



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:28 AM GMT

PDB ID : 3IE0  
Title : Crystal Structure of S378Y mutant TTHA0252 from *Thermus thermophilus* HB8  
Authors : Ishikawa, H.; Nakagawa, N.; Kuramitsu, S.; Yokoyama, S.; Masui, R.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2009-07-22  
Resolution : 2.73 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

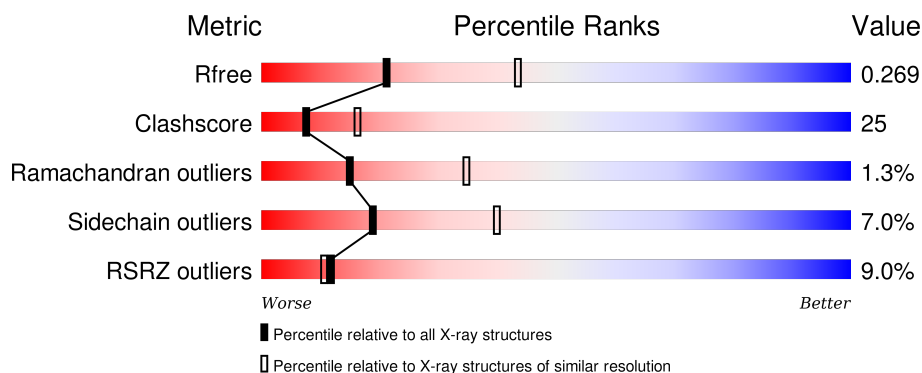
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.73 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	3050 (2.78-2.70)
Clashscore	102246	3424 (2.78-2.70)
Ramachandran outliers	100387	3367 (2.78-2.70)
Sidechain outliers	100360	3368 (2.78-2.70)
RSRZ outliers	91569	3055 (2.78-2.70)

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	431	<div> <div>2%</div> <div>67%</div> <div>29%</div> <div>.</div> </div>
1	B	431	<div> <div>%</div> <div>58%</div> <div>38%</div> <div>.</div> </div>
1	C	431	<div> <div>11%</div> <div>50%</div> <div>45%</div> <div>5%</div> </div>
1	D	431	<div> <div>21%</div> <div>49%</div> <div>48%</div> <div>.</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
2	SO4	A	438	-	-	-	X
2	SO4	A	442	-	-	-	X
2	SO4	A	448	-	-	-	X
2	SO4	B	433	-	-	X	-
2	SO4	B	437	-	-	-	X
2	SO4	B	441	-	-	-	X
2	SO4	B	446	-	-	X	-
2	SO4	B	447	-	-	-	X
2	SO4	B	448	-	-	X	-
2	SO4	C	434	-	-	-	X
2	SO4	C	436	-	-	-	X
2	SO4	C	441	-	-	-	X
2	SO4	D	433	-	-	X	-
2	SO4	D	434	-	-	-	X
3	FLC	B	451	-	-	X	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13790 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ribonuclease TTHA0252.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	0	0
			3332	2133	597	594	8			
1	B	431	Total	C	N	O	S	0	0	0
			3332	2133	597	594	8			
1	C	431	Total	C	N	O	S	0	0	0
			3332	2133	597	594	8			
1	D	431	Total	C	N	O	S	0	0	0
			3332	2133	597	594	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	378	TYR	SER	ENGINEERED	UNP Q5SLP1
B	378	TYR	SER	ENGINEERED	UNP Q5SLP1
C	378	TYR	SER	ENGINEERED	UNP Q5SLP1
D	378	TYR	SER	ENGINEERED	UNP Q5SLP1

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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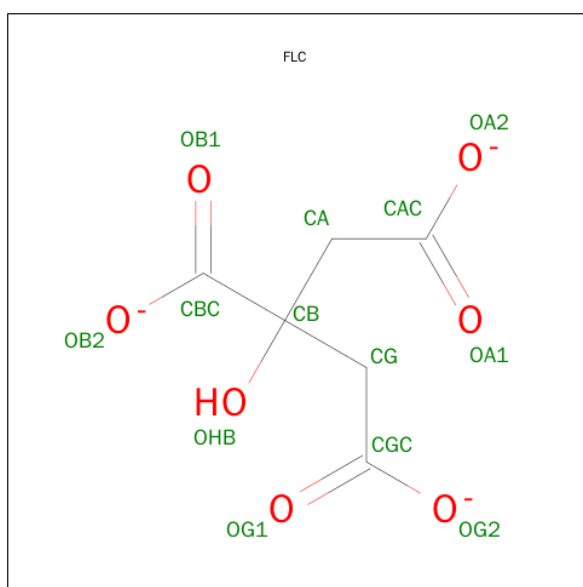
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula:  $C_6H_5O_7$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 13 6 7	0	0
3	A	1	Total C O 13 6 7	0	0
3	B	1	Total C O 13 6 7	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Zn 2 2	0	0
4	A	2	Total Zn 2 2	0	0
4	D	2	Total Zn 2 2	0	0
4	C	2	Total Zn 2 2	0	0

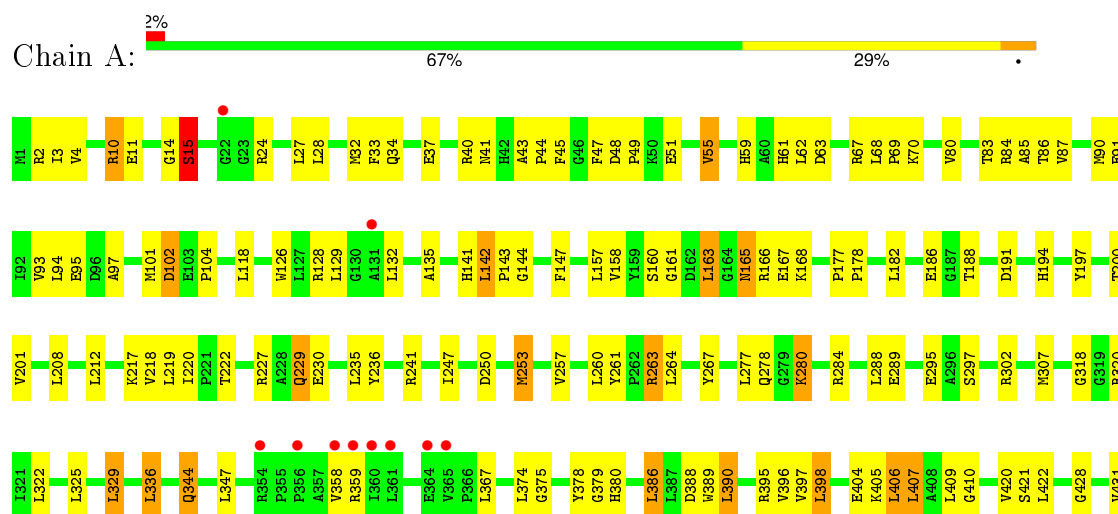
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	26	Total O 26 26	0	0
5	B	33	Total O 33 33	0	0
5	C	9	Total O 9 9	0	0
5	D	12	Total O 12 12	0	0

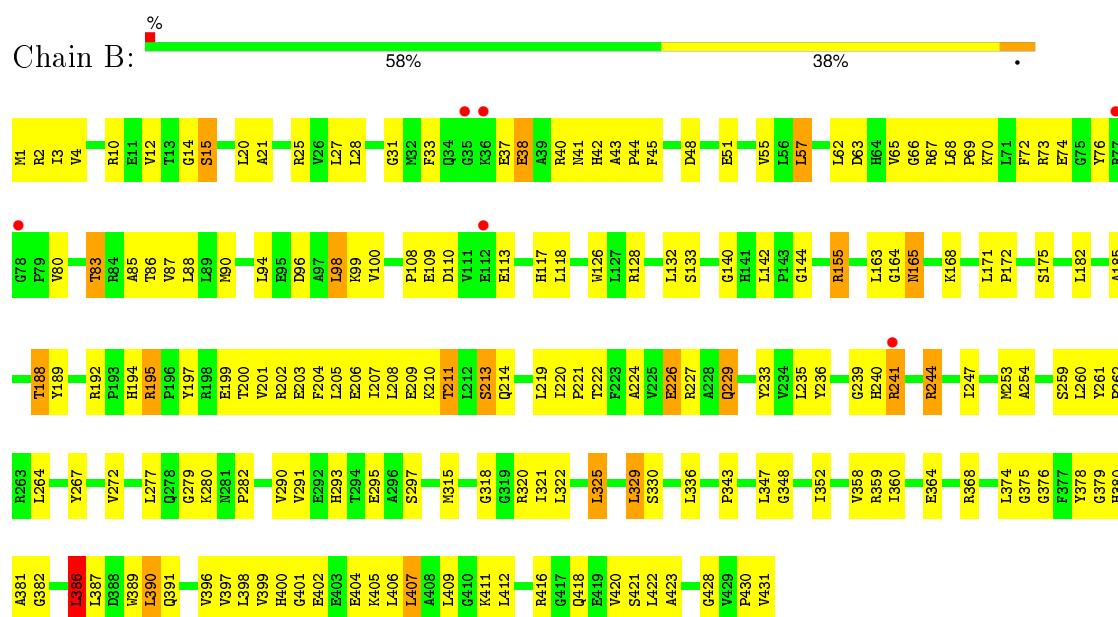
### 3 Residue-property plots

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: Ribonuclease TTHA0252

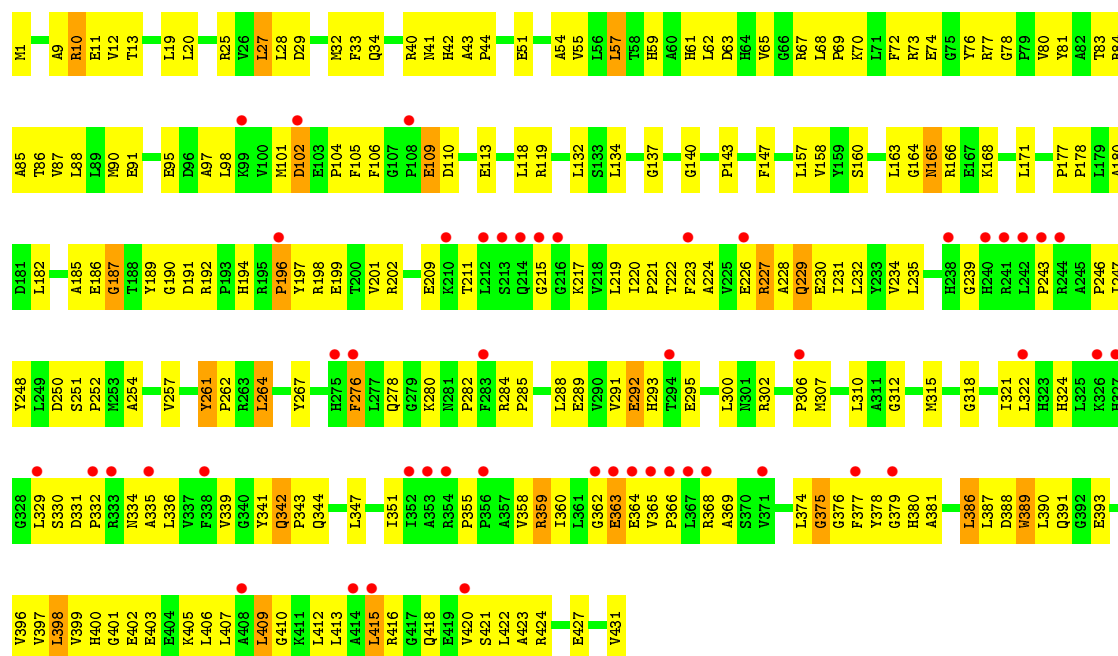


#### • Molecule 1: Ribonuclease TTHA0252

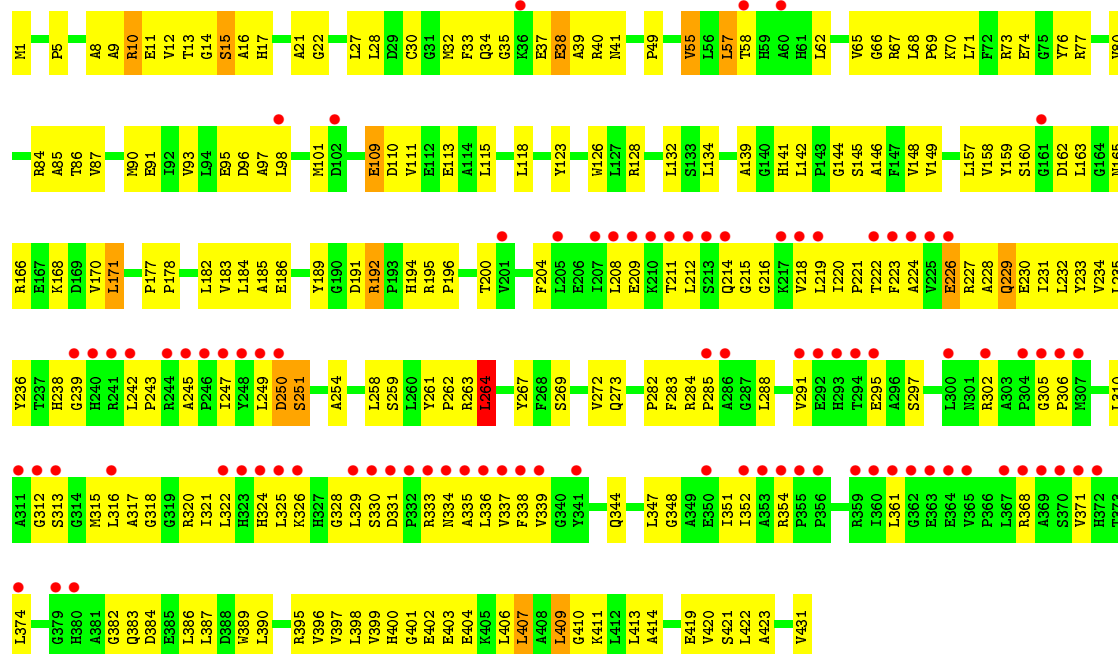


#### • Molecule 1: Ribonuclease TTHA0252





• Molecule 1: Ribonuclease TTHA0252



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	143.18Å 146.12Å 121.00Å 90.00° 109.51° 90.00°	Depositor
Resolution (Å)	50.00 – 2.73 41.86 – 2.73	Depositor EDS
% Data completeness (in resolution range)	96.1 (50.00-2.73) 96.1 (41.86-2.73)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.48 (at 2.73Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.218 , 0.272 0.216 , 0.269	Depositor DCC
$R_{free}$ test set	6035 reflections (10.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.6	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 55.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 61873 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13790	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FLC, ZN, 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	0.41	0/3414	0.68	2/4631 (0.0%)
1	B	0.39	0/3414	0.69	2/4631 (0.0%)
1	C	0.32	0/3414	0.59	0/4631
1	D	0.31	0/3414	0.58	0/4631
All	All	0.36	0/13656	0.64	4/18524 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	379	GLY	N-CA-C	7.17	131.03	113.10
1	B	379	GLY	N-CA-C	6.04	128.19	113.10
1	B	386	LEU	CA-CB-CG	5.79	128.62	115.30
1	A	161	GLY	N-CA-C	-5.29	99.86	113.10

There are no chirality outliers.

There are no planarity outliers.

### 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	3332	0	3355	121	0
1	B	3332	0	3355	162	0
1	C	3332	0	3355	208	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3332	0	3355	205	0
2	A	100	0	0	2	0
2	B	95	0	0	9	0
2	C	95	0	0	1	0
2	D	45	0	0	4	0
3	A	26	0	10	2	0
3	B	13	0	5	4	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	26	0	0	1	0
5	B	33	0	0	2	0
5	C	9	0	0	0	0
5	D	12	0	0	1	0
All	All	13790	0	13435	689	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

All (689) 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:A:263:ARG:HH21	1:A:263:ARG:HB3	1.00	1.14
1:C:73:ARG:HH21	1:C:106:PHE:HA	1.23	1.03
1:C:235:LEU:HD13	1:C:247:ILE:HD13	1.40	1.02
1:D:13:THR:CG2	1:D:33:PHE:HA	1.91	1.00
1:B:430:PRO:HG3	2:B:446:SO4:O3	1.62	0.98
1:B:83:THR:HG22	1:B:86:THR:H	1.29	0.96
1:C:33:PHE:H	1:C:41:ASN:HD21	1.12	0.94
1:B:33:PHE:H	1:B:41:ASN:HD21	1.11	0.93
1:A:263:ARG:HB3	1:A:263:ARG:NH2	1.85	0.92
1:D:235:LEU:HD13	1:D:247:ILE:HD13	1.50	0.91
1:A:263:ARG:CB	1:A:263:ARG:HH21	1.83	0.91
1:D:318:GLY:HA2	1:D:322:LEU:HD11	1.52	0.89
1:C:97:ALA:O	1:C:101:MET:HB2	1.75	0.86
1:C:342:GLN:HE21	1:C:342:GLN:HA	1.38	0.86
1:D:220:ILE:HG12	1:D:337:VAL:HB	1.59	0.85
1:B:37:GLU:HG3	1:B:40:ARG:HH11	1.40	0.85
1:B:48:ASP:OD2	1:B:51:GLU:HG2	1.78	0.84
1:B:359:ARG:HD2	1:B:364:GLU:OE1	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:387:LEU:HB3	1:C:416:ARG:HH12	1.44	0.82
1:D:211:THR:HG21	1:D:335:ALA:HB2	1.62	0.82
1:B:411:LYS:HG3	3:B:451:FLC:HA1	1.61	0.81
1:B:375:GLY:HA2	1:B:378:TYR:CE2	2.17	0.80
1:D:157:LEU:HD12	1:D:158:VAL:H	1.47	0.79
1:C:87:VAL:HG13	1:C:118:LEU:HD13	1.65	0.78
1:D:182:LEU:HD23	1:D:431:VAL:HG22	1.65	0.78
1:D:291:VAL:HG13	2:D:433:SO4:O1	1.83	0.78
1:B:83:THR:HG21	1:B:144:GLY:CA	2.13	0.78
1:D:284:ARG:HD3	1:D:288:LEU:HD23	1.66	0.78
1:B:31:GLY:O	1:B:67:ARG:HG3	1.83	0.77
1:D:13:THR:HG21	1:D:34:GLN:H	1.49	0.77
1:D:33:PHE:H	1:D:41:ASN:HD21	1.31	0.77
1:C:209:GLU:OE2	1:C:243:PRO:HD3	1.85	0.77
1:C:57:LEU:HD23	1:C:90:MET:HE1	1.67	0.76
1:A:91:GLU:O	1:A:95:GLU:HG2	1.86	0.76
1:C:342:GLN:HE21	1:C:343:PRO:HD2	1.51	0.76
1:B:12:VAL:HG12	1:B:401:GLY:HA2	1.68	0.76
1:A:10:ARG:HG2	1:A:10:ARG:HH11	1.51	0.76
1:C:222:THR:HG22	1:C:339:VAL:HG21	1.68	0.75
1:D:12:VAL:HG12	1:D:401:GLY:HA2	1.67	0.75
1:B:33:PHE:N	1:B:41:ASN:HD21	1.85	0.74
1:A:182:LEU:HD11	1:A:397:VAL:HG23	1.71	0.73
1:C:403:GLU:O	1:C:407:LEU:HD23	1.88	0.73
1:D:229:GLN:HG3	1:D:261:TYR:CE1	2.23	0.73
1:C:227:ARG:NH1	1:C:378:TYR:HA	2.04	0.73
1:C:73:ARG:NH2	1:C:106:PHE:HA	2.01	0.72
1:C:160:SER:HB2	1:C:163:LEU:HD21	1.72	0.72
1:C:25:ARG:HH11	1:C:51:GLU:HB3	1.53	0.72
1:B:43:ALA:HB1	1:B:44:PRO:HD2	1.71	0.72
1:D:12:VAL:CG1	1:D:401:GLY:HA2	2.21	0.71
1:D:160:SER:HB2	1:D:163:LEU:HD21	1.72	0.71
1:B:83:THR:HG21	1:B:144:GLY:HA3	1.71	0.71
1:B:70:LYS:HE3	1:B:74:GLU:OE1	1.90	0.71
1:A:128:ARG:O	1:A:129:LEU:HD23	1.90	0.71
1:D:13:THR:HG23	1:D:33:PHE:HA	1.70	0.71
1:B:99:LYS:HE2	5:B:472:HOH:O	1.91	0.71
1:A:97:ALA:O	1:A:101:MET:HB2	1.91	0.70
1:C:344:GLN:H	1:C:344:GLN:CD	1.95	0.70
1:B:37:GLU:HG3	1:B:40:ARG:NH1	2.07	0.70
1:D:325:LEU:HG	1:D:329:LEU:HD11	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:236:TYR:OH	1:B:280:LYS:HD3	1.90	0.70
1:C:198:ARG:HB3	1:C:198:ARG:NH2	2.06	0.69
1:B:1:MET:HG3	1:B:21:ALA:HB2	1.74	0.69
1:A:84:ARG:NH2	1:A:263:ARG:HH12	1.90	0.69
1:D:401:GLY:HA3	1:D:406:LEU:HD11	1.75	0.69
1:C:331:ASP:HB3	1:C:334:ASN:ND2	2.07	0.69
1:C:407:LEU:HD22	1:C:422:LEU:HD21	1.75	0.68
1:A:34:GLN:HE21	1:A:63:ASP:HB3	1.58	0.68
1:C:12:VAL:HG12	1:C:401:GLY:HA2	1.76	0.68
1:A:85:ALA:HB2	1:A:267:TYR:CD2	2.29	0.68
1:A:208:LEU:HD23	1:A:218:VAL:HG21	1.73	0.68
1:A:55:VAL:HG22	1:A:80:VAL:HG13	1.76	0.68
1:C:342:GLN:NE2	1:C:343:PRO:HD2	2.09	0.67
1:C:409:LEU:HD22	1:C:413:LEU:HG	1.76	0.67
1:B:57:LEU:HD23	1:B:90:MET:CE	2.25	0.67
1:A:83:THR:O	1:A:87:VAL:HG23	1.95	0.67
1:C:329:LEU:HD12	1:C:369:ALA:HB3	1.75	0.67
1:C:227:ARG:HH11	1:C:378:TYR:HA	1.60	0.66
1:D:258:LEU:HD11	1:D:283:PHE:HB3	1.75	0.66
1:A:302:ARG:HG2	1:A:302:ARG:HH21	1.59	0.66
1:D:326:LYS:HD2	1:D:361:LEU:HD12	1.76	0.66
1:C:229:GLN:HG3	1:C:261:TYR:CZ	2.29	0.66
1:A:85:ALA:HB2	1:A:267:TYR:CE2	2.32	0.65
1:C:27:LEU:HD13	1:C:29:ASP:O	1.96	0.65
1:C:160:SER:HB2	1:C:163:LEU:CD2	2.27	0.65
1:B:387:LEU:HB3	1:B:416:ARG:HH12	1.62	0.65
1:A:278:GLN:HB3	1:A:280:LYS:HE2	1.76	0.65
1:C:360:ILE:HD12	1:C:365:VAL:HG11	1.79	0.64
1:A:10:ARG:HG2	1:A:10:ARG:NH1	2.10	0.64
1:A:200:THR:CG2	1:A:374:LEU:HB3	2.27	0.64
1:C:86:THR:O	1:C:90:MET:HB2	1.97	0.64
1:D:62:LEU:HD13	1:D:93:VAL:HG12	1.79	0.64
1:D:321:ILE:O	1:D:325:LEU:HD13	1.98	0.64
1:D:222:THR:HG22	1:D:339:VAL:HG21	1.78	0.64
1:D:168:LYS:HD3	1:D:230:GLU:OE1	1.98	0.64
1:D:171:LEU:HD22	1:D:171:LEU:H	1.62	0.64
1:C:84:ARG:HB3	1:C:267:TYR:OH	1.98	0.64
1:D:209:GLU:OE1	1:D:242:LEU:HA	1.97	0.64
1:C:57:LEU:HD23	1:C:90:MET:CE	2.27	0.63
1:C:189:TYR:CE1	1:C:380:HIS:HB2	2.33	0.63
1:D:228:ALA:HB3	1:D:229:GLN:NE2	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:302:ARG:HG2	1:D:302:ARG:HH21	1.63	0.63
1:B:325:LEU:O	1:B:329:LEU:HB2	1.99	0.63
1:C:221:PRO:HB3	1:C:321:ILE:HG12	1.81	0.63
1:D:227:ARG:HG2	1:D:227:ARG:HH21	1.63	0.63
1:C:420:VAL:HG22	1:C:421:SER:N	2.13	0.63
1:A:288:LEU:HD12	1:A:289:GLU:H	1.62	0.63
1:D:291:VAL:CG1	2:D:433:SO4:O1	2.46	0.63
1:D:216:GLY:HA3	1:D:333:ARG:O	1.98	0.63
1:B:430:PRO:CG	2:B:446:SO4:O3	2.43	0.63
1:C:424:ARG:HD2	1:C:427:GLU:OE2	1.99	0.62
1:B:295:GLU:H	1:B:295:GLU:CD	2.01	0.62
1:A:347:LEU:HD11	1:A:358:VAL:HG11	1.81	0.62
1:C:415:LEU:HD23	1:C:416:ARG:N	2.14	0.62
1:D:295:GLU:CD	1:D:295:GLU:H	2.01	0.62
1:B:98:LEU:HD11	1:B:108:PRO:HA	1.81	0.62
1:B:406:LEU:N	1:B:406:LEU:HD12	2.14	0.62
1:D:86:THR:HG22	1:D:90:MET:HE2	1.80	0.62
1:C:73:ARG:HH21	1:C:106:PHE:CA	2.07	0.62
1:C:342:GLN:HE21	1:C:342:GLN:CA	2.07	0.62
1:B:65:VAL:HG11	1:B:90:MET:HG3	1.81	0.62
1:D:5:PRO:HG2	1:D:423:ALA:HB1	1.82	0.62
1:C:410:GLY:HA2	1:C:420:VAL:HG21	1.81	0.62
1:B:37:GLU:CG	1:B:40:ARG:HH11	2.10	0.62
1:A:220:ILE:HG22	1:A:222:THR:HG23	1.82	0.62
1:C:342:GLN:NE2	1:C:342:GLN:HA	2.10	0.62
1:D:76:TYR:O	1:D:77:ARG:HD2	2.00	0.62
1:C:251:SER:HB3	1:C:254:ALA:HB3	1.82	0.62
1:C:163:LEU:HD11	1:C:389:TRP:CE2	2.35	0.61
1:B:239:GLY:O	1:B:241:ARG:N	2.32	0.61
1:A:102:ASP:O	1:A:104:PRO:HD3	2.00	0.61
1:C:302:ARG:HG2	1:C:302:ARG:HH21	1.65	0.61
1:D:32:MET:HG2	1:D:66:GLY:HA3	1.82	0.61
1:A:165:ASN:C	1:A:165:ASN:HD22	2.03	0.61
1:C:83:THR:O	1:C:87:VAL:HG23	1.99	0.61
1:B:155:ARG:HD3	1:B:431:VAL:O	1.99	0.61
1:B:407:LEU:HD13	1:B:422:LEU:HD21	1.81	0.61
1:D:128:ARG:HD2	5:D:454:HOH:O	1.99	0.61
1:D:33:PHE:N	1:D:41:ASN:HD21	1.98	0.61
1:D:284:ARG:HD3	1:D:288:LEU:CD2	2.31	0.61
1:B:401:GLY:C	1:B:406:LEU:HD11	2.21	0.60
1:B:98:LEU:HD11	1:B:108:PRO:CA	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:291:VAL:HG12	1:C:292:GLU:N	2.16	0.60
1:B:229:GLN:HG3	1:B:261:TYR:CZ	2.36	0.60
1:A:84:ARG:HH22	1:A:263:ARG:HH12	1.49	0.60
1:D:347:LEU:O	1:D:351:ILE:HG13	2.01	0.60
1:C:318:GLY:HA2	1:C:322:LEU:CD1	2.30	0.60
1:A:235:LEU:HD13	1:A:247:ILE:HD13	1.84	0.60
1:D:239:GLY:HA2	1:D:242:LEU:HG	1.84	0.60
1:B:200:THR:HG23	1:B:374:LEU:HB3	1.81	0.60
1:D:259:SER:O	1:D:262:PRO:HD2	2.02	0.60
1:D:384:ASP:HA	1:D:387:LEU:HD12	1.82	0.60
1:A:344:GLN:CD	1:A:344:GLN:H	2.05	0.59
1:D:410:GLY:HA2	1:D:420:VAL:HG21	1.82	0.59
1:B:401:GLY:CA	1:B:406:LEU:HD11	2.32	0.59
1:A:404:GLU:CD	1:A:404:GLU:H	2.04	0.59
1:C:215:GLY:HA2	1:C:306:PRO:HD3	1.84	0.59
1:C:12:VAL:HG23	1:C:13:THR:HG23	1.84	0.59
1:C:54:ALA:HA	1:C:76:TYR:OH	2.02	0.59
1:C:331:ASP:HB3	1:C:334:ASN:HD22	1.67	0.59
1:C:359:ARG:HH11	1:C:359:ARG:HG2	1.68	0.59
1:D:91:GLU:HG3	1:D:115:LEU:HD13	1.84	0.59
1:C:182:LEU:HD23	1:C:431:VAL:HG22	1.85	0.59
1:B:33:PHE:H	1:B:41:ASN:ND2	1.92	0.59
1:C:229:GLN:NE2	1:C:229:GLN:H	2.01	0.58
1:C:86:THR:HG22	1:C:90:MET:CE	2.33	0.58
1:D:13:THR:HG22	1:D:33:PHE:CD1	2.38	0.58
1:D:219:LEU:HD23	1:D:325:LEU:HD12	1.85	0.58
1:A:168:LYS:HD3	1:A:230:GLU:OE1	2.03	0.58
1:C:409:LEU:CD2	1:C:413:LEU:HG	2.34	0.58
1:B:401:GLY:HA3	1:B:406:LEU:HD11	1.85	0.58
1:D:396:VAL:HG12	1:D:398:LEU:HD12	1.84	0.58
1:C:232:LEU:HA	1:C:235:LEU:HD12	1.86	0.58
1:C:420:VAL:HG22	1:C:421:SER:H	1.67	0.58
1:D:222:THR:HG22	1:D:339:VAL:CG2	2.34	0.58
1:B:142:LEU:CD2	1:B:226:GLU:HB3	2.33	0.58
1:A:87:VAL:HG13	1:A:118:LEU:HD13	1.85	0.58
1:D:383:GLN:O	1:D:387:LEU:HG	2.04	0.58
1:A:329:LEU:HD11	1:A:336:LEU:HD12	1.86	0.58
1:D:13:THR:HG21	1:D:33:PHE:HA	1.80	0.57
1:C:219:LEU:HD12	1:C:219:LEU:N	2.19	0.57
1:D:157:LEU:HD12	1:D:158:VAL:N	2.16	0.57
1:C:55:VAL:HG22	1:C:80:VAL:HG13	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:411:LYS:HB2	3:B:451:FLC:OHB	2.04	0.57
1:C:220:ILE:HG22	1:C:222:THR:HG23	1.85	0.57
1:B:83:THR:HG21	1:B:144:GLY:HA2	1.86	0.57
1:D:229:GLN:HG3	1:D:261:TYR:CZ	2.39	0.57
1:B:1:MET:HG3	1:B:21:ALA:CB	2.35	0.57
1:C:197:TYR:O	1:C:201:VAL:HG23	2.04	0.57
1:D:13:THR:HG22	1:D:33:PHE:HD1	1.68	0.57
1:A:34:GLN:NE2	1:A:63:ASP:HB3	2.19	0.57
1:C:252:PRO:HB2	2:C:434:SO4:O2	2.05	0.57
1:D:330:SER:O	1:D:368:ARG:HB2	2.04	0.57
1:C:229:GLN:CD	1:C:229:GLN:H	2.08	0.57
1:A:129:LEU:O	1:A:132:LEU:HB2	2.05	0.57
1:D:86:THR:O	1:D:90:MET:HB2	2.04	0.57
1:D:113:GLU:HA	1:D:113:GLU:OE2	2.05	0.56
1:D:37:GLU:HB3	1:D:40:ARG:HE	1.70	0.56
1:A:45:PHE:HB3	1:A:47:PHE:CE1	2.40	0.56
1:D:177:PRO:HD3	1:D:389:TRP:CE2	2.40	0.56
1:B:90:MET:O	1:B:94:LEU:HB2	2.04	0.56
1:A:398:LEU:HB3	1:A:406:LEU:HG	1.86	0.56
1:D:395:ARG:HG3	1:D:419:GLU:HB3	1.88	0.56
1:A:4:VAL:HG22	1:A:428:GLY:HA3	1.87	0.56
1:D:325:LEU:HA	1:D:329:LEU:HD13	1.86	0.56
1:C:388:ASP:O	1:C:391:GLN:HB3	2.05	0.56
1:C:295:GLU:CD	1:C:295:GLU:H	2.07	0.56
1:D:297:SER:HB2	1:D:320:ARG:NH2	2.20	0.56
1:B:209:GLU:O	1:B:213:SER:HB2	2.05	0.56
1:C:227:ARG:HH21	1:C:227:ARG:HG2	1.71	0.55
1:C:198:ARG:HH21	1:C:198:ARG:HB3	1.71	0.55
1:A:229:GLN:H	1:A:229:GLN:CD	2.08	0.55
1:B:290:VAL:HB	2:B:437:SO4:O3	2.06	0.55
1:B:396:VAL:HG12	1:B:398:LEU:HD12	1.88	0.55
1:B:100:VAL:O	1:B:100:VAL:HG12	2.07	0.55
1:C:315:MET:CE	1:C:343:PRO:HD3	2.37	0.55
1:D:354:ARG:NH1	1:D:371:VAL:HG23	2.22	0.55
1:B:165:ASN:HD22	1:B:165:ASN:C	2.10	0.55
1:C:393:GLU:O	1:C:418:GLN:HG2	2.06	0.55
1:D:221:PRO:HD2	1:D:337:VAL:O	2.06	0.55
1:A:86:THR:HG22	1:A:90:MET:HE2	1.88	0.55
1:D:177:PRO:HD3	1:D:389:TRP:NE1	2.21	0.55
1:B:411:LYS:CG	3:B:451:FLC:HA1	2.32	0.55
1:B:195:ARG:HD3	1:B:199:GLU:OE2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:412:LEU:O	1:C:415:LEU:HD22	2.07	0.55
1:C:248:TYR:CE2	1:C:289:GLU:HG2	2.42	0.55
1:B:33:PHE:CE2	1:B:67:ARG:NH1	2.75	0.54
1:D:163:LEU:N	1:D:163:LEU:HD22	2.22	0.54
1:D:354:ARG:HH12	1:D:371:VAL:HG23	1.72	0.54
1:C:231:ILE:O	1:C:235:LEU:HG	2.07	0.54
1:C:34:GLN:HE21	1:C:63:ASP:HB3	1.73	0.54
1:A:165:ASN:ND2	1:A:167:GLU:H	2.06	0.54
1:C:318:GLY:HA2	1:C:322:LEU:HD11	1.89	0.54
1:A:217:LYS:HE2	1:A:307:MET:CE	2.37	0.54
1:B:57:LEU:HD23	1:B:90:MET:HE2	1.89	0.54
1:C:359:ARG:HH12	1:C:362:GLY:C	2.11	0.54
1:D:49:PRO:HB3	1:D:71:LEU:HD12	1.89	0.54
1:B:142:LEU:HD21	1:B:226:GLU:HB3	1.88	0.54
1:C:293:HIS:HB3	1:C:295:GLU:OE1	2.08	0.54
1:B:20:LEU:HD21	1:B:25:ARG:HE	1.73	0.54
1:D:232:LEU:O	1:D:285:PRO:HD3	2.08	0.54
1:D:219:LEU:HD21	1:D:324:HIS:O	2.08	0.54
1:A:404:GLU:N	1:A:404:GLU:OE2	2.33	0.54
1:C:70:LYS:HE2	1:C:74:GLU:OE1	2.08	0.54
1:A:157:LEU:HG	1:A:158:VAL:N	2.22	0.54
1:C:315:MET:HE2	1:C:343:PRO:HD3	1.90	0.54
1:B:315:MET:SD	1:B:343:PRO:HD3	2.48	0.54
1:D:382:GLY:O	1:D:386:LEU:HD13	2.07	0.53
1:B:65:VAL:HG12	1:B:94:LEU:HD13	1.90	0.53
1:D:37:GLU:HB3	1:D:40:ARG:HH11	1.73	0.53
1:B:420:VAL:HG22	1:B:421:SER:N	2.23	0.53
1:A:33:PHE:H	1:A:41:ASN:HD21	1.56	0.53
1:D:182:LEU:HD11	1:D:397:VAL:HG23	1.90	0.53
1:A:41:ASN:O	1:A:70:LYS:HE3	2.08	0.53
1:D:204:PHE:CE1	1:D:208:LEU:HD11	2.43	0.53
1:A:250:ASP:OD2	1:A:297:SER:OG	2.26	0.53
1:D:171:LEU:N	1:D:171:LEU:HD22	2.24	0.53
1:A:396:VAL:HG12	1:A:398:LEU:HD13	1.91	0.53
1:D:13:THR:HG21	1:D:34:GLN:N	2.22	0.53
1:A:220:ILE:HG22	1:A:222:THR:CG2	2.39	0.53
1:B:68:LEU:N	1:B:69:PRO:HD2	2.23	0.53
1:A:288:LEU:HD12	1:A:289:GLU:N	2.23	0.53
1:A:329:LEU:HG	1:A:367:LEU:HD13	1.89	0.53
1:C:113:GLU:HA	1:C:113:GLU:OE2	2.09	0.53
1:C:401:GLY:HA3	1:C:406:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:GLU:O	1:D:95:GLU:HG3	2.07	0.53
1:C:374:LEU:C	1:C:376:GLY:H	2.13	0.53
1:A:302:ARG:NH2	1:A:302:ARG:HG2	2.24	0.53
1:A:68:LEU:N	1:A:69:PRO:HD2	2.23	0.52
1:B:295:GLU:OE2	1:B:295:GLU:N	2.31	0.52
1:A:229:GLN:NE2	1:A:229:GLN:H	2.07	0.52
1:A:284:ARG:HD2	3:A:452:FLC:HA2	1.92	0.52
1:D:160:SER:HB3	1:D:185:ALA:HA	1.91	0.52
1:B:204:PHE:CZ	1:B:208:LEU:HD11	2.45	0.52
1:D:420:VAL:HG22	1:D:421:SER:N	2.24	0.52
1:C:315:MET:HE2	1:C:341:TYR:O	2.10	0.52
1:B:389:TRP:HE3	1:B:390:LEU:HD13	1.75	0.52
1:A:142:LEU:HD22	1:A:143:PRO:HD2	1.92	0.52
1:A:320:ARG:HD3	3:A:453:FLC:OHB	2.10	0.52
1:A:395:ARG:NH2	1:A:431:VAL:OXT	2.40	0.52
1:C:227:ARG:HG2	1:C:227:ARG:NH2	2.24	0.52
1:B:83:THR:HG22	1:B:86:THR:N	2.12	0.52
1:D:11:GLU:C	1:D:401:GLY:H	2.13	0.52
1:C:407:LEU:CD2	1:C:422:LEU:HD21	2.38	0.52
1:C:1:MET:HG2	1:C:431:VAL:HG21	1.91	0.52
1:A:253:MET:O	1:A:257:VAL:HG23	2.10	0.52
1:D:325:LEU:HG	1:D:329:LEU:CD1	2.39	0.52
1:A:200:THR:HG23	1:A:374:LEU:HB3	1.93	0.51
1:D:209:GLU:HG3	1:D:243:PRO:HD3	1.91	0.51
1:B:239:GLY:C	1:B:241:ARG:H	2.12	0.51
1:D:409:LEU:HD22	1:D:413:LEU:HG	1.91	0.51
1:B:411:LYS:HA	3:B:451:FLC:HG1	1.91	0.51
1:C:227:ARG:HH11	1:C:378:TYR:CA	2.23	0.51
1:C:177:PRO:HD3	1:C:389:TRP:CE2	2.45	0.51
1:A:375:GLY:HA2	1:A:378:TYR:CE2	2.45	0.51
1:B:382:GLY:O	1:B:386:LEU:HD22	2.10	0.51
1:D:57:LEU:HD21	1:D:68:LEU:HD22	1.90	0.51
1:C:42:HIS:CE1	1:C:105:PHE:HB3	2.44	0.51
1:B:200:THR:OG1	1:B:376:GLY:HA3	2.11	0.51
1:D:84:ARG:HB2	1:D:267:TYR:OH	2.10	0.51
1:D:85:ALA:HB2	1:D:267:TYR:CD2	2.45	0.51
1:B:70:LYS:O	1:B:74:GLU:HG3	2.11	0.51
1:C:85:ALA:HB2	1:C:267:TYR:CD2	2.45	0.51
1:D:141:HIS:O	1:D:142:LEU:HD23	2.10	0.51
1:C:226:GLU:O	1:C:229:GLN:HG2	2.09	0.51
1:C:132:LEU:HD21	1:C:134:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:98:LEU:C	1:C:98:LEU:HD13	2.31	0.51
1:D:33:PHE:H	1:D:41:ASN:ND2	2.03	0.51
1:B:416:ARG:CG	2:B:433:SO4:O3	2.59	0.51
1:B:37:GLU:HA	1:B:37:GLU:OE2	2.10	0.51
1:A:37:GLU:HA	1:A:37:GLU:OE2	2.10	0.51
1:D:10:ARG:HH11	1:D:10:ARG:HG2	1.76	0.51
1:C:68:LEU:HD11	1:C:72:PHE:HE1	1.75	0.51
1:C:231:ILE:HG21	1:C:310:LEU:HD21	1.93	0.51
1:A:86:THR:O	1:A:90:MET:HB2	2.11	0.51
1:C:28:LEU:O	1:C:29:ASP:HB2	2.11	0.51
1:D:8:ALA:N	1:D:13:THR:O	2.37	0.50
1:C:12:VAL:HG12	1:C:401:GLY:CA	2.42	0.50
1:B:140:GLY:O	1:B:164:GLY:HA3	2.11	0.50
1:B:199:GLU:HA	1:B:202:ARG:HH11	1.77	0.50
1:D:70:LYS:NZ	1:D:74:GLU:OE1	2.44	0.50
1:C:73:ARG:HD2	1:C:110:ASP:OD2	2.10	0.50
1:D:411:LYS:O	1:D:414:ALA:HB3	2.12	0.50
1:B:12:VAL:HG12	1:B:401:GLY:CA	2.38	0.50
1:B:397:VAL:HG22	1:B:421:SER:OG	2.11	0.50
1:B:293:HIS:HB3	2:B:441:SO4:O4	2.11	0.50
1:A:318:GLY:HA2	1:A:322:LEU:CD1	2.41	0.50
1:C:165:ASN:HB2	1:C:379:GLY:O	2.11	0.50
1:D:62:LEU:HD13	1:D:93:VAL:CG1	2.42	0.50
1:D:211:THR:HG21	1:D:335:ALA:CB	2.38	0.50
1:C:228:ALA:HB3	1:C:229:GLN:NE2	2.27	0.50
1:B:73:ARG:HD2	1:B:110:ASP:OD2	2.12	0.50
1:C:33:PHE:CD2	1:C:40:ARG:HB2	2.46	0.50
1:A:325:LEU:O	1:A:329:LEU:HB2	2.12	0.50
1:B:168:LYS:HG2	1:B:197:TYR:CE2	2.47	0.50
1:D:251:SER:HB3	1:D:254:ALA:HB3	1.94	0.50
1:D:264:LEU:HD13	1:D:264:LEU:N	2.27	0.50
1:D:37:GLU:CB	1:D:40:ARG:HH11	2.25	0.50
1:C:95:GLU:O	1:C:98:LEU:HB3	2.11	0.50
1:D:139:ALA:HB2	1:D:146:ALA:HA	1.93	0.50
1:D:331:ASP:HB3	1:D:334:ASN:ND2	2.27	0.50
1:D:1:MET:HG3	1:D:21:ALA:HB2	1.92	0.50
1:D:401:GLY:CA	1:D:406:LEU:HD11	2.41	0.49
1:C:199:GLU:HA	1:C:202:ARG:HE	1.77	0.49
1:D:123:TYR:HE1	1:D:146:ALA:HB2	1.77	0.49
1:D:185:ALA:HB2	1:D:390:LEU:HD11	1.94	0.49
1:B:229:GLN:CD	1:B:229:GLN:H	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:GLN:HG3	1:A:261:TYR:CZ	2.47	0.49
1:C:13:THR:OG1	1:C:33:PHE:HA	2.12	0.49
1:A:289:GLU:OE2	1:B:291:VAL:HA	2.12	0.49
1:D:35:GLY:C	1:D:37:GLU:H	2.15	0.49
1:D:208:LEU:O	1:D:212:LEU:HG	2.12	0.49
1:A:344:GLN:H	1:A:344:GLN:NE2	2.09	0.49
1:B:85:ALA:HB2	1:B:267:TYR:CD2	2.47	0.49
1:C:415:LEU:HD23	1:C:415:LEU:C	2.32	0.49
1:B:396:VAL:HG12	1:B:398:LEU:CD1	2.42	0.49
1:A:217:LYS:HG2	1:A:307:MET:HG2	1.95	0.49
1:D:209:GLU:CD	1:D:243:PRO:HD3	2.32	0.49
1:C:109:GLU:H	1:C:109:GLU:CD	2.16	0.49
1:C:101:MET:CE	1:C:104:PRO:HA	2.43	0.49
1:D:32:MET:HA	1:D:67:ARG:HG3	1.95	0.49
1:B:163:LEU:HD21	1:B:389:TRP:CD2	2.48	0.49
1:B:387:LEU:HB3	1:B:416:ARG:NH1	2.27	0.48
1:C:158:VAL:HG23	1:C:180:ALA:HB2	1.94	0.48
1:C:358:VAL:O	1:C:365:VAL:HG12	2.13	0.48
1:D:86:THR:HG22	1:D:90:MET:CE	2.43	0.48
1:B:348:GLY:O	1:B:352:ILE:HG13	2.13	0.48
1:C:229:GLN:HG3	1:C:261:TYR:CE1	2.47	0.48
1:C:227:ARG:HH11	1:C:379:GLY:N	2.11	0.48
1:D:250:ASP:O	1:D:251:SER:HB2	2.12	0.48
1:C:359:ARG:NH1	1:C:359:ARG:HG2	2.28	0.48
1:C:73:ARG:NH2	1:C:106:PHE:CA	2.72	0.48
1:B:406:LEU:H	1:B:406:LEU:CD1	2.26	0.48
1:A:62:LEU:HD11	1:A:97:ALA:HB2	1.96	0.48
1:B:226:GLU:HG3	1:B:227:ARG:N	2.28	0.48
1:B:182:LEU:HD11	1:B:397:VAL:HG23	1.96	0.48
1:D:97:ALA:O	1:D:101:MET:HB2	2.13	0.48
1:B:203:GLU:O	1:B:206:GLU:HB2	2.13	0.48
1:C:12:VAL:CG1	1:C:401:GLY:HA2	2.43	0.48
1:D:325:LEU:HB3	1:D:329:LEU:HD22	1.96	0.48
1:D:420:VAL:HG22	1:D:421:SER:H	1.79	0.48
1:D:330:SER:O	1:D:368:ARG:HD2	2.14	0.48
1:B:165:ASN:C	1:B:165:ASN:ND2	2.66	0.48
1:D:245:ALA:HB1	1:D:306:PRO:O	2.14	0.48
1:A:241:ARG:HD3	2:A:441:SO4:O3	2.13	0.48
1:D:37:GLU:C	1:D:39:ALA:H	2.17	0.48
1:A:375:GLY:HA2	1:A:378:TYR:CZ	2.49	0.48
1:B:259:SER:O	1:B:262:PRO:HD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:231:ILE:C	1:D:233:TYR:H	2.16	0.48
1:A:43:ALA:HB1	1:A:44:PRO:HD2	1.95	0.48
1:C:381:ALA:HB3	1:C:386:LEU:CD1	2.44	0.48
1:D:13:THR:CG2	1:D:14:GLY:N	2.76	0.47
1:C:347:LEU:O	1:C:351:ILE:HG13	2.14	0.47
1:D:38:GLU:HG2	1:D:38:GLU:O	2.12	0.47
1:A:3:ILE:O	1:A:3:ILE:HG23	2.12	0.47
1:D:177:PRO:HD3	1:D:389:TRP:CD1	2.49	0.47
1:B:224:ALA:HB1	1:B:253:MET:HG2	1.96	0.47
1:C:235:LEU:HD13	1:C:247:ILE:HG21	1.96	0.47
1:B:347:LEU:HD11	1:B:358:VAL:HG11	1.95	0.47
1:A:87:VAL:HA	1:A:90:MET:HE3	1.95	0.47
1:D:170:VAL:HG12	1:D:171:LEU:HD13	1.97	0.47
1:D:204:PHE:HB2	1:D:374:LEU:HD13	1.96	0.47
1:D:219:LEU:CD2	1:D:324:HIS:HB3	2.45	0.47
1:D:258:LEU:CD1	1:D:283:PHE:HB3	2.43	0.47
1:C:32:MET:HE2	1:C:105:PHE:HZ	1.80	0.47
1:C:217:LYS:HG2	1:C:307:MET:HG2	1.96	0.47
1:C:86:THR:HG22	1:C:90:MET:HE2	1.96	0.47
1:C:331:ASP:OD2	1:C:332:PRO:HD2	2.15	0.47
1:B:416:ARG:HD2	1:B:418:GLN:OE1	2.15	0.47
1:A:4:VAL:HG22	1:A:428:GLY:CA	2.43	0.47
1:B:188:THR:HG22	1:B:189:TYR:CD1	2.49	0.47
1:B:207:ILE:O	1:B:211:THR:HG22	2.14	0.47
1:D:316:LEU:C	1:D:318:GLY:H	2.18	0.47
1:B:406:LEU:N	1:B:406:LEU:CD1	2.76	0.47
1:D:12:VAL:HG23	1:D:12:VAL:O	2.14	0.47
1:C:25:ARG:NH1	1:C:51:GLU:HB3	2.26	0.47
1:D:398:LEU:O	1:D:399:VAL:HG13	2.15	0.47
1:C:209:GLU:CD	1:C:243:PRO:HD3	2.35	0.47
1:B:404:GLU:HG3	1:B:405:LYS:N	2.30	0.47
1:D:37:GLU:O	1:D:39:ALA:N	2.48	0.47
1:D:65:VAL:HG11	1:D:90:MET:CG	2.45	0.47
1:A:318:GLY:HA2	1:A:322:LEU:HD12	1.97	0.47
1:D:312:GLY:HA2	1:D:313:SER:C	2.34	0.47
1:A:59:HIS:CD2	1:A:61:HIS:HB2	2.50	0.47
1:D:28:LEU:HB3	1:D:159:TYR:CD1	2.50	0.47
1:B:297:SER:OG	1:B:320:ARG:HD3	2.15	0.47
1:B:412:LEU:HD22	2:B:448:SO4:O3	2.15	0.46
1:D:348:GLY:O	1:D:352:ILE:HG13	2.14	0.46
1:D:148:VAL:HG12	1:D:149:VAL:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:168:LYS:CD	1:D:230:GLU:OE1	2.62	0.46
1:C:91:GLU:O	1:C:95:GLU:HG2	2.14	0.46
1:B:233:TYR:CE1	1:B:272:VAL:HG22	2.50	0.46
1:A:11:GLU:CD	1:A:40:ARG:HH12	2.18	0.46
1:A:2:ARG:HD3	5:A:461:HOH:O	2.15	0.46
1:B:253:MET:O	1:B:254:ALA:C	2.53	0.46
1:D:177:PRO:HB3	1:D:389:TRP:CZ2	2.50	0.46
1:D:55:VAL:HG13	1:D:80:VAL:HG22	1.98	0.46
1:B:229:GLN:HG3	1:B:261:TYR:CE1	2.51	0.46
1:B:31:GLY:HA3	1:B:63:ASP:C	2.35	0.46
1:D:226:GLU:O	1:D:229:GLN:HG2	2.16	0.46
1:C:9:ALA:O	1:C:11:GLU:HG2	2.15	0.46
1:C:88:LEU:HD12	1:C:264:LEU:HD11	1.98	0.46
1:C:43:ALA:O	1:C:70:LYS:NZ	2.48	0.46
1:C:191:ASP:OD2	1:C:192:ARG:N	2.49	0.46
1:C:234:VAL:HG21	1:C:377:PHE:HE2	1.81	0.46
1:A:420:VAL:HG22	1:A:421:SER:N	2.30	0.46
1:B:55:VAL:HG12	1:B:57:LEU:HD13	1.97	0.46
1:B:381:ALA:HB3	1:B:386:LEU:HD13	1.97	0.46
1:A:163:LEU:HD21	1:A:389:TRP:CD2	2.51	0.46
1:A:297:SER:OG	1:A:320:ARG:HG2	2.15	0.45
1:C:32:MET:HA	1:C:67:ARG:HG3	1.98	0.45
1:B:126:TRP:CE3	1:C:178:PRO:HB3	2.51	0.45
1:C:396:VAL:HG12	1:C:398:LEU:CD1	2.45	0.45
1:C:77:ARG:NE	1:C:113:GLU:OE1	2.49	0.45
1:C:191:ASP:CG	1:C:192:ARG:HG3	2.37	0.45
1:A:28:LEU:N	1:A:28:LEU:CD1	2.79	0.45
1:D:211:THR:OG1	1:D:218:VAL:HG22	2.16	0.45
1:B:402:GLU:O	1:B:406:LEU:HD13	2.16	0.45
1:B:43:ALA:HB1	1:B:44:PRO:CD	2.43	0.45
1:C:198:ARG:HH21	1:C:198:ARG:CB	2.29	0.45
1:A:24:ARG:HH11	1:A:24:ARG:HG2	1.82	0.45
1:B:3:ILE:HG23	1:B:3:ILE:O	2.16	0.45
1:D:58:THR:O	1:D:145:SER:HA	2.16	0.45
1:C:223:PHE:HZ	1:C:315:MET:HG3	1.81	0.45
1:B:358:VAL:HG12	1:B:359:ARG:N	2.31	0.45
1:B:406:LEU:HD12	1:B:406:LEU:H	1.81	0.45
1:C:375:GLY:HA2	1:C:378:TYR:CZ	2.51	0.45
1:D:55:VAL:CG1	1:D:80:VAL:HG22	2.47	0.45
1:D:291:VAL:HA	2:D:433:SO4:O1	2.17	0.45
1:C:220:ILE:HG22	1:C:222:THR:CG2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:421:SER:C	1:D:422:LEU:HD12	2.37	0.45
1:D:139:ALA:HB1	1:D:162:ASP:O	2.16	0.45
1:D:189:TYR:CE2	1:D:194:HIS:HE1	2.34	0.45
1:A:191:ASP:CG	1:A:405:LYS:HD2	2.36	0.45
1:C:284:ARG:HH21	1:C:288:LEU:HD23	1.82	0.45
1:A:194:HIS:NE2	1:A:380:HIS:O	2.50	0.45
1:D:224:ALA:CB	1:D:254:ALA:HB2	2.46	0.45
1:B:171:LEU:HB3	1:B:172:PRO:HD2	1.97	0.45
1:D:191:ASP:OD2	1:D:192:ARG:HG3	2.17	0.45
1:D:232:LEU:HD11	1:D:249:LEU:HD13	1.97	0.45
1:A:4:VAL:HA	1:A:428:GLY:HA2	1.99	0.45
1:A:217:LYS:HE2	1:A:307:MET:HE3	1.97	0.45
1:B:73:ARG:HG3	1:B:73:ARG:HH21	1.81	0.45
1:B:113:GLU:HA	1:B:113:GLU:OE2	2.17	0.45
1:A:407:LEU:HD13	1:A:422:LEU:HD21	1.99	0.45
1:D:269:SER:O	1:D:273:GLN:HG3	2.17	0.45
1:B:210:LYS:O	1:B:214:GLN:HG2	2.17	0.45
1:C:399:VAL:HG12	1:C:423:ALA:CB	2.46	0.45
1:C:420:VAL:CG2	1:C:421:SER:N	2.80	0.45
1:C:76:TYR:CZ	1:C:78:GLY:HA3	2.52	0.45
1:C:246:PRO:HG2	1:C:248:TYR:HE1	1.82	0.45
1:C:262:PRO:HA	1:C:276:PHE:CZ	2.52	0.45
1:D:14:GLY:O	1:D:15:SER:C	2.55	0.45
1:C:43:ALA:HB1	1:C:44:PRO:HD2	1.99	0.45
1:D:85:ALA:HB2	1:D:267:TYR:CE2	2.52	0.45
1:D:10:ARG:NH1	1:D:10:ARG:HG2	2.32	0.45
1:D:215:GLY:O	1:D:305:GLY:HA3	2.16	0.45
1:B:201:VAL:O	1:B:205:LEU:HG	2.17	0.45
1:B:72:PHE:HE2	1:B:117:HIS:CG	2.34	0.45
1:B:399:VAL:HG12	1:B:423:ALA:HB3	1.98	0.44
1:B:244:ARG:H	1:B:244:ARG:NE	2.15	0.44
1:D:310:LEU:N	1:D:310:LEU:HD12	2.32	0.44
1:C:235:LEU:O	1:C:239:GLY:N	2.50	0.44
1:B:375:GLY:HA2	1:B:378:TYR:CZ	2.51	0.44
1:D:302:ARG:HG2	1:D:302:ARG:NH2	2.30	0.44
1:C:291:VAL:CG1	1:C:292:GLU:N	2.80	0.44
1:D:68:LEU:N	1:D:69:PRO:HD2	2.31	0.44
1:D:223:PHE:CZ	1:D:315:MET:HG3	2.53	0.44
1:A:386:LEU:HD12	1:A:386:LEU:HA	1.88	0.44
1:A:62:LEU:HD13	1:A:93:VAL:HG12	1.99	0.44
1:D:200:THR:CG2	1:D:374:LEU:HB3	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:9:ALA:C	1:C:11:GLU:H	2.21	0.44
1:A:389:TRP:HE3	1:A:390:LEU:HD13	1.82	0.44
1:B:235:LEU:HD13	1:B:247:ILE:HD13	1.99	0.44
1:C:224:ALA:O	1:C:257:VAL:HG21	2.18	0.44
1:C:168:LYS:HE3	1:C:378:TYR:O	2.17	0.44
1:C:65:VAL:HG11	1:C:90:MET:HG3	1.98	0.44
1:A:208:LEU:O	1:A:212:LEU:HG	2.18	0.44
1:C:302:ARG:HG2	1:C:302:ARG:NH2	2.32	0.44
1:C:359:ARG:NH1	1:C:363:GLU:N	2.65	0.44
1:D:215:GLY:HA2	1:D:306:PRO:HB3	2.00	0.44
1:C:191:ASP:OD2	1:C:192:ARG:HG3	2.18	0.44
1:B:330:SER:O	1:B:368:ARG:HD2	2.18	0.44
1:B:396:VAL:O	1:B:420:VAL:HA	2.18	0.44
1:B:325:LEU:HG	1:B:329:LEU:HD22	2.00	0.44
1:D:404:GLU:CD	1:D:404:GLU:H	2.21	0.44
1:B:220:ILE:HG22	1:B:222:THR:HG23	1.98	0.44
1:B:221:PRO:HB3	1:B:321:ILE:HG12	2.00	0.44
1:A:263:ARG:HH21	1:A:263:ARG:CG	2.31	0.44
1:C:409:LEU:HD22	1:C:413:LEU:CG	2.46	0.44
1:C:98:LEU:O	1:C:98:LEU:HD13	2.17	0.44
1:D:132:LEU:HG	1:D:134:LEU:HD11	1.99	0.44
1:D:182:LEU:HD12	1:D:183:VAL:H	1.82	0.44
1:C:226:GLU:HG3	1:C:227:ARG:N	2.31	0.44
1:B:236:TYR:CD2	1:B:236:TYR:C	2.90	0.44
1:C:410:GLY:CA	1:C:420:VAL:HG21	2.48	0.44
1:B:207:ILE:O	1:B:211:THR:CG2	2.66	0.44
1:C:81:TYR:HA	1:C:119:ARG:O	2.18	0.44
1:C:20:LEU:HD23	1:C:25:ARG:HG2	2.00	0.43
1:B:416:ARG:O	1:B:416:ARG:HG2	2.17	0.43
1:D:236:TYR:N	1:D:285:PRO:HB3	2.34	0.43
1:D:221:PRO:HG3	1:D:338:PHE:CE1	2.54	0.43
1:C:359:ARG:HH12	1:C:363:GLU:N	2.16	0.43
1:D:37:GLU:C	1:D:39:ALA:N	2.71	0.43
1:B:233:TYR:CE1	1:B:282:PRO:HB2	2.53	0.43
1:D:87:VAL:HG13	1:D:118:LEU:HD13	1.99	0.43
1:A:295:GLU:CD	1:A:295:GLU:H	2.21	0.43
1:B:325:LEU:HA	1:B:325:LEU:HD12	1.82	0.43
1:C:219:LEU:HD21	1:C:324:HIS:O	2.18	0.43
1:B:195:ARG:HH11	1:B:195:ARG:HG2	1.83	0.43
1:A:260:LEU:HD12	1:A:263:ARG:HD3	2.01	0.43
1:B:40:ARG:C	1:B:42:HIS:H	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:GLY:O	1:B:15:SER:C	2.56	0.43
1:D:9:ALA:O	1:D:11:GLU:HG2	2.19	0.43
1:C:20:LEU:CD2	1:C:25:ARG:HG2	2.48	0.43
1:D:85:ALA:HB3	1:D:144:GLY:HA3	2.01	0.43
1:C:235:LEU:CD1	1:C:247:ILE:HG21	2.48	0.43
1:C:420:VAL:CG2	1:C:421:SER:H	2.32	0.43
1:B:98:LEU:HD11	1:B:108:PRO:HB3	2.00	0.43
1:D:37:GLU:HA	1:D:37:GLU:OE2	2.19	0.43
1:C:284:ARG:HD3	1:C:288:LEU:HD23	2.00	0.43
1:D:223:PHE:HZ	1:D:315:MET:HG3	1.82	0.43
1:D:16:ALA:C	1:D:17:HIS:CD2	2.91	0.43
1:A:165:ASN:C	1:A:165:ASN:ND2	2.68	0.43
1:D:73:ARG:NH2	1:D:110:ASP:OD2	2.52	0.43
1:A:85:ALA:HB3	1:A:144:GLY:HA3	2.01	0.43
1:B:80:VAL:HB	1:B:118:LEU:HD23	2.00	0.43
1:A:167:GLU:HB3	1:A:197:TYR:HB2	2.01	0.43
1:A:407:LEU:O	1:A:410:GLY:N	2.52	0.43
1:D:195:ARG:O	1:D:196:PRO:C	2.57	0.43
1:A:347:LEU:CD1	1:A:358:VAL:HG11	2.49	0.43
1:B:188:THR:OG1	1:B:400:HIS:ND1	2.52	0.43
1:B:126:TRP:CD2	1:C:178:PRO:HB3	2.53	0.43
1:B:277:LEU:C	1:B:279:GLY:N	2.72	0.43
1:D:211:THR:O	1:D:214:GLN:HG2	2.18	0.43
1:C:168:LYS:HD3	1:C:230:GLU:OE1	2.19	0.43
1:A:197:TYR:O	1:A:201:VAL:HG23	2.19	0.43
1:A:177:PRO:HD3	1:A:389:TRP:CE2	2.54	0.43
1:D:234:VAL:HG13	1:D:238:HIS:HD2	1.83	0.43
1:C:374:LEU:O	1:C:376:GLY:N	2.52	0.42
1:D:17:HIS:ND1	1:D:184:LEU:HD21	2.34	0.42
1:B:318:GLY:HA2	1:B:322:LEU:HD11	1.99	0.42
1:D:109:GLU:H	1:D:109:GLU:CD	2.22	0.42
1:D:316:LEU:HB3	1:D:347:LEU:HD23	2.01	0.42
1:C:355:PRO:HG2	1:C:358:VAL:HG22	2.00	0.42
1:D:209:GLU:CG	1:D:243:PRO:HD3	2.49	0.42
1:D:111:VAL:O	1:D:115:LEU:HG	2.19	0.42
1:C:34:GLN:NE2	1:C:63:ASP:HB3	2.32	0.42
1:D:227:ARG:CG	1:D:227:ARG:HH21	2.32	0.42
1:A:329:LEU:HD12	1:A:329:LEU:HA	1.91	0.42
1:D:231:ILE:C	1:D:233:TYR:N	2.72	0.42
1:A:126:TRP:CE3	1:A:135:ALA:HB2	2.55	0.42
1:B:37:GLU:O	1:B:38:GLU:C	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:194:HIS:CE1	1:C:378:TYR:HD1	2.37	0.42
1:D:110:ASP:O	1:D:113:GLU:N	2.52	0.42
1:D:182:LEU:HD12	1:D:183:VAL:N	2.34	0.42
1:B:57:LEU:HD22	1:B:80:VAL:CG1	2.50	0.42
1:C:312:GLY:O	1:C:321:ILE:HG22	2.19	0.42
1:D:49:PRO:HB3	1:D:71:LEU:CD1	2.49	0.42
1:D:395:ARG:HD2	1:D:419:GLU:OE2	2.19	0.42
1:C:386:LEU:O	1:C:390:LEU:HD23	2.20	0.42
1:B:185:ALA:O	1:B:399:VAL:HG22	2.20	0.42
1:C:19:LEU:HD13	1:C:157:LEU:HD23	2.01	0.42
1:C:59:HIS:CD2	1:C:61:HIS:HB2	2.55	0.42
1:D:291:VAL:HG13	2:D:433:SO4:S	2.60	0.42
1:D:386:LEU:O	1:D:390:LEU:HD23	2.19	0.42
1:B:87:VAL:HG13	1:B:118:LEU:HD13	2.01	0.42
1:D:170:VAL:HA	1:D:272:VAL:HG21	2.02	0.42
1:D:91:GLU:HG3	1:D:115:LEU:CD1	2.49	0.42
1:C:10:ARG:HG2	1:C:10:ARG:HH11	1.85	0.42
1:D:220:ILE:HG23	1:D:337:VAL:O	2.20	0.42
1:B:391:GLN:NE2	2:B:433:SO4:O2	2.53	0.42
1:C:1:MET:HG2	1:C:431:VAL:CG2	2.50	0.42
1:B:20:LEU:CD2	1:B:25:ARG:HE	2.32	0.42
1:B:68:LEU:HD11	1:B:72:PHE:HE1	1.85	0.42
1:C:330:SER:HA	1:C:366:PRO:O	2.20	0.42
1:C:402:GLU:HB2	1:C:405:LYS:CG	2.49	0.42
1:C:190:GLY:HA3	1:C:409:LEU:HB2	2.02	0.42
1:B:387:LEU:HD13	2:B:448:SO4:O1	2.20	0.42
1:C:143:PRO:HG3	1:C:171:LEU:HD11	2.02	0.42
1:B:194:HIS:NE2	1:B:380:HIS:O	2.52	0.42
1:C:65:VAL:HG11	1:C:90:MET:CG	2.50	0.42
1:C:330:SER:O	1:C:368:ARG:HD2	2.19	0.42
1:D:336:LEU:C	1:D:336:LEU:HD23	2.41	0.42
1:C:222:THR:HG22	1:C:339:VAL:CG2	2.44	0.41
1:B:45:PHE:CZ	1:B:70:LYS:HG2	2.54	0.41
1:A:32:MET:HA	1:A:67:ARG:HG3	2.02	0.41
1:A:41:ASN:HD22	1:A:67:ARG:HD3	1.85	0.41
1:D:98:LEU:C	1:D:98:LEU:HD23	2.40	0.41
1:A:147:PHE:HB2	1:A:160:SER:HA	2.02	0.41
1:B:359:ARG:HH11	1:B:359:ARG:HG2	1.86	0.41
1:C:32:MET:HG2	1:C:62:LEU:O	2.20	0.41
1:C:235:LEU:HB2	1:C:285:PRO:HB3	2.02	0.41
1:C:177:PRO:HD3	1:C:389:TRP:NE1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:PRO:HB3	1:D:126:TRP:CE3	2.54	0.41
1:C:140:GLY:O	1:C:164:GLY:HA3	2.20	0.41
1:A:277:LEU:HD21	1:D:263:ARG:HG2	2.01	0.41
1:B:40:ARG:C	1:B:42:HIS:N	2.73	0.41
1:C:291:VAL:HG12	1:C:292:GLU:H	1.84	0.41
1:A:194:HIS:CE1	1:A:378:TYR:HB2	2.55	0.41
1:B:4:VAL:HA	1:B:428:GLY:HA2	2.02	0.41
1:B:88:LEU:HB3	1:B:260:LEU:HD21	2.01	0.41
1:A:48:ASP:OD2	1:A:51:GLU:HG2	2.20	0.41
1:D:409:LEU:HD22	1:D:413:LEU:CD1	2.50	0.41
1:A:37:GLU:CA	1:A:37:GLU:OE2	2.69	0.41
1:A:163:LEU:HD12	1:A:163:LEU:HA	1.83	0.41
1:A:48:ASP:HA	1:A:49:PRO:HD2	1.95	0.41
1:B:325:LEU:HB3	1:B:360:ILE:HD13	2.02	0.41
1:C:137:GLY:HA3	1:C:147:PHE:CZ	2.56	0.41
1:D:344:GLN:H	1:D:344:GLN:CD	2.24	0.41
1:D:232:LEU:HD23	1:D:235:LEU:HD12	2.03	0.41
1:C:227:ARG:O	1:C:228:ALA:C	2.59	0.41
1:C:77:ARG:HD3	1:C:77:ARG:HA	1.85	0.41
1:D:409:LEU:HD22	1:D:413:LEU:CG	2.50	0.41
1:C:196:PRO:HB2	1:C:199:GLU:HG2	2.02	0.41
1:D:264:LEU:CD1	1:D:264:LEU:N	2.84	0.41
1:C:137:GLY:HA3	1:C:147:PHE:CE1	2.56	0.41
1:C:375:GLY:HA2	1:C:378:TYR:CE1	2.56	0.41
1:A:358:VAL:HG12	1:A:359:ARG:N	2.35	0.41
1:C:182:LEU:HD11	1:C:397:VAL:HG23	2.03	0.41
1:C:374:LEU:C	1:C:376:GLY:N	2.73	0.41
1:C:68:LEU:HB3	1:C:69:PRO:HD3	2.01	0.41
1:D:17:HIS:CD2	1:D:17:HIS:N	2.88	0.41
1:C:186:GLU:HG3	1:C:187:GLY:N	2.35	0.41
1:A:236:TYR:C	1:A:236:TYR:CD2	2.94	0.41
1:D:407:LEU:HA	1:D:407:LEU:HD13	1.88	0.41
1:A:14:GLY:O	1:A:15:SER:C	2.58	0.41
1:B:402:GLU:OE1	1:B:405:LYS:HD2	2.21	0.41
1:D:325:LEU:CA	1:D:329:LEU:HD13	2.51	0.41
1:B:236:TYR:HH	1:B:280:LYS:HD3	1.82	0.41
1:B:416:ARG:HG3	2:B:433:SO4:O3	2.21	0.41
1:C:101:MET:O	1:C:102:ASP:C	2.59	0.40
1:A:126:TRP:CD2	1:D:178:PRO:HB3	2.56	0.40
1:D:402:GLU:O	1:D:403:GLU:C	2.60	0.40
1:B:2:ARG:CG	5:B:459:HOH:O	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:LEU:HD12	1:B:133:SER:H	1.85	0.40
1:C:402:GLU:O	1:C:406:LEU:HD13	2.21	0.40
1:C:160:SER:OG	1:C:185:ALA:HA	2.21	0.40
1:C:250:ASP:HA	1:C:291:VAL:HB	2.03	0.40
1:B:290:VAL:HG12	1:B:290:VAL:O	2.20	0.40
1:B:72:PHE:HA	1:B:76:TYR:O	2.21	0.40
1:C:192:ARG:HG2	1:C:192:ARG:HH11	1.87	0.40
1:B:244:ARG:H	1:B:244:ARG:CD	2.34	0.40
1:A:141:HIS:HA	2:A:448:SO4:O2	2.22	0.40
1:A:227:ARG:HH21	1:A:227:ARG:HG2	1.85	0.40
1:C:280:LYS:O	1:C:282:PRO:HD3	2.20	0.40
1:C:248:TYR:CE2	1:C:300:LEU:HD21	2.56	0.40
1:A:178:PRO:HB3	1:D:126:TRP:CD2	2.56	0.40
1:D:11:GLU:O	1:D:400:HIS:HA	2.22	0.40
1:C:211:THR:HG21	1:C:335:ALA:CB	2.52	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	429/431 (100%)	400 (93%)	28 (6%)	1 (0%)	52	80
1	B	429/431 (100%)	387 (90%)	36 (8%)	6 (1%)	14	33
1	C	429/431 (100%)	370 (86%)	54 (13%)	5 (1%)	16	37
1	D	429/431 (100%)	376 (88%)	43 (10%)	10 (2%)	8	18
All	All	1716/1724 (100%)	1533 (89%)	161 (9%)	22 (1%)	15	35

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	240	HIS
1	B	38	GLU
1	B	188	THR
1	B	241	ARG
1	C	375	GLY
1	C	400	HIS
1	D	38	GLU
1	D	226	GLU
1	D	317	ALA
1	D	328	GLY
1	A	15	SER
1	B	15	SER
1	C	102	ASP
1	D	22	GLY
1	D	30	CYS
1	D	282	PRO
1	D	15	SER
1	D	264	LEU
1	D	251	SER
1	B	66	GLY
1	C	196	PRO
1	C	187	GLY

### 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	342/342 (100%)	314 (92%)	28 (8%)	14	30
1	B	342/342 (100%)	313 (92%)	29 (8%)	13	28
1	C	342/342 (100%)	319 (93%)	23 (7%)	20	42
1	D	342/342 (100%)	326 (95%)	16 (5%)	32	61
All	All	1368/1368 (100%)	1272 (93%)	96 (7%)	19	40

All (96) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	10	ARG
1	A	15	SER
1	A	27	LEU
1	A	55	VAL
1	A	94	LEU
1	A	102	ASP
1	A	142	LEU
1	A	163	LEU
1	A	165	ASN
1	A	166	ARG
1	A	186	GLU
1	A	188	THR
1	A	219	LEU
1	A	229	GLN
1	A	253	MET
1	A	263	ARG
1	A	264	LEU
1	A	280	LYS
1	A	329	LEU
1	A	336	LEU
1	A	344	GLN
1	A	386	LEU
1	A	388	ASP
1	A	390	LEU
1	A	398	LEU
1	A	406	LEU
1	A	407	LEU
1	A	409	LEU
1	B	10	ARG
1	B	27	LEU
1	B	28	LEU
1	B	57	LEU
1	B	62	LEU
1	B	83	THR
1	B	96	ASP
1	B	98	LEU
1	B	109	GLU
1	B	128	ARG
1	B	155	ARG
1	B	165	ASN
1	B	175	SER
1	B	192	ARG
1	B	195	ARG

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Mol	Chain	Res	Type
1	B	211	THR
1	B	213	SER
1	B	219	LEU
1	B	226	GLU
1	B	229	GLN
1	B	244	ARG
1	B	264	LEU
1	B	325	LEU
1	B	329	LEU
1	B	336	LEU
1	B	386	LEU
1	B	390	LEU
1	B	407	LEU
1	B	409	LEU
1	C	10	ARG
1	C	27	LEU
1	C	57	LEU
1	C	109	GLU
1	C	165	ASN
1	C	166	ARG
1	C	227	ARG
1	C	229	GLN
1	C	261	TYR
1	C	264	LEU
1	C	276	PHE
1	C	278	GLN
1	C	292	GLU
1	C	336	LEU
1	C	342	GLN
1	C	359	ARG
1	C	363	GLU
1	C	364	GLU
1	C	386	LEU
1	C	389	TRP
1	C	398	LEU
1	C	409	LEU
1	C	415	LEU
1	D	10	ARG
1	D	27	LEU
1	D	55	VAL
1	D	57	LEU
1	D	96	ASP

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Mol	Chain	Res	Type
1	D	109	GLU
1	D	165	ASN
1	D	166	ARG
1	D	171	LEU
1	D	186	GLU
1	D	192	ARG
1	D	229	GLN
1	D	250	ASP
1	D	264	LEU
1	D	407	LEU
1	D	409	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	41	ASN
1	A	59	HIS
1	A	165	ASN
1	A	214	GLN
1	A	229	GLN
1	A	344	GLN
1	A	383	GLN
1	B	34	GLN
1	B	41	ASN
1	B	42	HIS
1	B	165	ASN
1	B	383	GLN
1	C	34	GLN
1	C	41	ASN
1	C	42	HIS
1	C	59	HIS
1	C	165	ASN
1	C	194	HIS
1	C	229	GLN
1	C	275	HIS
1	C	323	HIS
1	C	342	GLN
1	C	380	HIS
1	D	34	GLN
1	D	41	ASN
1	D	59	HIS

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Mol	Chain	Res	Type
1	D	165	ASN
1	D	194	HIS
1	D	214	GLN
1	D	229	GLN
1	D	238	HIS
1	D	301	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 78 ligands modelled in this entry, 8 are monoatomic - leaving 70 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	A	432	-	4,4,4	1.54	0	6,6,6	0.93	0
2	SO4	A	433	-	4,4,4	1.54	0	6,6,6	0.91	0
2	SO4	A	434	-	4,4,4	1.49	0	6,6,6	0.92	0
2	SO4	A	435	-	4,4,4	1.50	0	6,6,6	0.93	0
2	SO4	A	436	-	4,4,4	1.52	0	6,6,6	0.94	0
2	SO4	A	437	-	4,4,4	1.56	0	6,6,6	0.93	0
2	SO4	A	438	-	4,4,4	1.53	0	6,6,6	0.93	0
2	SO4	A	439	-	4,4,4	1.51	0	6,6,6	0.89	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	A	440	-	4,4,4	1.50	0	6,6,6	0.92	0
2	SO4	A	441	-	4,4,4	1.52	0	6,6,6	0.95	0
2	SO4	A	442	-	4,4,4	1.53	0	6,6,6	0.91	0
2	SO4	A	443	-	4,4,4	1.49	0	6,6,6	0.96	0
2	SO4	A	444	-	4,4,4	1.52	0	6,6,6	0.92	0
2	SO4	A	445	-	4,4,4	1.48	0	6,6,6	0.93	0
2	SO4	A	446	-	4,4,4	1.51	0	6,6,6	0.95	0
2	SO4	A	447	-	4,4,4	1.51	0	6,6,6	0.94	0
2	SO4	A	448	-	4,4,4	1.52	0	6,6,6	0.97	0
2	SO4	A	449	-	4,4,4	1.59	0	6,6,6	0.79	0
2	SO4	A	450	-	4,4,4	1.47	0	6,6,6	1.00	0
2	SO4	A	451	-	4,4,4	1.49	0	6,6,6	1.02	0
3	FLC	A	452	-	3,12,12	1.14	0	3,17,17	0.58	0
3	FLC	A	453	-	3,12,12	1.04	0	3,17,17	0.52	0
2	SO4	B	432	-	4,4,4	1.46	0	6,6,6	1.01	0
2	SO4	B	433	-	4,4,4	1.48	0	6,6,6	0.94	0
2	SO4	B	434	-	4,4,4	1.54	0	6,6,6	0.95	0
2	SO4	B	435	-	4,4,4	1.47	0	6,6,6	1.01	0
2	SO4	B	436	-	4,4,4	1.52	0	6,6,6	0.95	0
2	SO4	B	437	-	4,4,4	1.49	0	6,6,6	0.93	0
2	SO4	B	438	-	4,4,4	1.53	0	6,6,6	0.93	0
2	SO4	B	439	-	4,4,4	1.40	0	6,6,6	1.02	0
2	SO4	B	440	-	4,4,4	1.58	0	6,6,6	0.91	0
2	SO4	B	441	-	4,4,4	1.50	0	6,6,6	0.96	0
2	SO4	B	442	-	4,4,4	1.53	0	6,6,6	0.94	0
2	SO4	B	443	-	4,4,4	1.54	0	6,6,6	0.97	0
2	SO4	B	444	-	4,4,4	1.52	0	6,6,6	0.93	0
2	SO4	B	445	-	4,4,4	1.49	0	6,6,6	0.96	0
2	SO4	B	446	-	4,4,4	1.55	0	6,6,6	0.92	0
2	SO4	B	447	-	4,4,4	1.50	0	6,6,6	0.95	0
2	SO4	B	448	-	4,4,4	1.48	0	6,6,6	0.94	0
2	SO4	B	449	-	4,4,4	1.55	0	6,6,6	0.92	0
2	SO4	B	450	-	4,4,4	1.50	0	6,6,6	0.95	0
3	FLC	B	451	-	3,12,12	1.06	0	3,17,17	0.27	0
2	SO4	C	432	-	4,4,4	1.53	0	6,6,6	0.92	0
2	SO4	C	433	-	4,4,4	1.53	0	6,6,6	0.94	0
2	SO4	C	434	-	4,4,4	1.52	0	6,6,6	0.94	0
2	SO4	C	435	-	4,4,4	1.50	0	6,6,6	0.95	0
2	SO4	C	436	-	4,4,4	1.52	0	6,6,6	0.94	0
2	SO4	C	437	-	4,4,4	1.55	0	6,6,6	0.93	0
2	SO4	C	438	-	4,4,4	1.55	0	6,6,6	0.93	0
2	SO4	C	439	-	4,4,4	1.53	0	6,6,6	0.93	0
2	SO4	C	440	-	4,4,4	1.53	0	6,6,6	0.96	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	C	441	-	4,4,4	1.51	0	6,6,6	0.96	0
2	SO4	C	442	-	4,4,4	1.52	0	6,6,6	0.94	0
2	SO4	C	443	-	4,4,4	1.55	0	6,6,6	0.90	0
2	SO4	C	444	-	4,4,4	1.53	0	6,6,6	0.95	0
2	SO4	C	445	-	4,4,4	1.52	0	6,6,6	0.93	0
2	SO4	C	446	-	4,4,4	1.52	0	6,6,6	0.93	0
2	SO4	C	447	-	4,4,4	1.49	0	6,6,6	0.96	0
2	SO4	C	448	-	4,4,4	1.56	0	6,6,6	0.91	0
2	SO4	C	449	-	4,4,4	1.54	0	6,6,6	0.92	0
2	SO4	C	450	-	4,4,4	1.50	0	6,6,6	0.98	0
2	SO4	D	432	-	4,4,4	1.51	0	6,6,6	0.99	0
2	SO4	D	433	-	4,4,4	1.49	0	6,6,6	1.02	0
2	SO4	D	434	-	4,4,4	1.56	0	6,6,6	0.92	0
2	SO4	D	435	-	4,4,4	1.50	0	6,6,6	0.94	0
2	SO4	D	436	-	4,4,4	1.50	0	6,6,6	0.94	0
2	SO4	D	437	-	4,4,4	1.56	0	6,6,6	0.92	0
2	SO4	D	438	-	4,4,4	1.45	0	6,6,6	0.98	0
2	SO4	D	439	-	4,4,4	1.55	0	6,6,6	0.95	0
2	SO4	D	440	-	4,4,4	1.56	0	6,6,6	0.91	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
2	SO4	A	432	-	-	0/0/0/0	0/0/0/0
2	SO4	A	433	-	-	0/0/0/0	0/0/0/0
2	SO4	A	434	-	-	0/0/0/0	0/0/0/0
2	SO4	A	435	-	-	0/0/0/0	0/0/0/0
2	SO4	A	436	-	-	0/0/0/0	0/0/0/0
2	SO4	A	437	-	-	0/0/0/0	0/0/0/0
2	SO4	A	438	-	-	0/0/0/0	0/0/0/0
2	SO4	A	439	-	-	0/0/0/0	0/0/0/0
2	SO4	A	440	-	-	0/0/0/0	0/0/0/0
2	SO4	A	441	-	-	0/0/0/0	0/0/0/0
2	SO4	A	442	-	-	0/0/0/0	0/0/0/0
2	SO4	A	443	-	-	0/0/0/0	0/0/0/0
2	SO4	A	444	-	-	0/0/0/0	0/0/0/0
2	SO4	A	445	-	-	0/0/0/0	0/0/0/0
2	SO4	A	446	-	-	0/0/0/0	0/0/0/0
2	SO4	A	447	-	-	0/0/0/0	0/0/0/0
2	SO4	A	448	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	A	449	-	-	0/0/0/0	0/0/0/0
2	SO4	A	450	-	-	0/0/0/0	0/0/0/0
2	SO4	A	451	-	-	0/0/0/0	0/0/0/0
3	FLC	A	452	-	-	0/6/16/16	0/0/0/0
3	FLC	A	453	-	-	0/6/16/16	0/0/0/0
2	SO4	B	432	-	-	0/0/0/0	0/0/0/0
2	SO4	B	433	-	-	0/0/0/0	0/0/0/0
2	SO4	B	434	-	-	0/0/0/0	0/0/0/0
2	SO4	B	435	-	-	0/0/0/0	0/0/0/0
2	SO4	B	436	-	-	0/0/0/0	0/0/0/0
2	SO4	B	437	-	-	0/0/0/0	0/0/0/0
2	SO4	B	438	-	-	0/0/0/0	0/0/0/0
2	SO4	B	439	-	-	0/0/0/0	0/0/0/0
2	SO4	B	440	-	-	0/0/0/0	0/0/0/0
2	SO4	B	441	-	-	0/0/0/0	0/0/0/0
2	SO4	B	442	-	-	0/0/0/0	0/0/0/0
2	SO4	B	443	-	-	0/0/0/0	0/0/0/0
2	SO4	B	444	-	-	0/0/0/0	0/0/0/0
2	SO4	B	445	-	-	0/0/0/0	0/0/0/0
2	SO4	B	446	-	-	0/0/0/0	0/0/0/0
2	SO4	B	447	-	-	0/0/0/0	0/0/0/0
2	SO4	B	448	-	-	0/0/0/0	0/0/0/0
2	SO4	B	449	-	-	0/0/0/0	0/0/0/0
2	SO4	B	450	-	-	0/0/0/0	0/0/0/0
3	FLC	B	451	-	-	0/6/16/16	0/0/0/0
2	SO4	C	432	-	-	0/0/0/0	0/0/0/0
2	SO4	C	433	-	-	0/0/0/0	0/0/0/0
2	SO4	C	434	-	-	0/0/0/0	0/0/0/0
2	SO4	C	435	-	-	0/0/0/0	0/0/0/0
2	SO4	C	436	-	-	0/0/0/0	0/0/0/0
2	SO4	C	437	-	-	0/0/0/0	0/0/0/0
2	SO4	C	438	-	-	0/0/0/0	0/0/0/0
2	SO4	C	439	-	-	0/0/0/0	0/0/0/0
2	SO4	C	440	-	-	0/0/0/0	0/0/0/0
2	SO4	C	441	-	-	0/0/0/0	0/0/0/0
2	SO4	C	442	-	-	0/0/0/0	0/0/0/0
2	SO4	C	443	-	-	0/0/0/0	0/0/0/0
2	SO4	C	444	-	-	0/0/0/0	0/0/0/0
2	SO4	C	445	-	-	0/0/0/0	0/0/0/0
2	SO4	C	446	-	-	0/0/0/0	0/0/0/0
2	SO4	C	447	-	-	0/0/0/0	0/0/0/0
2	SO4	C	448	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	C	449	-	-	0/0/0/0	0/0/0/0
2	SO4	C	450	-	-	0/0/0/0	0/0/0/0
2	SO4	D	432	-	-	0/0/0/0	0/0/0/0
2	SO4	D	433	-	-	0/0/0/0	0/0/0/0
2	SO4	D	434	-	-	0/0/0/0	0/0/0/0
2	SO4	D	435	-	-	0/0/0/0	0/0/0/0
2	SO4	D	436	-	-	0/0/0/0	0/0/0/0
2	SO4	D	437	-	-	0/0/0/0	0/0/0/0
2	SO4	D	438	-	-	0/0/0/0	0/0/0/0
2	SO4	D	439	-	-	0/0/0/0	0/0/0/0
2	SO4	D	440	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	441	SO4	1	0
2	A	448	SO4	1	0
3	A	452	FLC	1	0
3	A	453	FLC	1	0
2	B	433	SO4	3	0
2	B	437	SO4	1	0
2	B	441	SO4	1	0
2	B	446	SO4	2	0
2	B	448	SO4	2	0
3	B	451	FLC	4	0
2	C	434	SO4	1	0
2	D	433	SO4	4	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, 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	431/431 (100%)	-0.07	10 (2%) 64 66	22, 40, 63, 89	0
1	B	431/431 (100%)	-0.01	6 (1%) 78 79	22, 43, 74, 93	0
1	C	431/431 (100%)	0.66	49 (11%) 7 6	26, 72, 125, 136	0
1	D	431/431 (100%)	0.99	91 (21%) 1 1	34, 75, 147, 153	0
All	All	1724/1724 (100%)	0.39	156 (9%) 12 10	22, 51, 129, 153	0

All (156) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	216	GLY	6.6
1	D	218	VAL	6.2
1	D	212	LEU	5.9
1	D	242	LEU	5.6
1	D	360	ILE	5.4
1	C	353	ALA	5.0
1	D	370	SER	4.9
1	D	213	SER	4.9
1	D	334	ASN	4.9
1	C	214	GLN	4.8
1	D	208	LEU	4.7
1	D	367	LEU	4.7
1	C	415	LEU	4.6
1	D	286	ALA	4.5
1	D	302	ARG	4.5
1	D	333	ARG	4.4
1	D	306	PRO	4.4
1	D	326	LYS	4.3
1	D	332	PRO	4.3
1	D	363	GLU	4.2
1	D	293	HIS	4.2

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Mol	Chain	Res	Type	RSRZ
1	D	356	PRO	4.2
1	D	201	VAL	4.2
1	D	335	ALA	4.2
1	D	239	GLY	4.1
1	D	316	LEU	4.1
1	D	245	ALA	4.1
1	D	369	ALA	4.1
1	C	244	ARG	4.0
1	C	326	LYS	4.0
1	D	304	PRO	4.0
1	A	364	GLU	4.0
1	D	325	LEU	3.9
1	D	311	ALA	3.9
1	C	354	ARG	3.9
1	C	213	SER	3.9
1	D	244	ARG	3.9
1	C	356	PRO	3.9
1	C	362	GLY	3.9
1	D	207	ILE	3.8
1	D	361	LEU	3.8
1	D	374	LEU	3.7
1	C	99	LYS	3.7
1	B	78	GLY	3.7
1	C	329	LEU	3.7
1	C	240	HIS	3.6
1	D	295	GLU	3.6
1	C	367	LEU	3.6
1	D	354	ARG	3.6
1	C	276	PHE	3.6
1	D	362	GLY	3.5
1	D	211	THR	3.5
1	C	306	PRO	3.5
1	C	363	GLU	3.4
1	D	353	ALA	3.4
1	D	217	LYS	3.4
1	D	364	GLU	3.4
1	C	352	ILE	3.3
1	D	338	PHE	3.3
1	D	214	GLN	3.3
1	D	324	HIS	3.3
1	D	330	SER	3.2
1	D	246	PRO	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	322	LEU	3.1
1	D	240	HIS	3.1
1	D	250	ASP	3.1
1	B	35	GLY	3.0
1	C	333	ARG	3.0
1	C	371	VAL	3.0
1	C	275	HIS	3.0
1	D	292	GLU	3.0
1	D	225	VAL	3.0
1	D	368	ARG	2.9
1	D	331	ASP	2.9
1	C	215	GLY	2.9
1	D	359	ARG	2.9
1	C	368	ARG	2.9
1	C	335	ALA	2.8
1	D	248	TYR	2.8
1	C	241	ARG	2.8
1	D	249	LEU	2.8
1	C	243	PRO	2.8
1	D	36	LYS	2.8
1	C	294	THR	2.8
1	A	365	VAL	2.8
1	D	307	MET	2.7
1	C	210	LYS	2.7
1	C	366	PRO	2.7
1	D	223	PHE	2.7
1	D	300	LEU	2.7
1	C	226	GLU	2.7
1	D	219	LEU	2.7
1	C	238	HIS	2.6
1	C	223	PHE	2.6
1	B	36	LYS	2.6
1	D	98	LEU	2.6
1	C	242	LEU	2.6
1	C	365	VAL	2.5
1	C	322	LEU	2.5
1	D	371	VAL	2.5
1	C	327	HIS	2.5
1	D	365	VAL	2.5
1	C	212	LEU	2.5
1	D	305	GLY	2.4
1	A	358	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	364	GLU	2.4
1	D	337	VAL	2.4
1	C	420	VAL	2.4
1	D	323	HIS	2.4
1	D	372	HIS	2.4
1	D	313	SER	2.4
1	A	356	PRO	2.4
1	C	408	ALA	2.3
1	C	102	ASP	2.3
1	D	352	ILE	2.3
1	D	209	GLU	2.3
1	D	210	LYS	2.3
1	A	131	ALA	2.3
1	A	361	LEU	2.3
1	C	283	PHE	2.3
1	C	338	PHE	2.3
1	C	377	PHE	2.3
1	D	222	THR	2.3
1	D	205	LEU	2.3
1	A	354	ARG	2.3
1	D	312	GLY	2.3
1	D	329	LEU	2.3
1	D	60	ALA	2.2
1	D	161	GLY	2.2
1	D	380	HIS	2.2
1	D	350	GLU	2.2
1	D	339	VAL	2.2
1	D	341	TYR	2.2
1	D	336	LEU	2.2
1	A	22	GLY	2.1
1	D	355	PRO	2.1
1	C	414	ALA	2.1
1	C	332	PRO	2.1
1	D	379	GLY	2.1
1	C	379	GLY	2.1
1	D	291	VAL	2.1
1	C	108	PRO	2.1
1	D	102	ASP	2.1
1	A	359	ARG	2.1
1	D	241	ARG	2.1
1	D	247	ILE	2.1
1	D	226	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	58	THR	2.1
1	D	294	THR	2.1
1	B	241	ARG	2.1
1	B	112	GLU	2.1
1	D	224	ALA	2.1
1	A	360	ILE	2.0
1	C	196	PRO	2.0
1	B	77	ARG	2.0
1	D	285	PRO	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](#)

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	SO4	B	437	5/5	0.68	0.45	21.19	169,169,170,170	0
2	SO4	B	441	5/5	0.89	0.31	8.16	117,118,119,119	0
2	SO4	A	448	5/5	0.89	0.35	5.83	135,135,136,136	0
3	FLC	B	451	13/13	0.90	0.33	5.37	68,70,79,80	0
2	SO4	C	441	5/5	0.77	0.46	3.77	147,147,147,147	0
2	SO4	D	434	5/5	0.67	0.48	3.75	163,163,164,164	0
2	SO4	A	442	5/5	0.72	0.30	3.70	141,141,141,142	0
2	SO4	C	436	5/5	0.93	0.45	3.58	139,139,139,139	0
2	SO4	A	438	5/5	0.80	0.35	3.51	130,130,131,131	0
2	SO4	B	447	5/5	0.94	0.22	2.76	121,121,121,121	0
2	SO4	A	450	5/5	0.81	0.29	1.78	145,145,145,145	0
2	SO4	C	434	5/5	0.80	0.50	1.77	146,146,147,147	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	A	439	5/5	0.96	0.24	1.39	91,92,92,93	0
2	SO4	B	440	5/5	0.94	0.18	1.03	81,81,82,83	0
2	SO4	D	432	5/5	0.96	0.19	0.58	80,80,81,82	0
2	SO4	A	449	5/5	0.97	0.18	0.52	48,49,52,53	0
2	SO4	D	433	5/5	0.76	0.38	0.51	156,157,158,158	0
2	SO4	A	443	5/5	0.77	0.19	0.25	123,124,124,124	0
2	SO4	B	439	5/5	0.97	0.17	0.01	45,45,49,49	0
2	SO4	B	443	5/5	0.96	0.15	-0.20	57,59,60,61	0
2	SO4	D	436	5/5	0.53	0.32	-0.31	170,170,170,170	0
2	SO4	A	441	5/5	0.98	0.13	-0.31	43,45,48,49	0
2	SO4	C	448	5/5	0.92	0.17	-0.34	97,97,98,98	0
4	ZN	C	452	1/1	0.89	0.18	-0.53	125,125,125,125	0
2	SO4	C	446	5/5	0.90	0.29	-0.70	119,120,120,120	0
2	SO4	D	440	5/5	0.94	0.25	-0.79	85,85,85,86	0
2	SO4	D	438	5/5	0.89	0.15	-0.84	110,110,111,111	0
4	ZN	D	442	1/1	0.84	0.21	-1.28	121,121,121,121	0
2	SO4	A	440	5/5	0.97	0.12	-1.45	81,81,82,82	0
4	ZN	D	441	1/1	0.93	0.20	-1.47	98,98,98,98	0
4	ZN	A	455	1/1	0.57	0.15	-1.66	88,88,88,88	0
2	SO4	C	440	5/5	0.96	0.15	-2.05	87,87,88,88	0
4	ZN	C	451	1/1	0.80	0.10	-2.05	82,82,82,82	0
4	ZN	B	452	1/1	0.87	0.13	-2.57	74,74,74,74	0
2	SO4	A	451	5/5	0.98	0.11	-2.65	56,58,60,62	0
4	ZN	B	453	1/1	0.93	0.09	-3.72	88,88,88,88	0
4	ZN	A	454	1/1	0.95	0.08	-5.84	72,72,72,72	0
2	SO4	A	434	5/5	0.85	0.21	-	117,117,117,118	0
2	SO4	A	435	5/5	0.65	0.33	-	142,142,143,143	0
2	SO4	C	437	5/5	0.80	0.19	-	133,134,134,134	0
2	SO4	B	436	5/5	0.52	0.33	-	148,148,149,149	0
2	SO4	D	439	5/5	0.98	0.10	-	67,67,68,69	0
2	SO4	B	450	5/5	0.71	0.30	-	137,137,138,138	0
2	SO4	A	436	5/5	0.84	0.32	-	131,131,131,131	0
2	SO4	C	445	5/5	0.56	0.33	-	162,162,163,163	0
2	SO4	A	433	5/5	0.85	0.23	-	121,121,122,122	0
2	SO4	A	447	5/5	0.90	0.20	-	125,126,126,126	0
2	SO4	B	444	5/5	0.87	0.16	-	124,124,124,124	0
3	FLC	A	453	13/13	0.71	0.41	-	122,123,124,124	0
2	SO4	C	432	5/5	0.90	0.18	-	131,131,132,132	0
2	SO4	C	435	5/5	0.98	0.09	-	71,72,73,73	0
2	SO4	A	437	5/5	0.78	0.28	-	148,148,149,149	0
2	SO4	B	432	5/5	0.96	0.09	-	76,77,79,79	0
3	FLC	A	452	13/13	0.78	0.38	-	108,111,112,112	0

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*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	C	449	5/5	0.92	0.10	-	114,114,114,115	0
2	SO4	C	444	5/5	0.93	0.24	-	118,118,118,118	0
2	SO4	B	449	5/5	0.93	0.17	-	98,98,99,99	0
2	SO4	A	432	5/5	0.94	0.22	-	103,103,104,104	0
2	SO4	C	438	5/5	0.71	0.24	-	138,138,139,139	0
2	SO4	B	438	5/5	0.93	0.24	-	110,110,111,111	0
2	SO4	B	433	5/5	0.78	0.55	-	171,171,171,171	0
2	SO4	B	435	5/5	0.92	0.20	-	101,101,102,103	0
2	SO4	B	434	5/5	0.86	0.23	-	136,136,136,137	0
2	SO4	C	443	5/5	0.91	0.11	-	102,102,103,103	0
2	SO4	B	445	5/5	0.92	0.25	-	114,115,115,115	0
2	SO4	B	448	5/5	0.66	0.58	-	178,178,178,178	0
2	SO4	D	437	5/5	0.89	0.22	-	109,110,110,110	0
2	SO4	C	433	5/5	0.91	0.38	-	141,141,141,141	0
2	SO4	B	442	5/5	0.77	0.25	-	121,122,123,123	0
2	SO4	D	435	5/5	0.82	0.24	-	126,127,127,127	0
2	SO4	C	450	5/5	0.92	0.34	-	116,116,116,116	0
2	SO4	C	439	5/5	0.94	0.11	-	105,105,105,105	0
2	SO4	C	442	5/5	0.77	0.28	-	139,140,140,140	0
2	SO4	A	445	5/5	0.92	0.21	-	101,102,103,103	0
2	SO4	C	447	5/5	0.81	0.17	-	153,154,154,154	0
2	SO4	B	446	5/5	0.78	0.57	-	154,154,155,155	0
2	SO4	A	444	5/5	0.85	0.27	-	111,111,111,111	0
2	SO4	A	446	5/5	0.86	0.17	-	113,114,114,114	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.