:409:VAL:CG1	1:F:480:ILE:HG23	2.47	0.45
1:C:490:TYR:HB3	1:C:493:LEU:HB2	1.99	0.45
1:D:200:ILE:HD11	1:D:208:ILE:HD12	1.97	0.45
1:A:208:ILE:HD13	1:A:260:VAL:HG13	1.97	0.45
1:G:405:SER:C	1:G:406:GLU:HG3	2.37	0.45
1:G:227:ARG:O	1:G:276:ILE:HA	2.17	0.45
1:F:350:HIS:CE1	1:F:448:ALA:O	2.70	0.45
1:B:342:HIS:CE1	1:B:441:VAL:HG21	2.52	0.45
1:A:341:LEU:HG	7:A:2115:HOH:O	2.17	0.45
1:G:320:ASP:CG	1:G:333:HIS:HE1	2.21	0.45
1:C:306:GLY:O	1:C:310:VAL:HG22	2.17	0.45
1:A:83:ASP:OD2	1:D:435:PHE:HB3	2.16	0.45
1:E:281:THR:OG1	1:E:295:ASN:ND2	2.48	0.44
1:F:280:ASN:HD22	1:F:281:THR:N	2.08	0.44
1:G:350:HIS:CB	1:G:416:VAL:HG11	2.46	0.44
1:B:409:VAL:CG1	1:B:480:ILE:HG23	2.45	0.44
1:C:232:SER:HB3	1:C:282:SER:HA	1.99	0.44
1:D:43:GLN:HE22	1:D:48:PHE:HB2	1.82	0.44
1:E:362:LEU:HD11	1:E:365:ARG:HB2	2.00	0.44
1:G:102:PHE:HB3	1:G:120:ASN:O	2.18	0.44
1:G:95:ARG:HG3	7:G:2021:HOH:O	2.17	0.44
1:F:71:GLY:HA2	7:F:2025:HOH:O	2.18	0.44
1:F:114:VAL:HG13	1:F:115:PHE:CD1	2.52	0.44
1:B:103:MET:HE3	1:B:104:PRO:HD2	2.00	0.44
1:E:429:GLN:NE2	1:G:454:THR:OG1	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:GLY:O	1:B:78:ASN:HB3	2.17	0.44
1:A:103:MET:CG	1:A:122:THR:O	2.59	0.44
1:G:162:ASN:ND2	1:G:204:SER:HB3	2.32	0.44
1:C:3:VAL:HG13	1:C:399:GLN:HB2	1.99	0.44
1:C:457:ARG:NH1	1:C:466:LEU:HD23	2.32	0.44
1:F:185:ALA:O	1:F:189:VAL:HG23	2.18	0.44
1:B:278:GLU:HG2	1:B:316:TRP:CD2	2.53	0.44
1:G:328:PRO:HB3	1:G:333:HIS:CD2	2.53	0.44
1:A:46:ILE:HD13	1:A:352:PHE:CB	2.48	0.44
1:F:43:GLN:HE22	1:F:48:PHE:HB2	1.83	0.44
1:B:54:HIS:HE1	1:B:159:ASN:CG	2.21	0.44
1:G:350:HIS:ND1	1:G:450:PRO:CG	2.79	0.44
1:D:103:MET:CE	1:D:107:LEU:HD13	2.47	0.44
1:H:228:HIS:CE1	1:H:278:GLU:HG3	2.53	0.44
1:B:423:ALA:HB2	1:B:448:ALA:HB2	1.99	0.44
1:B:320:ASP:CG	1:B:333:HIS:HE1	2.20	0.44
1:E:196:GLY:HA3	1:E:224:PHE:CE1	2.53	0.44
1:E:449:GLN:NE2	7:E:2164:HOH:O	2.50	0.44
1:D:105:LYS:HZ2	1:D:120:ASN:HD22	1.62	0.44
1:E:400:LEU:HD23	1:E:402:ILE:HD11	1.98	0.44
1:H:281:THR:OG1	1:H:295:ASN:ND2	2.51	0.44
1:F:256:GLN:O	1:F:260:VAL:HG23	2.18	0.44
1:B:374:ARG:NH2	1:B:479:GLU:OE1	2.51	0.44
1:B:197:GLY:O	1:B:225:VAL:HA	2.18	0.44
1:E:190:ASP:HB3	1:E:193:LEU:HG	2.00	0.44
1:B:446:GLN:HE22	1:D:412:LYS:HZ1	1.66	0.44
1:A:64:TYR:HB3	1:A:104:PRO:HB3	1.99	0.43
1:G:256:GLN:O	1:G:260:VAL:HG23	2.18	0.43
1:E:30:ALA:HA	1:E:35:TYR:CD2	2.53	0.43
1:G:127:TYR:CD1	1:G:177:LYS:HE2	2.52	0.43
1:E:335:GLY:O	1:E:346:LYS:NZ	2.51	0.43
1:H:18:TRP:CE3	1:H:19:LYS:HB3	2.53	0.43
1:H:63:ILE:HD11	1:H:82:ILE:CG1	2.46	0.43
1:D:278:GLU:OE2	4:D:1507:XYS:O2	2.36	0.43
1:D:303:LEU:O	7:D:2097:HOH:O	2.21	0.43
1:A:492:GLY:O	1:C:237:LYS:NZ	2.50	0.43
1:B:417:ASN:HB3	1:B:474:GLU:HA	1.99	0.43
1:E:56:LEU:CD1	1:E:82:ILE:HG21	2.48	0.43
1:H:373:ARG:CD	7:H:2139:HOH:O	2.65	0.43
1:D:298:TYR:C	1:D:298:TYR:CD2	2.92	0.43
1:E:285:PRO:HB3	1:E:336:PHE:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:290:HIS:CB	1:H:335:GLY:O	2.67	0.43
1:F:103:MET:HE1	1:F:107:LEU:HB3	2.00	0.43
1:A:106:ALA:O	1:A:125:LYS:NZ	2.41	0.43
1:A:468:ILE:HG22	1:A:470:LEU:HD23	2.01	0.43
1:H:63:ILE:O	1:H:77:TYR:HA	2.19	0.43
1:A:426:VAL:HG21	1:A:447:VAL:CG1	2.48	0.43
1:F:63:ILE:HD11	1:F:82:ILE:HG12	2.01	0.43
1:D:324:GLU:OE1	4:D:1505:XYP:O4B	2.37	0.43
7:B:2042:HOH:O	1:C:342:HIS:HE1	2.00	0.43
1:G:79:PHE:HD2	1:G:82:ILE:HD11	1.84	0.43
1:D:79:PHE:CG	1:D:140:HIS:CD2	3.06	0.43
1:F:339:VAL:CG1	1:F:343:SER:HA	2.49	0.43
1:F:414:GLN:O	1:F:476:THR:HA	2.19	0.43
1:B:493:LEU:C	1:B:493:LEU:HD23	2.39	0.43
1:H:30:ALA:HA	1:H:35:TYR:CD2	2.53	0.43
1:C:139:SER:O	1:C:143:GLU:HG3	2.19	0.43
1:D:415:ILE:CD1	1:D:417:ASN:ND2	2.82	0.43
1:E:350:HIS:HA	1:E:353:THR:HB	2.01	0.43
1:G:54:HIS:CE1	1:G:159:ASN:CG	2.87	0.43
1:G:374:ARG:NH2	1:G:479:GLU:OE1	2.51	0.43
1:B:229:ALA:O	1:B:279:TYR:HA	2.19	0.43
1:C:350:HIS:NE2	1:C:448:ALA:O	2.52	0.43
1:B:232:SER:OG	1:B:282:SER:HA	2.19	0.43
1:E:38:HIS:ND1	1:E:339:VAL:HG12	2.34	0.43
1:G:38:HIS:ND1	1:G:339:VAL:HG12	2.33	0.43
1:H:127:TYR:CD1	1:H:177:LYS:HE2	2.54	0.43
1:G:437:SER:HB2	1:G:439:GLN:NE2	2.33	0.43
1:H:79:PHE:CG	1:H:140:HIS:CD2	3.07	0.43
1:D:323:GLU:O	1:D:324:GLU:C	2.55	0.43
1:C:103:MET:HE2	1:C:107:LEU:HB3	1.97	0.43
1:C:79:PHE:CD2	1:C:82:ILE:HD11	2.46	0.43
1:F:54:HIS:HB2	7:F:2006:HOH:O	2.17	0.43
1:H:43:GLN:HE22	1:H:48:PHE:N	2.15	0.43
1:C:157:VAL:HG11	1:C:179:TYR:HA	2.00	0.43
1:A:444:LEU:HA	1:A:444:LEU:HD23	1.88	0.43
1:F:67:VAL:HG12	1:F:67:VAL:O	2.18	0.42
1:D:138:VAL:HG12	1:D:189:VAL:HG11	2.01	0.42
1:H:417:ASN:HB2	7:H:2180:HOH:O	2.18	0.42
1:B:50:TYR:HA	1:B:95:ARG:O	2.19	0.42
1:B:329:LYS:NZ	7:B:2110:HOH:O	2.52	0.42
1:F:215:CYS:SG	1:F:222:VAL:HG22	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:TRP:CZ3	1:D:19:LYS:HB3	2.54	0.42
1:C:191:PRO:HB3	1:E:213:HIS:CE1	2.54	0.42
1:F:451:HIS:CD2	7:F:2123:HOH:O	2.71	0.42
1:G:155:PHE:O	1:G:195:VAL:HA	2.19	0.42
1:D:182:THR:O	1:D:186:VAL:HG23	2.19	0.42
1:D:213:HIS:CB	7:D:2081:HOH:O	2.40	0.42
1:F:470:LEU:HD21	1:F:476:THR:CG2	2.48	0.42
1:F:187:LYS:HG3	1:F:221:PRO:CG	2.49	0.42
1:H:353:THR:HG23	7:H:2006:HOH:O	2.19	0.42
1:G:257:PHE:HB3	1:G:309:TYR:HB2	2.01	0.42
1:G:4:VAL:HB	1:G:400:LEU:HD12	2.02	0.42
1:F:402:ILE:CG2	1:F:403:PRO:HD2	2.49	0.42
1:G:447:VAL:HG13	7:G:2135:HOH:O	2.19	0.42
1:B:102:PHE:HB3	1:B:120:ASN:O	2.20	0.42
1:G:157:VAL:HG11	1:G:179:TYR:HA	2.02	0.42
1:H:28:GLY:HA3	1:H:60:ASP:OD2	2.20	0.42
1:G:291:ASP:HA	1:G:346:LYS:HD3	2.02	0.42
1:C:229:ALA:O	1:C:279:TYR:HA	2.19	0.42
1:B:298:TYR:CA	1:B:386:LEU:HD13	2.49	0.42
1:E:157:VAL:HG11	1:E:179:TYR:HA	2.01	0.42
1:F:102:PHE:HB3	1:F:120:ASN:O	2.18	0.42
1:G:313:PHE:N	1:G:313:PHE:CD1	2.88	0.42
1:H:79:PHE:HD2	1:H:82:ILE:HD11	1.83	0.42
1:F:228:HIS:ND1	1:F:278:GLU:HB2	2.35	0.42
1:B:223:ASP:O	1:B:273:PRO:HD2	2.19	0.42
1:H:299:ILE:HG12	1:H:315:TYR:HE1	1.84	0.42
1:C:350:HIS:CB	1:C:416:VAL:HG11	2.48	0.42
1:C:86:VAL:HB	1:C:145:TYR:OH	2.20	0.42
1:F:253:MET:O	1:F:256:GLN:HB2	2.20	0.42
1:H:52:ARG:NH2	1:H:228:HIS:HE1	2.18	0.42
1:C:34:GLU:O	1:C:38:HIS:CD2	2.73	0.42
1:C:157:VAL:HG22	1:C:182:THR:HG21	2.00	0.42
1:A:497:GLU:HB2	1:C:244:TYR:CG	2.55	0.42
1:G:38:HIS:CE1	1:G:339:VAL:HG12	2.54	0.42
1:G:54:HIS:CE1	1:G:159:ASN:ND2	2.86	0.42
1:H:400:LEU:HD23	1:H:402:ILE:HD11	2.01	0.42
1:H:50:TYR:HA	1:H:95:ARG:O	2.20	0.42
1:E:361:GLU:O	1:E:372:THR:HA	2.20	0.42
1:D:257:PHE:CE1	1:D:276:ILE:HG13	2.55	0.42
1:A:353:THR:HG22	1:A:354:PHE:CD2	2.54	0.42
1:F:204:SER:OG	1:F:207:TRP:CD1	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:446:GLN:HE22	1:D:412:LYS:CE	2.33	0.42
1:F:350:HIS:CG	1:F:416:VAL:HG11	2.54	0.41
1:G:330:ALA:O	1:G:333:HIS:HB3	2.19	0.41
1:H:316:TRP:O	1:H:336:PHE:HB3	2.20	0.41
1:C:256:GLN:O	1:C:260:VAL:HG23	2.20	0.41
1:F:419:GLN:OE1	7:F:2109:HOH:O	2.21	0.41
1:E:422:ASN:HD21	1:E:424:TRP:HB3	1.85	0.41
1:D:102:PHE:HB3	1:D:120:ASN:O	2.20	0.41
1:A:19:LYS:HZ3	1:A:356:ASN:ND2	2.18	0.41
1:A:66:GLU:HG3	1:A:106:ALA:HB1	2.03	0.41
1:A:342:HIS:CD2	7:A:2129:HOH:O	2.74	0.41
1:A:335:GLY:O	1:A:346:LYS:NZ	2.53	0.41
1:F:39:LEU:HB3	1:F:92:LEU:HD13	2.02	0.41
1:E:100:PHE:CD2	1:E:134:ILE:HD12	2.55	0.41
1:A:289:VAL:HB	1:C:498:ILE:HG23	2.02	0.41
1:E:428:LYS:HE3	1:G:495:ASP:OD2	2.20	0.41
1:C:103:MET:CE	1:C:104:PRO:HD2	2.50	0.41
1:B:43:GLN:HE22	1:B:48:PHE:N	2.17	0.41
1:E:342:HIS:ND1	1:E:441:VAL:HG21	2.35	0.41
1:A:317:THR:N	1:A:336:PHE:HB3	2.35	0.41
1:A:103:MET:HE3	1:A:104:PRO:HD2	2.00	0.41
1:D:19:LYS:HZ2	1:D:356:ASN:HD21	1.68	0.41
1:D:175:TYR:OH	1:D:198:PRO:HA	2.19	0.41
1:H:374:ARG:HA	5:H:1505:SO4:O1	2.20	0.41
1:B:161:PRO:HA	1:B:167:TRP:HB2	2.02	0.41
1:F:291:ASP:HA	1:F:346:LYS:HD3	2.03	0.41
1:C:353:THR:HG22	1:C:354:PHE:CD2	2.56	0.41
1:D:406:GLU:H	1:D:406:GLU:HG3	1.65	0.41
1:E:278:GLU:HG3	1:E:316:TRP:CE3	2.54	0.41
1:H:95:ARG:HD2	1:H:149:GLU:OE2	2.20	0.41
1:A:157:VAL:HG22	1:A:182:THR:HG21	2.03	0.41
1:G:264:ILE:O	1:G:270:PRO:HA	2.20	0.41
1:H:157:VAL:HG11	1:H:179:TYR:HA	2.03	0.41
1:C:26:ARG:HD3	1:C:117:TRP:CD2	2.55	0.41
1:H:165:ASN:H	1:H:165:ASN:HD22	1.68	0.41
1:F:497:GLU:HB3	1:H:244:TYR:CG	2.56	0.41
1:D:103:MET:HB3	1:D:120:ASN:HB3	2.03	0.41
1:B:316:TRP:O	1:B:336:PHE:HB3	2.21	0.41
1:H:492:GLY:O	1:H:493:LEU:C	2.57	0.41
6:H:1504:XYC1	7:H:2193:HOH:O	2.68	0.41
1:G:290:HIS:HB3	1:G:335:GLY:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:346:LYS:O	1:G:349:PHE:HB3	2.21	0.41
1:B:266:GLN:NE2	7:B:2085:HOH:O	2.54	0.41
1:D:304:SER:OG	1:D:365:ARG:HD2	2.20	0.41
1:B:294:LEU:O	1:B:294:LEU:HG	2.21	0.41
1:C:200:ILE:HD11	1:C:208:ILE:HD12	2.03	0.41
1:C:103:MET:HE1	1:C:104:PRO:HD2	2.02	0.41
1:A:79:PHE:CD1	1:A:140:HIS:ND1	2.88	0.41
1:G:350:HIS:CE1	1:G:448:ALA:O	2.74	0.41
1:G:64:TYR:HB3	1:G:104:PRO:CB	2.51	0.41
1:G:278:GLU:OE2	6:G:1504:XYS:O2	2.32	0.41
1:E:30:ALA:HA	1:E:35:TYR:CG	2.55	0.41
1:H:97:PHE:CE1	1:H:154:LEU:HD12	2.55	0.41
1:F:358:LEU:HD21	1:F:382:VAL:HG23	2.02	0.41
1:B:18:TRP:CE3	1:B:19:LYS:HB3	2.56	0.41
1:C:24:THR:C	1:C:25:GLY:O	2.55	0.41
1:E:240:PHE:CD1	1:H:67:VAL:HG13	2.56	0.41
1:G:63:ILE:HA	1:G:78:ASN:O	2.21	0.41
1:E:411:ILE:O	1:E:454:THR:HA	2.21	0.41
1:F:38:HIS:CE1	1:F:340:ALA:O	2.72	0.41
1:D:215:CYS:SG	1:D:222:VAL:HG22	2.60	0.41
1:C:38:HIS:HE1	1:C:340:ALA:O	2.04	0.41
1:F:490:TYR:HB3	1:F:493:LEU:HB2	2.02	0.41
1:C:115:PHE:HZ	6:C:1504:XYS:O3	2.04	0.41
1:C:419:GLN:HG2	7:C:2144:HOH:O	2.19	0.41
1:G:83:ASP:OD1	1:G:140:HIS:NE2	2.36	0.41
1:F:301:ARG:CB	7:F:2083:HOH:O	2.69	0.41
1:E:164:VAL:HG13	7:E:2054:HOH:O	2.21	0.41
1:B:4:VAL:HG11	1:B:364:TYR:CE2	2.55	0.41
1:E:354:PHE:CG	1:E:477:LEU:HB2	2.56	0.41
1:D:457:ARG:NH1	1:D:466:LEU:HD23	2.36	0.41
1:D:363:LEU:HD11	1:D:373:ARG:HB2	2.02	0.41
1:C:183:ALA:HA	1:C:195:VAL:HG21	2.02	0.41
1:A:103:MET:HE1	1:A:107:LEU:HB3	2.01	0.41
1:G:316:TRP:HA	1:G:317:THR:HA	1.88	0.41
1:E:197:GLY:O	1:E:225:VAL:HA	2.21	0.41
1:C:121:VAL:HB	1:C:166:PHE:O	2.21	0.41
1:B:301:ARG:O	1:B:304:SER:HB3	2.21	0.41
1:D:350:HIS:HB3	1:D:416:VAL:HG11	2.02	0.40
1:H:18:TRP:CZ3	1:H:19:LYS:HB3	2.56	0.40
1:C:426:VAL:HG21	1:C:447:VAL:CG1	2.50	0.40
1:E:338:LEU:CD2	1:E:348:THR:HG22	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:LEU:O	1:B:63:ILE:HD12	2.21	0.40
1:A:350:HIS:NE2	1:A:448:ALA:O	2.41	0.40
1:H:275:HIS:HB3	1:H:312:SER:OG	2.20	0.40
1:D:415:ILE:HD11	1:D:417:ASN:ND2	2.36	0.40
1:A:169:ASP:O	1:A:170:ALA:C	2.59	0.40
1:F:19:LYS:HZ1	1:F:47:GLY:HA3	1.86	0.40
1:D:159:ASN:OD1	1:D:228:HIS:NE2	2.45	0.40
1:H:370:ILE:O	1:H:381:ALA:HA	2.21	0.40
1:H:296:ALA:HB3	7:H:2113:HOH:O	2.22	0.40
1:H:301:ARG:O	1:H:304:SER:HB3	2.21	0.40
1:A:103:MET:O	1:A:120:ASN:HB3	2.21	0.40
1:G:232:SER:CB	1:G:282:SER:HA	2.50	0.40
1:B:353:THR:HG22	1:B:354:PHE:HD2	1.86	0.40
1:E:306:GLY:O	1:E:310:VAL:HG22	2.21	0.40
1:D:114:VAL:O	1:D:115:PHE:HB2	2.22	0.40
1:A:267:SER:HB2	1:A:268:PRO:HD2	2.02	0.40
1:F:499:THR:HG22	1:H:294:LEU:CD1	2.51	0.40
1:C:369:MET:HB2	1:C:383:LEU:HG	2.03	0.40
1:G:38:HIS:ND1	1:G:339:VAL:CG1	2.83	0.40
1:H:414:GLN:HA	1:H:451:HIS:O	2.22	0.40
1:F:200:ILE:HD12	7:F:2058:HOH:O	2.21	0.40
1:F:126:ASP:OD1	1:F:128:ASN:HB2	2.22	0.40
1:H:313:PHE:N	1:H:313:PHE:CD1	2.89	0.40
1:G:227:ARG:HD2	1:G:260:VAL:HG21	2.02	0.40
1:F:38:HIS:CE1	1:F:339:VAL:HG12	2.56	0.40
1:F:187:LYS:HG3	1:F:221:PRO:HG2	2.03	0.40
1:F:232:SER:OG	1:F:282:SER:HA	2.22	0.40
1:B:406:GLU:O	1:B:408:ALA:N	2.54	0.40
1:F:357:ALA:CB	1:F:477:LEU:HD11	2.52	0.40
1:C:318:PHE:CE1	1:C:319:SER:HB2	2.57	0.40
1:D:317:THR:N	1:D:336:PHE:HB3	2.37	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)
1:E:392:GLU:O	1:F:399:GLN:NE2[1_655]	2.19	0.01

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	499/503 (99%)	465 (93%)	32 (6%)	2 (0%)	39	56
1	B	499/503 (99%)	469 (94%)	28 (6%)	2 (0%)	39	56
1	C	499/503 (99%)	475 (95%)	22 (4%)	2 (0%)	39	56
1	D	499/503 (99%)	466 (93%)	29 (6%)	4 (1%)	24	35
1	E	499/503 (99%)	470 (94%)	27 (5%)	2 (0%)	39	56
1	F	499/503 (99%)	468 (94%)	28 (6%)	3 (1%)	30	43
1	G	499/503 (99%)	469 (94%)	27 (5%)	3 (1%)	30	43
1	H	499/503 (99%)	469 (94%)	25 (5%)	5 (1%)	19	28
All	All	3992/4024 (99%)	3751 (94%)	218 (6%)	23 (1%)	30	43

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	404	VAL
1	E	67	VAL
1	E	407	SER
1	F	67	VAL
1	G	67	VAL
1	H	67	VAL
1	A	67	VAL
1	B	67	VAL
1	B	407	SER
1	C	67	VAL
1	D	67	VAL
1	H	70	ASP
1	H	407	SER
1	A	204	SER
1	D	70	ASP
1	F	407	SER
1	H	204	SER

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Mol	Chain	Res	Type
1	C	407	SER
1	D	281	THR
1	F	281	THR
1	G	204	SER
1	G	326	ASP
1	H	321	VAL

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	439/441 (100%)	397 (90%)	42 (10%)	10	15
1	B	439/441 (100%)	395 (90%)	44 (10%)	9	14
1	C	438/441 (99%)	398 (91%)	40 (9%)	12	17
1	D	439/441 (100%)	396 (90%)	43 (10%)	10	14
1	E	439/441 (100%)	401 (91%)	38 (9%)	13	19
1	F	439/441 (100%)	403 (92%)	36 (8%)	14	21
1	G	439/441 (100%)	409 (93%)	30 (7%)	20	31
1	H	439/441 (100%)	407 (93%)	32 (7%)	17	27
All	All	3511/3528 (100%)	3206 (91%)	305 (9%)	13	19

All (305) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	11	ARG
1	A	16	LYS
1	A	33	LYS
1	A	35	TYR
1	A	39	LEU
1	A	66	GLU
1	A	74	LYS
1	A	82	ILE

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Mol	Chain	Res	Type
1	A	95	ARG
1	A	98	ILE
1	A	105	LYS
1	A	107	LEU
1	A	133	LEU
1	A	173	GLN
1	A	201	CYS
1	A	222	VAL
1	A	251	GLU
1	A	280	ASN
1	A	294	LEU
1	A	299	ILE
1	A	319	SER
1	A	325	MET
1	A	353	THR
1	A	374	ARG
1	A	394	LEU
1	A	397	GLU
1	A	400	LEU
1	A	404	VAL
1	A	409	VAL
1	A	415	ILE
1	A	419	GLN
1	A	422	ASN
1	A	425	ARG
1	A	439	GLN
1	A	447	VAL
1	A	463	VAL
1	A	465	HIS
1	A	467	SER
1	A	470	LEU
1	A	477	LEU
1	A	481	GLU
1	B	3	VAL
1	B	5	ASN
1	B	9	ASN
1	B	11	ARG
1	B	15	LYS
1	B	27	LEU
1	B	39	LEU
1	B	74	LYS
1	B	82	ILE

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Mol	Chain	Res	Type
1	B	95	ARG
1	B	97	PHE
1	B	98	ILE
1	B	107	LEU
1	B	116	TYR
1	B	133	LEU
1	B	154	LEU
1	B	164	VAL
1	B	165	ASN
1	B	201	CYS
1	B	204	SER
1	B	251	GLU
1	B	258	LYS
1	B	265	ARG
1	B	280	ASN
1	B	294	LEU
1	B	299	ILE
1	B	325	MET
1	B	353	THR
1	B	374	ARG
1	B	404	VAL
1	B	406	GLU
1	B	407	SER
1	B	409	VAL
1	B	415	ILE
1	B	422	ASN
1	B	428	LYS
1	B	442	GLU
1	B	445	ARG
1	B	447	VAL
1	B	464	ILE
1	B	467	SER
1	B	477	LEU
1	B	481	GLU
1	B	500	SER
1	C	3	VAL
1	C	8	SER
1	C	11	ARG
1	C	27	LEU
1	C	35	TYR
1	C	39	LEU
1	C	66	GLU

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Mol	Chain	Res	Type
1	C	82	ILE
1	C	95	ARG
1	C	97	PHE
1	C	98	ILE
1	C	103	MET
1	C	105	LYS
1	C	107	LEU
1	C	133	LEU
1	C	201	CYS
1	C	219	ARG
1	C	251	GLU
1	C	259	THR
1	C	280	ASN
1	C	282	SER
1	C	299	ILE
1	C	325	MET
1	C	328	PRO
1	C	353	THR
1	C	374	ARG
1	C	389	GLU
1	C	392	GLU
1	C	396	LYS
1	C	400	LEU
1	C	415	ILE
1	C	416	VAL
1	C	419	GLN
1	C	422	ASN
1	C	425	ARG
1	C	447	VAL
1	C	455	GLU
1	C	463	VAL
1	C	464	ILE
1	C	477	LEU
1	D	3	VAL
1	D	9	ASN
1	D	27	LEU
1	D	39	LEU
1	D	66	GLU
1	D	82	ILE
1	D	95	ARG
1	D	97	PHE
1	D	98	ILE

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Mol	Chain	Res	Type
1	D	105	LYS
1	D	107	LEU
1	D	125	LYS
1	D	133	LEU
1	D	164	VAL
1	D	201	CYS
1	D	219	ARG
1	D	228	HIS
1	D	231	THR
1	D	251	GLU
1	D	265	ARG
1	D	280	ASN
1	D	282	SER
1	D	294	LEU
1	D	328	PRO
1	D	353	THR
1	D	373	ARG
1	D	374	ARG
1	D	390	LYS
1	D	394	LEU
1	D	397	GLU
1	D	404	VAL
1	D	406	GLU
1	D	407	SER
1	D	415	ILE
1	D	416	VAL
1	D	422	ASN
1	D	425	ARG
1	D	438	ARG
1	D	458	ARG
1	D	464	ILE
1	D	471	SER
1	D	477	LEU
1	D	481	GLU
1	E	12	GLU
1	E	19	LYS
1	E	27	LEU
1	E	33	LYS
1	E	39	LEU
1	E	70	ASP
1	E	82	ILE
1	E	95	ARG

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Mol	Chain	Res	Type
1	E	97	PHE
1	E	98	ILE
1	E	107	LEU
1	E	133	LEU
1	E	173	GLN
1	E	201	CYS
1	E	219	ARG
1	E	222	VAL
1	E	233	LYS
1	E	251	GLU
1	E	280	ASN
1	E	282	SER
1	E	299	ILE
1	E	319	SER
1	E	325	MET
1	E	374	ARG
1	E	375	LYS
1	E	389	GLU
1	E	404	VAL
1	E	415	ILE
1	E	416	VAL
1	E	419	GLN
1	E	422	ASN
1	E	425	ARG
1	E	447	VAL
1	E	464	ILE
1	E	467	SER
1	E	477	LEU
1	E	481	GLU
1	E	500	SER
1	F	3	VAL
1	F	8	SER
1	F	19	LYS
1	F	33	LYS
1	F	39	LEU
1	F	69	ILE
1	F	82	ILE
1	F	95	ARG
1	F	97	PHE
1	F	107	LEU
1	F	116	TYR
1	F	133	LEU

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Mol	Chain	Res	Type
1	F	164	VAL
1	F	168	LYS
1	F	201	CYS
1	F	219	ARG
1	F	279	TYR
1	F	280	ASN
1	F	282	SER
1	F	299	ILE
1	F	304	SER
1	F	319	SER
1	F	325	MET
1	F	353	THR
1	F	374	ARG
1	F	396	LYS
1	F	397	GLU
1	F	400	LEU
1	F	422	ASN
1	F	425	ARG
1	F	428	LYS
1	F	453	MET
1	F	464	ILE
1	F	467	SER
1	F	477	LEU
1	F	502	SER
1	G	39	LEU
1	G	66	GLU
1	G	82	ILE
1	G	95	ARG
1	G	97	PHE
1	G	98	ILE
1	G	105	LYS
1	G	107	LEU
1	G	133	LEU
1	G	201	CYS
1	G	218	ARG
1	G	222	VAL
1	G	233	LYS
1	G	251	GLU
1	G	280	ASN
1	G	282	SER
1	G	299	ILE
1	G	313	PHE

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Mol	Chain	Res	Type
1	G	325	MET
1	G	353	THR
1	G	374	ARG
1	G	396	LYS
1	G	409	VAL
1	G	416	VAL
1	G	422	ASN
1	G	425	ARG
1	G	439	GLN
1	G	447	VAL
1	G	464	ILE
1	G	477	LEU
1	H	15	LYS
1	H	27	LEU
1	H	33	LYS
1	H	35	TYR
1	H	39	LEU
1	H	70	ASP
1	H	74	LYS
1	H	82	ILE
1	H	95	ARG
1	H	116	TYR
1	H	133	LEU
1	H	165	ASN
1	H	201	CYS
1	H	222	VAL
1	H	227	ARG
1	H	280	ASN
1	H	282	SER
1	H	313	PHE
1	H	328	PRO
1	H	374	ARG
1	H	396	LYS
1	H	407	SER
1	H	409	VAL
1	H	416	VAL
1	H	422	ASN
1	H	425	ARG
1	H	439	GLN
1	H	457	ARG
1	H	458	ARG
1	H	464	ILE

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Mol	Chain	Res	Type
1	H	467	SER
1	H	477	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (104) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	236	HIS
1	A	256	GLN
1	A	280	ASN
1	A	290	HIS
1	A	295	ASN
1	A	333	HIS
1	A	342	HIS
1	A	356	ASN
1	A	385	ASN
1	A	422	ASN
1	A	429	GLN
1	A	439	GLN
1	A	449	GLN
1	B	9	ASN
1	B	43	GLN
1	B	165	ASN
1	B	192	HIS
1	B	228	HIS
1	B	256	GLN
1	B	280	ASN
1	B	295	ASN
1	B	356	ASN
1	B	385	ASN
1	B	422	ASN
1	B	429	GLN
1	B	439	GLN
1	B	446	GLN
1	B	449	GLN
1	C	43	GLN
1	C	54	HIS
1	C	236	HIS
1	C	256	GLN
1	C	280	ASN
1	C	290	HIS
1	C	342	HIS

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Mol	Chain	Res	Type
1	C	356	ASN
1	C	385	ASN
1	C	422	ASN
1	C	439	GLN
1	C	446	GLN
1	C	449	GLN
1	D	43	GLN
1	D	120	ASN
1	D	213	HIS
1	D	236	HIS
1	D	256	GLN
1	D	266	GLN
1	D	280	ASN
1	D	290	HIS
1	D	295	ASN
1	D	356	ASN
1	D	385	ASN
1	D	419	GLN
1	D	422	ASN
1	E	43	GLN
1	E	213	HIS
1	E	236	HIS
1	E	256	GLN
1	E	280	ASN
1	E	356	ASN
1	E	385	ASN
1	E	422	ASN
1	E	429	GLN
1	E	449	GLN
1	F	43	GLN
1	F	165	ASN
1	F	256	GLN
1	F	280	ASN
1	F	356	ASN
1	F	385	ASN
1	F	399	GLN
1	F	422	ASN
1	F	429	GLN
1	F	449	GLN
1	F	451	HIS
1	G	38	HIS
1	G	43	GLN

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Mol	Chain	Res	Type
1	G	54	HIS
1	G	256	GLN
1	G	280	ASN
1	G	290	HIS
1	G	295	ASN
1	G	342	HIS
1	G	356	ASN
1	G	385	ASN
1	G	422	ASN
1	G	429	GLN
1	G	439	GLN
1	G	451	HIS
1	H	9	ASN
1	H	43	GLN
1	H	54	HIS
1	H	165	ASN
1	H	236	HIS
1	H	256	GLN
1	H	266	GLN
1	H	280	ASN
1	H	295	ASN
1	H	356	ASN
1	H	385	ASN
1	H	422	ASN
1	H	449	GLN
1	H	451	HIS

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 ⓘ

4 carbohydrates 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
4	XYP	A	1505	3,4	9,9,10	2.58	2 (22%)	12,12,14	1.53	2 (16%)
4	XYS	A	1507	1,4	9,9,10	1.90	3 (33%)	12,12,14	1.80	3 (25%)
4	XYP	D	1505	3,4	9,9,10	2.65	2 (22%)	12,12,14	1.78	2 (16%)
4	XYS	D	1507	1,4	9,9,10	1.92	3 (33%)	12,12,14	2.11	5 (41%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	XYP	A	1505	3,4	-	0/0/14/17	0/1/1/1
4	XYS	A	1507	1,4	-	0/0/14/17	0/1/1/1
4	XYP	D	1505	3,4	1/1/3/4	0/0/14/17	1/1/1/1
4	XYS	D	1507	1,4	-	0/0/14/17	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1505	XYP	O2B-C2B	-7.19	1.27	1.43
4	A	1505	XYP	O2B-C2B	-6.85	1.28	1.43
4	D	1507	XYS	C4-C3	2.04	1.55	1.52
4	A	1507	XYS	O5-C5	2.64	1.48	1.42
4	A	1507	XYS	C4-C3	2.65	1.56	1.52
4	D	1507	XYS	O5-C5	2.95	1.48	1.42
4	D	1505	XYP	C2B-C3B	3.03	1.56	1.52
4	D	1507	XYS	O5-C1	3.16	1.49	1.42
4	A	1507	XYS	O5-C1	3.18	1.49	1.42
4	A	1505	XYP	C2B-C3B	3.47	1.57	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1507	XYS	C4-C3-C2	-3.91	107.38	111.24
4	D	1507	XYS	C4-C3-C2	-3.89	107.39	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1507	XYS	C1-C2-C3	-3.47	105.44	109.54
4	D	1505	XYP	C4B-C3B-C2B	-3.36	107.92	111.24
4	A	1507	XYS	C1-C2-C3	-3.02	105.97	109.54
4	D	1507	XYS	O5-C1-C2	-2.48	105.67	110.31
4	A	1507	XYS	O5-C1-C2	-2.31	105.99	110.31
4	A	1505	XYP	C4B-C3B-C2B	-2.29	108.98	111.24
4	D	1507	XYS	C5-C4-C3	2.42	112.40	109.54
4	D	1507	XYS	C5-O5-C1	2.67	115.88	111.57
4	A	1505	XYP	C5B-O5B-C1B	4.02	118.04	111.57
4	D	1505	XYP	C5B-O5B-C1B	4.55	118.90	111.57

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	D	1505	XYP	C1B

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1505	XYP	C1B-C2B-C3B-C4B-C5B-O5B

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1505	XYP	2	0
4	A	1507	XYS	1	0
4	D	1505	XYP	4	0
4	D	1507	XYS	1	0

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 8 are monoatomic - leaving 16 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
3	ANX	A	1504	4	8,13,13	4.26	2 (25%)	10,18,18	2.17	4 (40%)
5	SO4	A	1506	-	4,4,4	0.24	0	6,6,6	0.33	0
6	XYS	B	1504	1	9,9,10	2.13	3 (33%)	12,12,14	2.09	3 (25%)
5	SO4	B	1505	-	4,4,4	0.36	0	6,6,6	0.33	0
6	XYS	C	1504	1	9,9,10	2.24	4 (44%)	12,12,14	2.68	4 (33%)
5	SO4	C	1505	-	4,4,4	0.35	0	6,6,6	0.25	0
3	ANX	D	1504	1,4	8,13,13	4.04	2 (25%)	10,18,18	2.90	4 (40%)
5	SO4	D	1506	-	4,4,4	0.29	0	6,6,6	0.19	0
6	XYS	E	1504	1	9,9,10	2.23	4 (44%)	12,12,14	2.85	5 (41%)
5	SO4	E	1505	-	4,4,4	0.21	0	6,6,6	0.69	0
6	XYS	F	1504	1	9,9,10	2.29	4 (44%)	12,12,14	2.72	3 (25%)
5	SO4	F	1505	-	4,4,4	0.39	0	6,6,6	0.37	0
6	XYS	G	1504	1	9,9,10	2.03	3 (33%)	12,12,14	2.74	5 (41%)
5	SO4	G	1505	-	4,4,4	0.47	0	6,6,6	0.74	0
6	XYS	H	1504	1	9,9,10	2.27	4 (44%)	12,12,14	2.51	6 (50%)
5	SO4	H	1505	-	4,4,4	0.45	0	6,6,6	0.26	0

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
3	ANX	A	1504	4	-	2/7/8/8	0/1/1/1
5	SO4	A	1506	-	-	0/0/0/0	0/0/0/0
6	XYS	B	1504	1	-	0/0/14/17	0/1/1/1
5	SO4	B	1505	-	-	0/0/0/0	0/0/0/0
6	XYS	C	1504	1	-	0/0/14/17	0/1/1/1
5	SO4	C	1505	-	-	0/0/0/0	0/0/0/0
3	ANX	D	1504	1,4	-	0/7/8/8	0/1/1/1
5	SO4	D	1506	-	-	0/0/0/0	0/0/0/0
6	XYS	E	1504	1	-	0/0/14/17	0/1/1/1
5	SO4	E	1505	-	-	0/0/0/0	0/0/0/0
6	XYS	F	1504	1	-	0/0/14/17	0/1/1/1
5	SO4	F	1505	-	-	0/0/0/0	0/0/0/0
6	XYS	G	1504	1	-	0/0/14/17	0/1/1/1
5	SO4	G	1505	-	-	0/0/0/0	0/0/0/0
6	XYS	H	1504	1	-	0/0/14/17	0/1/1/1
5	SO4	H	1505	-	-	0/0/0/0	0/0/0/0

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	1504	XYS	C2-C3	2.07	1.55	1.52
6	G	1504	XYS	O5-C5	2.20	1.47	1.42
6	B	1504	XYS	C5-C4	2.21	1.57	1.52
6	F	1504	XYS	C4-C3	2.25	1.55	1.52
6	E	1504	XYS	O5-C5	2.33	1.47	1.42
3	D	1504	ANX	O1-C1	2.42	1.41	1.36
6	F	1504	XYS	C5-C4	2.46	1.58	1.52
6	C	1504	XYS	C2-C3	2.50	1.55	1.52
6	C	1504	XYS	O5-C5	2.61	1.48	1.42
6	H	1504	XYS	O5-C5	2.63	1.48	1.42
6	G	1504	XYS	C4-C3	2.65	1.56	1.52
6	C	1504	XYS	C4-C3	2.68	1.56	1.52
6	E	1504	XYS	C2-C3	2.75	1.56	1.52
6	H	1504	XYS	C4-C3	2.84	1.56	1.52
6	E	1504	XYS	C4-C3	3.05	1.56	1.52
6	B	1504	XYS	O5-C5	3.07	1.48	1.42
6	F	1504	XYS	O5-C5	3.19	1.49	1.42
3	A	1504	ANX	O1-C1	3.39	1.43	1.36
6	G	1504	XYS	O5-C1	3.61	1.50	1.42
6	E	1504	XYS	O5-C1	4.17	1.51	1.42
6	B	1504	XYS	O5-C1	4.27	1.51	1.42
6	C	1504	XYS	O5-C1	4.48	1.51	1.42
6	F	1504	XYS	O5-C1	4.49	1.51	1.42
6	H	1504	XYS	O5-C1	4.73	1.52	1.42
3	D	1504	ANX	O42-N1	10.72	1.44	1.22
3	A	1504	ANX	O42-N1	11.15	1.44	1.22

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	1504	XYS	C1-C2-C3	-5.82	102.66	109.54
6	E	1504	XYS	C1-C2-C3	-5.71	102.79	109.54
6	G	1504	XYS	O5-C1-C2	-5.58	99.88	110.31
6	C	1504	XYS	C1-C2-C3	-5.49	103.04	109.54
6	F	1504	XYS	C1-C2-C3	-5.46	103.08	109.54
6	F	1504	XYS	C4-C3-C2	-5.46	105.85	111.24
6	C	1504	XYS	O5-C1-C2	-5.43	100.16	110.31
6	E	1504	XYS	O5-C1-C2	-5.11	100.76	110.31
6	B	1504	XYS	O5-C1-C2	-4.74	101.44	110.31
6	F	1504	XYS	O5-C1-C2	-4.64	101.64	110.31
6	H	1504	XYS	C1-C2-C3	-4.55	104.15	109.54
6	H	1504	XYS	O5-C1-C2	-4.20	102.46	110.31
6	H	1504	XYS	C4-C3-C2	-4.19	107.10	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1504	XYS	C1-C2-C3	-3.37	105.56	109.54
6	C	1504	XYS	O3-C3-C4	-3.28	104.08	110.00
6	E	1504	XYS	C4-C3-C2	-2.77	108.50	111.24
6	C	1504	XYS	O5-C5-C4	-2.76	105.16	110.31
3	A	1504	ANX	C3-C2-N2	-2.72	113.07	116.59
6	E	1504	XYS	O5-C5-C4	-2.71	105.23	110.31
3	D	1504	ANX	C3-C2-N2	-2.69	113.11	116.59
3	A	1504	ANX	O42-N1-C5	-2.34	114.69	118.89
6	H	1504	XYS	O4-C4-C5	-2.27	104.65	109.21
3	D	1504	ANX	C4-C3-C2	2.10	122.32	118.96
6	G	1504	XYS	C5-O5-C1	2.12	114.99	111.57
6	H	1504	XYS	O2-C2-C1	2.13	113.48	109.21
3	A	1504	ANX	C4-C5-N1	2.28	121.32	119.48
6	H	1504	XYS	O2-C2-C3	2.32	114.78	110.12
6	G	1504	XYS	C5-C4-C3	2.38	112.36	109.54
6	G	1504	XYS	O2-C2-C3	2.65	115.44	110.12
6	B	1504	XYS	C5-O5-C1	3.07	116.52	111.57
3	D	1504	ANX	C4-C5-N1	3.46	122.27	119.48
6	E	1504	XYS	O2-C2-C3	4.07	118.31	110.12
3	A	1504	ANX	C5-C6-C1	4.68	121.68	118.59
3	D	1504	ANX	C5-C6-C1	7.20	123.34	118.59

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1504	ANX	C6-C5-N1-O42
3	A	1504	ANX	C4-C5-N1-O42

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1504	ANX	1	0
6	B	1504	XYS	1	0
6	C	1504	XYS	1	0
6	G	1504	XYS	1	0
5	G	1505	SO4	1	0
6	H	1504	XYS	2	0
5	H	1505	SO4	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	501/503 (99%)	0.19	18 (3%) 46 47	17, 24, 43, 51	0
1	B	501/503 (99%)	0.27	28 (5%) 28 28	16, 24, 44, 52	0
1	C	501/503 (99%)	0.16	23 (4%) 36 37	16, 24, 43, 52	0
1	D	501/503 (99%)	0.25	19 (3%) 44 45	16, 24, 43, 51	0
1	E	501/503 (99%)	0.14	12 (2%) 62 61	15, 24, 41, 51	0
1	F	501/503 (99%)	0.35	32 (6%) 23 23	16, 24, 44, 52	0
1	G	501/503 (99%)	0.16	14 (2%) 56 55	16, 23, 42, 51	0
1	H	501/503 (99%)	0.14	18 (3%) 46 47	15, 23, 43, 51	0
All	All	4008/4024 (99%)	0.21	164 (4%) 41 42	15, 24, 43, 52	0

All (164) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	405	SER	9.0
1	D	405	SER	8.3
1	H	2	GLY	8.2
1	G	2	GLY	8.0
1	G	405	SER	6.0
1	F	404	VAL	5.9
1	A	405	SER	5.9
1	F	405	SER	5.7
1	G	393	GLY	5.6
1	A	71	GLY	5.5
1	A	461	ASP	5.3
1	H	70	ASP	4.9
1	B	459	ALA	4.9
1	B	461	ASP	4.8
1	C	405	SER	4.7
1	F	460	THR	4.6

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Mol	Chain	Res	Type	RSRZ
1	F	403	PRO	4.5
1	C	11	ARG	4.5
1	H	395	THR	4.4
1	C	461	ASP	4.3
1	B	460	THR	4.2
1	G	461	ASP	4.2
1	G	5	ASN	4.2
1	C	459	ALA	4.2
1	C	393	GLY	4.1
1	B	2	GLY	4.1
1	F	128	ASN	4.1
1	F	459	ALA	4.1
1	G	70	ASP	4.1
1	A	393	GLY	4.0
1	H	405	SER	4.0
1	D	395	THR	4.0
1	C	394	LEU	3.9
1	F	461	ASP	3.9
1	G	3	VAL	3.9
1	G	394	LEU	3.9
1	A	460	THR	3.9
1	B	213	HIS	3.9
1	B	463	VAL	3.8
1	F	70	ASP	3.8
1	H	461	ASP	3.8
1	F	8	SER	3.8
1	D	70	ASP	3.7
1	H	393	GLY	3.7
1	B	11	ARG	3.6
1	G	404	VAL	3.6
1	D	394	LEU	3.6
1	C	395	THR	3.5
1	D	3	VAL	3.5
1	B	3	VAL	3.5
1	B	458	ARG	3.5
1	B	407	SER	3.4
1	B	72	GLU	3.4
1	A	404	VAL	3.4
1	D	8	SER	3.3
1	C	404	VAL	3.3
1	A	72	GLU	3.3
1	H	462	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	H	11	ARG	3.3
1	F	463	VAL	3.2
1	D	393	GLY	3.2
1	C	460	THR	3.2
1	A	403	PRO	3.2
1	D	404	VAL	3.2
1	G	395	THR	3.2
1	G	392	GLU	3.2
1	E	11	ARG	3.2
1	C	70	ASP	3.2
1	A	462	GLY	3.2
1	H	394	LEU	3.1
1	A	465	HIS	3.1
1	B	173	GLN	3.1
1	E	405	SER	3.1
1	D	461	ASP	3.1
1	E	393	GLY	3.1
1	D	2	GLY	3.1
1	E	465	HIS	3.0
1	H	5	ASN	3.0
1	D	148	GLU	3.0
1	B	404	VAL	3.0
1	C	458	ARG	3.0
1	F	458	ARG	3.0
1	B	69	ILE	2.9
1	F	67	VAL	2.9
1	H	392	GLU	2.9
1	E	460	THR	2.9
1	H	3	VAL	2.9
1	E	461	ASP	2.9
1	A	407	SER	2.9
1	B	408	ALA	2.9
1	F	246	GLU	2.8
1	F	265	ARG	2.8
1	A	406	GLU	2.8
1	H	213	HIS	2.8
1	F	406	GLU	2.8
1	C	3	VAL	2.8
1	C	392	GLU	2.8
1	F	47	GLY	2.8
1	C	2	GLY	2.8
1	C	403	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	8	SER	2.8
1	F	9	ASN	2.8
1	F	213	HIS	2.8
1	D	458	ARG	2.7
1	F	71	GLY	2.7
1	B	482	GLN	2.7
1	B	5	ASN	2.7
1	B	406	GLU	2.7
1	F	68	GLU	2.7
1	A	463	VAL	2.7
1	F	11	ARG	2.6
1	A	70	ASP	2.6
1	E	458	ARG	2.6
1	H	397	GLU	2.6
1	D	392	GLU	2.6
1	B	484	ARG	2.6
1	F	462	GLY	2.6
1	B	266	GLN	2.6
1	H	404	VAL	2.5
1	C	463	VAL	2.5
1	A	7	PRO	2.5
1	F	10	GLY	2.5
1	F	393	GLY	2.5
1	C	213	HIS	2.5
1	A	459	ALA	2.5
1	E	392	GLU	2.5
1	F	3	VAL	2.5
1	B	402	ILE	2.5
1	A	392	GLU	2.4
1	A	394	LEU	2.4
1	F	72	GLU	2.4
1	B	403	PRO	2.4
1	B	70	ASP	2.4
1	F	373	ARG	2.4
1	E	2	GLY	2.4
1	C	111	ASP	2.4
1	G	407	SER	2.4
1	C	217	GLU	2.4
1	F	5	ASN	2.3
1	B	393	GLY	2.3
1	H	111	ASP	2.3
1	F	394	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	12	GLU	2.2
1	E	459	ALA	2.2
1	G	391	GLY	2.2
1	H	463	VAL	2.2
1	B	462	GLY	2.2
1	C	360	ASP	2.2
1	B	465	HIS	2.2
1	G	375	LYS	2.2
1	E	3	VAL	2.1
1	D	111	ASP	2.1
1	D	496	GLY	2.1
1	D	397	GLU	2.1
1	F	130	TRP	2.1
1	H	458	ARG	2.1
1	D	213	HIS	2.1
1	C	407	SER	2.1
1	C	484	ARG	2.0
1	E	111	ASP	2.0
1	D	71	GLY	2.0
1	D	203	GLY	2.0
1	B	360	ASP	2.0
1	F	132	ASP	2.0

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](#)

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	XYS	A	1507	9/10	0.91	0.21	1.87	37,37,37,38	9
4	XYP	A	1505	9/10	0.91	0.20	1.38	37,37,38,38	9
4	XYS	D	1507	9/10	0.92	0.23	1.30	39,39,40,40	9
4	XYP	D	1505	9/10	0.90	0.20	0.73	39,39,40,41	9

6.4 Ligands ⓘ

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
3	ANX	A	1504	13/13	0.57	0.47	15.43	43,50,53,54	13
3	ANX	D	1504	13/13	0.77	0.38	5.89	41,44,46,46	13
6	XYS	F	1504	9/10	0.79	0.25	4.99	40,42,42,42	0
2	NA	A	1503	1/1	0.99	0.36	4.84	19,19,19,19	0
6	XYS	C	1504	9/10	0.76	0.26	3.26	35,38,40,41	0
6	XYS	G	1504	9/10	0.86	0.24	2.80	35,36,36,38	0
2	NA	E	1503	1/1	0.99	0.23	2.24	6,6,6,6	0
2	NA	F	1503	1/1	0.98	0.21	2.20	9,9,9,9	0
6	XYS	E	1504	9/10	0.77	0.25	2.14	36,37,38,39	0
5	SO4	H	1505	5/5	0.96	0.31	1.99	64,64,65,66	0
6	XYS	H	1504	9/10	0.84	0.20	1.94	29,29,32,33	0
6	XYS	B	1504	9/10	0.83	0.23	1.74	39,39,41,42	0
2	NA	D	1503	1/1	0.99	0.19	1.61	10,10,10,10	0
5	SO4	G	1505	5/5	0.96	0.31	1.18	55,55,55,56	0
2	NA	G	1503	1/1	0.99	0.22	0.88	9,9,9,9	0
5	SO4	A	1506	5/5	0.96	0.26	0.76	55,56,57,57	0
5	SO4	E	1505	5/5	0.96	0.24	0.69	56,58,58,59	0
5	SO4	F	1505	5/5	0.94	0.28	0.54	56,56,57,58	0
2	NA	C	1503	1/1	0.99	0.20	0.49	7,7,7,7	0
2	NA	B	1503	1/1	0.99	0.21	0.11	5,5,5,5	0
5	SO4	C	1505	5/5	0.96	0.21	-0.00	60,60,62,62	0
2	NA	H	1503	1/1	0.99	0.17	-0.04	4,4,4,4	0
5	SO4	B	1505	5/5	0.97	0.22	-0.07	58,59,60,61	0
5	SO4	D	1506	5/5	0.98	0.17	-0.45	58,59,59,60	0

6.5 Other polymers ⓘ

There are no such residues in this entry.