



# Full wwPDB X-ray Structure Validation Report ⓘ

May 4, 2016 – 04:38 PM EDT

PDB ID : 5FI7  
Title : Crystal structure of human GAC in complex with inhibitor UPGL\_00015: 2-phenyl- {N}-[5-[(3 {S})-3-[[5-(2-phenylethanoylamino)-1,3,4-thiadiazol-2-yl]oxy]pyrrolidin-1-yl]-1,3,4-thiadiazol-2-yl]ethanamide  
Authors : Huang, Q.; Cerione, R.  
Deposited on : 2015-12-22  
Resolution : 2.50 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027457  
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) : rb-20027457

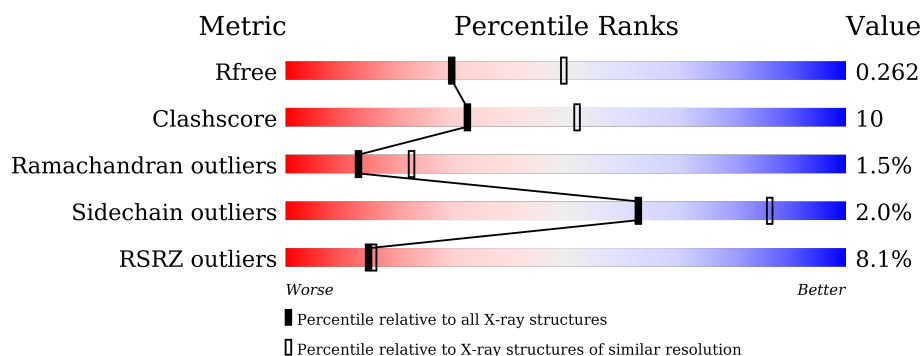
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	539	<div> <div>7%</div> <div> <div></div> <div>59%</div> <div>15%</div> <div>••</div> <div>24%</div> </div> </div>
1	B	539	<div> <div>6%</div> <div> <div></div> <div>61%</div> <div>14%</div> <div>•</div> <div>24%</div> </div> </div>
1	C	539	<div> <div>7%</div> <div> <div></div> <div>60%</div> <div>14%</div> <div>•</div> <div>24%</div> </div> </div>
1	D	539	<div> <div>5%</div> <div> <div></div> <div>60%</div> <div>14%</div> <div>•</div> <div>24%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13050 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 Glutaminase kidney isoform, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	410	Total	C	N	O	S	1	0	0
			3194	2036	540	590	28			
1	B	410	Total	C	N	O	S	1	0	0
			3194	2036	540	590	28			
1	C	410	Total	C	N	O	S	1	0	0
			3194	2036	540	590	28			
1	D	410	Total	C	N	O	S	1	0	0
			3194	2036	540	590	28			

There are 48 discrepancies between the modelled and reference sequences:

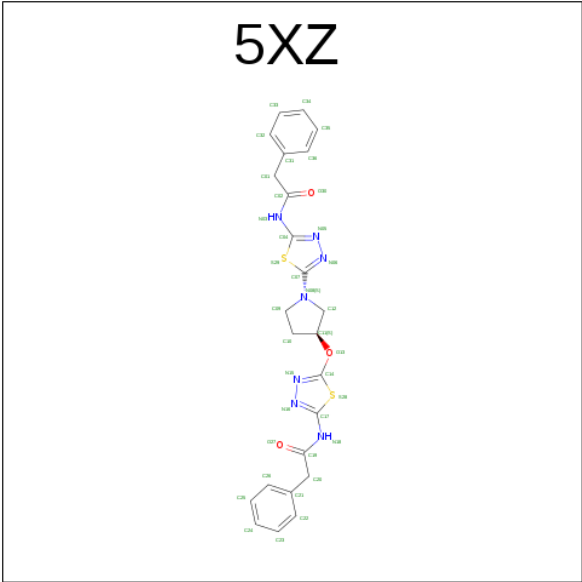
Chain	Residue	Modelled	Actual	Comment	Reference
A	59	MET	-	initiating methionine	UNP O94925
A	60	ARG	-	expression tag	UNP O94925
A	61	GLY	-	expression tag	UNP O94925
A	62	SER	-	expression tag	UNP O94925
A	63	HIS	-	expression tag	UNP O94925
A	64	HIS	-	expression tag	UNP O94925
A	65	HIS	-	expression tag	UNP O94925
A	66	HIS	-	expression tag	UNP O94925
A	67	HIS	-	expression tag	UNP O94925
A	68	HIS	-	expression tag	UNP O94925
A	69	GLY	-	expression tag	UNP O94925
A	70	SER	-	expression tag	UNP O94925
B	59	MET	-	initiating methionine	UNP O94925
B	60	ARG	-	expression tag	UNP O94925
B	61	GLY	-	expression tag	UNP O94925
B	62	SER	-	expression tag	UNP O94925
B	63	HIS	-	expression tag	UNP O94925
B	64	HIS	-	expression tag	UNP O94925
B	65	HIS	-	expression tag	UNP O94925
B	66	HIS	-	expression tag	UNP O94925
B	67	HIS	-	expression tag	UNP O94925

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Chain	Residue	Modelled	Actual	Comment	Reference
B	68	HIS	-	expression tag	UNP O94925
B	69	GLY	-	expression tag	UNP O94925
B	70	SER	-	expression tag	UNP O94925
C	59	MET	-	initiating methionine	UNP O94925
C	60	ARG	-	expression tag	UNP O94925
C	61	GLY	-	expression tag	UNP O94925
C	62	SER	-	expression tag	UNP O94925
C	63	HIS	-	expression tag	UNP O94925
C	64	HIS	-	expression tag	UNP O94925
C	65	HIS	-	expression tag	UNP O94925
C	66	HIS	-	expression tag	UNP O94925
C	67	HIS	-	expression tag	UNP O94925
C	68	HIS	-	expression tag	UNP O94925
C	69	GLY	-	expression tag	UNP O94925
C	70	SER	-	expression tag	UNP O94925
D	59	MET	-	initiating methionine	UNP O94925
D	60	ARG	-	expression tag	UNP O94925
D	61	GLY	-	expression tag	UNP O94925
D	62	SER	-	expression tag	UNP O94925
D	63	HIS	-	expression tag	UNP O94925
D	64	HIS	-	expression tag	UNP O94925
D	65	HIS	-	expression tag	UNP O94925
D	66	HIS	-	expression tag	UNP O94925
D	67	HIS	-	expression tag	UNP O94925
D	68	HIS	-	expression tag	UNP O94925
D	69	GLY	-	expression tag	UNP O94925
D	70	SER	-	expression tag	UNP O94925

- Molecule 2 is 2-phenyl- {N}-[5-[(3 {S})-3-[[5-(2-phenylethanoylamino)-1,3,4-thiadiazol-2-yl]oxy]pyrrolidin-1-yl]-1,3,4-thiadiazol-2-yl]ethanamide (three-letter code: 5XZ) (formula: C<sub>24</sub>H<sub>23</sub>N<sub>7</sub>O<sub>3</sub>S<sub>2</sub>).



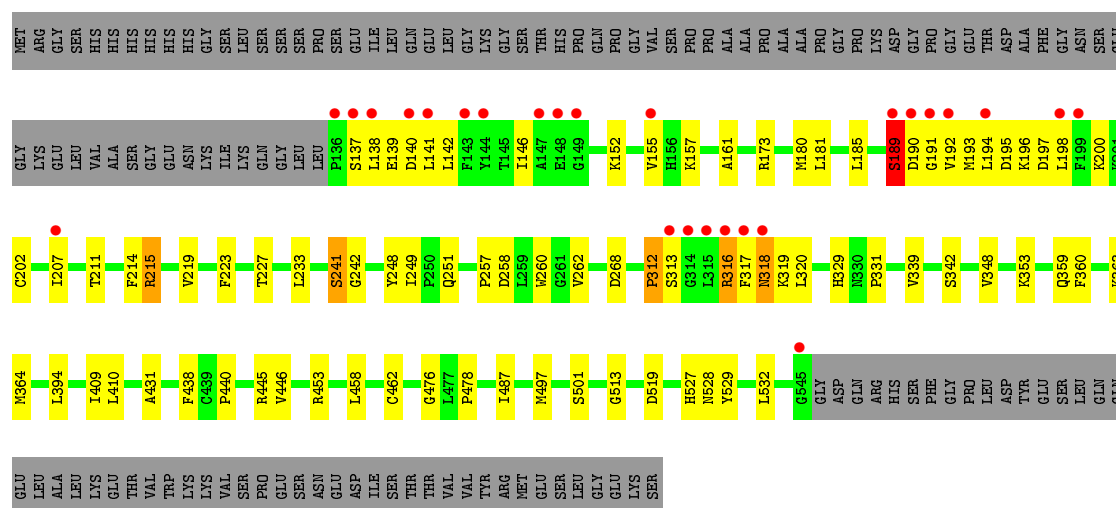
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			36	24	7	3	2		
2	C	1	Total	C	N	O	S	0	0
			36	24	7	3	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	51	Total	O	0	0
			51	51		
3	B	53	Total	O	0	0
			53	53		
3	C	48	Total	O	0	0
			48	48		
3	D	50	Total	O	0	0
			50	50		



- Chain C: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.17Å 138.83Å 176.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.90 – 2.50 49.59 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.5 (44.90-2.50) 83.4 (49.59-2.30)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.12 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, $R_{free}$	0.218 , 0.267 0.211 , 0.262	Depositor DCC
$R_{free}$ test set	1386 reflections (1.87%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.3	Xtriage
Anisotropy	0.823	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 41.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13050	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	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 57.61 % 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 2.3086e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: 5XZ

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	0.43	0/3266	0.63	3/4408 (0.1%)
1	B	0.43	0/3266	0.60	0/4408
1	C	0.49	1/3266 (0.0%)	0.64	2/4408 (0.0%)
1	D	0.44	0/3266	0.61	2/4408 (0.0%)
All	All	0.45	1/13064 (0.0%)	0.62	7/17632 (0.0%)

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	B	0	1
1	C	0	2
1	D	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	255	PHE	CE2-CZ	-5.81	1.26	1.37

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	LEU	CA-CB-CG	-6.80	99.66	115.30
1	C	316	ARG	NE-CZ-NH2	6.01	123.31	120.30
1	C	316	ARG	NE-CZ-NH1	-5.88	117.36	120.30
1	A	317	PHE	CB-CG-CD2	5.62	124.73	120.80
1	D	173	ARG	NE-CZ-NH2	-5.52	117.54	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	173	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	D	194	LEU	CA-CB-CG	5.07	126.95	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	314	GLY	Peptide
1	C	252	LEU	Peptide
1	C	315	LEU	Peptide
1	D	312	PRO	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	3194	0	3167	78	0
1	B	3194	0	3167	58	0
1	C	3194	0	3167	82	0
1	D	3194	0	3167	70	0
2	A	36	0	0	2	0
2	C	36	0	0	1	0
3	A	51	0	0	2	0
3	B	53	0	0	1	0
3	C	48	0	0	2	0
3	D	50	0	0	1	0
All	All	13050	0	12668	268	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 10.

All (268) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:ASP:OD2	1:C:196:LYS:NZ	1.86	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:489:LEU:HD23	1:B:497:MET:HE2	1.42	0.99
1:D:146:ILE:O	1:D:157:LYS:NZ	2.01	0.93
1:C:345:LYS:HE3	1:C:356:TYR:CE2	2.06	0.90
1:B:489:LEU:HD23	1:B:497:MET:CE	2.03	0.88
1:C:137:SER:OG	1:C:140:ASP:OD1	1.94	0.84
1:A:148:GLU:HG3	1:A:150:GLN:HG2	1.58	0.83
1:D:313:SER:HA	1:D:316:ARG:CZ	2.08	0.83
1:C:316:ARG:HD2	1:C:317:PHE:CE2	2.12	0.83
1:B:362:ASN:ND2	3:B:602:HOH:O	2.13	0.81
1:D:139:GLU:N	1:D:139:GLU:OE1	2.13	0.81
1:B:316:ARG:HH21	1:B:317:PHE:HE1	1.28	0.80
1:A:142:LEU:HD22	1:A:199:PHE:HZ	1.49	0.78
1:D:140:ASP:OD2	1:D:196:LYS:NZ	2.15	0.77
1:C:312:PRO:HA	1:C:462:CYS:SG	2.25	0.77
1:C:297:ASN:HD22	1:C:448:SER:H	1.33	0.76
1:C:508:GLY:O	3:C:701:HOH:O	2.02	0.76
1:D:195:ASP:OD1	1:D:198:LEU:N	2.17	0.76
1:A:315:LEU:HD11	1:A:466:ASP:O	1.86	0.76
1:C:215:ARG:HA	1:C:215:ARG:HE	1.50	0.75
1:C:345:LYS:HE3	1:C:356:TYR:CD2	2.22	0.74
1:B:187:THR:HG23	1:B:188:THR:HG23	1.70	0.74
1:A:233:LEU:HD22	1:A:519:ASP:HB3	1.71	0.73
1:B:493:ASN:HD21	1:D:532:LEU:H	1.37	0.73
1:B:251:GLN:OE1	1:B:251:GLN:N	2.19	0.70
1:B:493:ASN:ND2	1:D:532:LEU:H	1.88	0.70
1:D:207:ILE:O	1:D:211:THR:HG23	1.92	0.70
1:C:184:THR:HA	1:C:187:THR:HB	1.74	0.69
1:C:316:ARG:CZ	1:C:317:PHE:CD2	2.76	0.69
1:A:148:GLU:CG	1:A:150:GLN:HG2	2.23	0.69
1:B:313:SER:OG	1:B:314:GLY:N	2.26	0.68
1:B:528:ASN:OD1	1:D:528:ASN:ND2	2.27	0.68
1:C:146:ILE:O	1:C:157:LYS:NZ	2.23	0.68
1:C:316:ARG:NH1	1:C:317:PHE:CE2	2.62	0.67
1:A:142:LEU:HD23	1:A:146:ILE:HD13	1.76	0.67
1:C:313:SER:HA	1:C:316:ARG:CZ	2.25	0.67
1:A:397:LYS:NZ	3:A:702:HOH:O	2.29	0.66
1:B:233:LEU:HD22	1:B:519:ASP:HB3	1.77	0.66
1:C:313:SER:OG	1:C:314:GLY:N	2.29	0.66
1:A:316:ARG:HA	1:A:316:ARG:NE	2.12	0.65
1:C:255:PHE:HD1	1:C:259:LEU:HD13	1.61	0.65
1:C:306:ARG:NH2	1:D:258:ASP:OD1	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:537:LYS:H	1:A:537:LYS:HD3	1.62	0.65
1:C:345:LYS:CE	1:C:356:TYR:CE2	2.80	0.64
1:C:323:ASN:HB3	1:C:329:HIS:HD2	1.62	0.64
1:C:302:GLU:OE2	1:D:241:SER:HB3	1.98	0.63
1:A:152:LYS:HG2	1:A:195:ASP:HA	1.81	0.63
1:C:306:ARG:HH12	1:D:257:PRO:HB2	1.63	0.63
1:D:215:ARG:HA	1:D:215:ARG:HE	1.64	0.63
1:C:381:ARG:NH2	1:C:411:ASP:OD2	2.31	0.62
1:C:316:ARG:HG2	1:C:317:PHE:H	1.64	0.62
1:D:181:LEU:O	1:D:185:LEU:HD12	1.99	0.62
1:A:142:LEU:HD22	1:A:199:PHE:CZ	2.33	0.62
1:A:161:ALA:HB1	1:A:214:PHE:HE1	1.65	0.61
1:D:317:PHE:O	1:D:319:LYS:N	2.33	0.61
1:B:251:GLN:NE2	1:B:379:SER:OG	2.25	0.61
1:D:348:VAL:HG23	1:D:353:LYS:HG3	1.81	0.61
1:A:317:PHE:CE1	1:C:316:ARG:HG3	2.36	0.61
1:C:316:ARG:CG	1:C:317:PHE:H	2.13	0.61
1:A:194:LEU:O	1:A:196:LYS:N	2.32	0.61
1:C:323:ASN:HB3	1:C:329:HIS:CD2	2.36	0.60
1:D:139:GLU:HB2	1:D:200:LYS:HD2	1.84	0.60
1:C:144:TYR:O	1:C:148:GLU:HG3	2.02	0.60
1:A:137:SER:OG	1:A:138:LEU:N	2.35	0.60
1:A:469:GLY:HA3	1:C:311:GLU:HG2	1.83	0.60
1:A:142:LEU:HD12	1:A:211:THR:HG23	1.84	0.59
1:B:287:VAL:HG13	1:B:291:LYS:HD3	1.85	0.59
1:C:142:LEU:HD22	1:C:199:PHE:HZ	1.67	0.59
1:D:248:TYR:CD1	1:D:249:ILE:HG12	2.37	0.59
1:D:152:LYS:HB3	1:D:193:MET:HB3	1.83	0.59
1:A:244:LYS:HE2	1:A:245:VAL:O	2.02	0.59
1:A:195:ASP:O	1:A:197:ASP:N	2.36	0.59
1:B:152:LYS:HG3	1:B:193:MET:SD	2.43	0.58
1:D:313:SER:HA	1:D:316:ARG:NH1	2.19	0.58
1:C:312:PRO:HB3	1:C:461:SER:HB2	1.86	0.58
1:D:316:ARG:HH22	1:D:329:HIS:CG	2.20	0.58
1:A:363:LYS:NZ	3:A:706:HOH:O	2.37	0.58
1:B:143:PHE:CE2	1:B:196:LYS:HG2	2.39	0.57
1:C:161:ALA:HB1	1:C:214:PHE:HE1	1.68	0.57
1:C:313:SER:HA	1:C:316:ARG:NH1	2.19	0.57
1:D:331:PRO:HD2	1:D:458:LEU:HD13	1.87	0.57
1:A:315:LEU:C	1:A:317:PHE:H	2.08	0.57
1:B:142:LEU:O	1:B:145:THR:OG1	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:GLN:HE22	1:B:379:SER:CB	2.17	0.57
1:B:285:SER:OG	1:B:288:LYS:NZ	2.36	0.57
1:B:251:GLN:HE21	1:B:375:ALA:C	2.08	0.57
1:B:150:GLN:NE2	1:B:152:LYS:HD3	2.20	0.56
1:B:316:ARG:NH2	1:D:316:ARG:HH11	2.05	0.55
1:C:181:LEU:HD23	1:C:202:CYS:SG	2.46	0.55
1:A:290:LEU:HD22	1:A:364:MET:CE	2.37	0.55
1:D:313:SER:O	1:D:316:ARG:HB2	2.07	0.55
1:C:181:LEU:O	1:C:185:LEU:HD12	2.07	0.54
1:C:316:ARG:HD2	1:C:317:PHE:CZ	2.41	0.54
1:D:487:ILE:HD12	1:D:513:GLY:HA3	1.88	0.54
1:A:364:MET:HG3	1:A:446:VAL:HG11	1.89	0.54
1:D:316:ARG:HG2	1:D:317:PHE:CD2	2.43	0.54
1:B:524:CYS:HA	1:B:539:LEU:O	2.06	0.54
1:A:223:PHE:O	1:A:227:THR:HG23	2.08	0.54
1:B:497:MET:HE1	1:B:516:PHE:HE1	1.72	0.54
1:C:357:VAL:O	1:C:361:LEU:HG	2.08	0.54
1:C:487:ILE:HD12	1:C:513:GLY:HA3	1.90	0.54
1:B:247:ASP:HA	1:B:253:ALA:HB2	1.90	0.53
1:D:313:SER:O	1:D:316:ARG:HD3	2.09	0.53
1:D:142:LEU:CD2	1:D:211:THR:HG22	2.39	0.53
1:A:319:LYS:HE3	2:A:601:5XZ:C24	2.38	0.53
1:B:453:ARG:HD3	1:D:527:HIS:CD2	2.42	0.53
1:A:144:TYR:OH	1:A:196:LYS:NZ	2.25	0.53
1:B:184:THR:O	1:B:187:THR:HG22	2.09	0.53
1:A:528:ASN:ND2	1:C:528:ASN:OD1	2.40	0.52
1:D:233:LEU:HD22	1:D:519:ASP:HB3	1.91	0.52
1:A:316:ARG:NH2	1:A:318:ASN:OD1	2.40	0.52
1:C:297:ASN:ND2	1:C:448:SER:H	2.03	0.52
1:B:184:THR:HG21	1:B:198:LEU:HD21	1.92	0.52
1:A:150:GLN:HG3	1:A:151:GLU:N	2.25	0.51
1:A:266:THR:HA	1:A:495:MET:HA	1.91	0.51
1:A:251:GLN:HG2	1:A:254:LYS:NZ	2.25	0.51
1:B:312:PRO:HA	1:B:462:CYS:SG	2.51	0.51
1:A:245:VAL:HG22	1:A:502:PRO:HB2	1.93	0.51
1:A:292:TYR:OH	1:A:305:HIS:NE2	2.33	0.51
1:C:191:GLY:HA3	1:C:193:MET:H	1.75	0.50
1:A:251:GLN:O	1:A:254:LYS:HG2	2.11	0.50
1:B:489:LEU:CD2	1:B:497:MET:HE2	2.28	0.50
1:C:342:SER:HA	1:C:409:ILE:HD12	1.94	0.50
1:D:138:LEU:HD23	1:D:141:LEU:HD21	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:431:ALA:HB1	1:C:440:PRO:HG2	1.93	0.50
1:B:151:GLU:OE1	1:B:196:LYS:NZ	2.33	0.50
1:B:231:ASP:O	1:B:235:GLU:HG2	2.11	0.50
1:D:476:GLY:O	1:D:528:ASN:HB2	2.10	0.50
1:C:247:ASP:HA	1:C:253:ALA:HB2	1.94	0.50
1:A:316:ARG:HH21	1:A:318:ASN:CG	2.15	0.49
1:D:161:ALA:HB1	1:D:214:PHE:HE1	1.76	0.49
1:D:248:TYR:O	1:D:249:ILE:HD13	2.13	0.49
1:D:251:GLN:NE2	1:D:251:GLN:H	2.10	0.49
1:C:465:TYR:HE1	3:C:701:HOH:O	1.94	0.49
1:B:527:HIS:CD2	1:D:453:ARG:HD2	2.48	0.49
1:A:147:ALA:C	1:A:149:GLY:H	2.16	0.49
1:C:255:PHE:HD1	1:C:259:LEU:CD1	2.25	0.48
1:C:316:ARG:NH1	1:C:317:PHE:CD2	2.81	0.48
1:C:301:THR:OG1	1:C:454:ASN:OD1	2.29	0.48
1:A:452:VAL:O	1:A:456:LEU:HG	2.12	0.48
1:C:244:LYS:O	1:C:244:LYS:HG2	2.12	0.48
1:A:315:LEU:C	1:A:317:PHE:N	2.67	0.48
1:A:316:ARG:HH22	1:A:319:LYS:NZ	2.11	0.48
1:A:247:ASP:O	1:A:249:ILE:N	2.46	0.48
1:C:252:LEU:HD23	1:C:252:LEU:O	2.13	0.48
1:B:431:ALA:HB1	1:B:440:PRO:HG3	1.95	0.48
1:B:478:PRO:HG3	1:D:529:TYR:CE1	2.50	0.47
1:A:151:GLU:O	1:A:152:LYS:HG3	2.14	0.47
1:A:248:TYR:CD1	1:A:249:ILE:HG23	2.49	0.47
1:C:151:GLU:CD	1:C:152:LYS:H	2.17	0.47
1:A:150:GLN:CG	1:A:151:GLU:H	2.27	0.47
1:B:315:LEU:O	1:B:318:ASN:ND2	2.46	0.47
1:D:317:PHE:O	1:D:319:LYS:HG3	2.14	0.47
1:B:161:ALA:HB1	1:B:214:PHE:HE1	1.79	0.47
1:C:266:THR:HA	1:C:495:MET:HA	1.96	0.47
1:A:528:ASN:HD21	1:C:528:ASN:CG	2.17	0.47
1:B:478:PRO:HD2	1:B:490:VAL:O	2.14	0.47
1:A:524:CYS:HA	1:A:539:LEU:O	2.14	0.47
1:A:363:LYS:HD3	1:A:444:GLU:OE2	2.14	0.47
1:B:361:LEU:HD22	1:B:429:MET:CE	2.45	0.47
1:C:187:THR:HG22	1:C:188:THR:HG23	1.97	0.47
1:D:223:PHE:O	1:D:227:THR:HG23	2.15	0.47
1:A:269:GLY:O	1:A:271:ARG:HG2	2.15	0.46
1:C:255:PHE:CD1	1:C:259:LEU:HD13	2.47	0.46
1:C:476:GLY:O	1:C:528:ASN:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:ARG:O	1:A:327:LYS:HD3	2.15	0.46
1:A:150:GLN:HG3	1:A:151:GLU:H	1.79	0.46
1:C:299:LEU:HD13	1:C:303:TYR:CE2	2.50	0.46
1:B:317:PHE:N	1:B:317:PHE:CD1	2.83	0.46
1:C:146:ILE:HD12	1:C:146:ILE:H	1.80	0.46
1:C:251:GLN:NE2	1:C:251:GLN:HA	2.30	0.46
1:A:348:VAL:O	1:A:353:LYS:HE3	2.16	0.46
1:A:476:GLY:O	1:A:528:ASN:HB2	2.16	0.46
1:C:316:ARG:NE	1:C:317:PHE:CD2	2.84	0.46
1:A:453:ARG:HD3	1:C:527:HIS:CD2	2.51	0.46
1:D:318:ASN:N	1:D:318:ASN:OD1	2.48	0.46
1:A:148:GLU:H	1:A:148:GLU:HG2	1.59	0.46
1:A:378:GLN:NE2	1:A:381:ARG:HD3	2.31	0.46
1:C:152:LYS:HB3	1:C:193:MET:HB3	1.98	0.46
1:D:219:VAL:N	1:D:268:ASP:OD2	2.48	0.46
1:B:244:LYS:HE3	1:B:245:VAL:O	2.17	0.45
1:A:151:GLU:HB2	1:A:152:LYS:H	1.52	0.45
1:D:138:LEU:O	1:D:142:LEU:HD23	2.16	0.45
1:C:479:ALA:HB2	1:C:489:LEU:HD12	1.99	0.45
1:A:152:LYS:HE2	1:A:195:ASP:OD2	2.17	0.45
1:C:215:ARG:HA	1:C:215:ARG:NE	2.24	0.45
1:D:195:ASP:OD1	1:D:197:ASP:N	2.50	0.45
1:A:140:ASP:HA	1:A:143:PHE:HB3	1.99	0.45
1:C:302:GLU:OE2	1:D:241:SER:CB	2.64	0.45
1:D:241:SER:HB2	1:D:242:GLY:H	1.56	0.45
1:D:260:TRP:CE3	1:D:501:SER:HB2	2.52	0.45
1:C:151:GLU:OE1	1:C:152:LYS:N	2.50	0.45
1:D:262:VAL:HG13	1:D:497:MET:CE	2.46	0.45
1:D:438:PHE:CE2	1:D:445:ARG:HB2	2.52	0.45
1:A:316:ARG:HH21	1:A:318:ASN:ND2	2.15	0.44
1:C:314:GLY:O	1:C:316:ARG:HB3	2.17	0.44
1:B:529:TYR:OH	1:D:478:PRO:HD3	2.17	0.44
1:B:266:THR:HA	1:B:495:MET:HA	1.99	0.44
1:B:489:LEU:HD23	1:B:497:MET:HE3	1.94	0.44
1:C:316:ARG:NH1	1:C:317:PHE:HE2	2.12	0.44
1:C:191:GLY:HA3	1:C:193:MET:N	2.33	0.44
1:C:316:ARG:HD2	1:C:317:PHE:CD2	2.50	0.44
1:A:244:LYS:HE3	1:A:247:ASP:OD2	2.17	0.44
1:D:364:MET:HG3	1:D:446:VAL:HG11	1.99	0.44
1:A:431:ALA:HB1	1:A:440:PRO:HG2	2.00	0.44
1:B:476:GLY:O	1:B:528:ASN:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:313:SER:OG	1:D:316:ARG:NH2	2.51	0.44
1:B:398:LYS:HA	1:B:398:LYS:HD3	1.81	0.44
1:B:537:LYS:HA	1:B:537:LYS:HE2	1.98	0.44
1:C:256:SER:O	1:C:259:LEU:HD12	2.18	0.44
1:D:141:LEU:HD23	1:D:142:LEU:HD22	1.99	0.44
1:B:144:TYR:CE1	1:B:149:GLY:HA2	2.52	0.44
1:B:180:MET:HE1	1:B:201:LYS:HE2	2.00	0.44
1:C:140:ASP:OD2	1:C:196:LYS:HG3	2.18	0.44
1:C:320:LEU:HD22	2:C:601:5XZ:C07	2.48	0.44
1:A:316:ARG:HH22	1:A:319:LYS:CE	2.31	0.43
1:D:191:GLY:HA3	1:D:192:VAL:HA	1.61	0.43
1:D:339:VAL:HG23	1:D:394:LEU:HD13	2.00	0.43
1:A:150:GLN:NE2	1:A:151:GLU:OE2	2.52	0.43
1:A:312:PRO:HA	1:A:462:CYS:SG	2.59	0.43
1:D:155:VAL:HG23	1:D:192:VAL:O	2.19	0.43
1:D:142:LEU:HG	1:D:211:THR:HG22	2.00	0.43
1:D:317:PHE:CE1	1:D:320:LEU:HB2	2.52	0.43
1:B:227:THR:HB	1:B:272:HIS:CE1	2.54	0.43
1:C:302:GLU:O	1:C:306:ARG:HG3	2.19	0.43
1:A:316:ARG:HH22	1:A:319:LYS:HE2	1.83	0.43
1:B:141:LEU:HA	1:B:141:LEU:HD23	1.78	0.43
1:B:529:TYR:CE1	1:D:478:PRO:HG3	2.54	0.43
1:A:319:LYS:HE3	2:A:601:5XZ:C25	2.49	0.43
1:B:331:PRO:HD2	1:B:458:LEU:HD13	2.01	0.43
1:A:251:GLN:HG2	1:A:254:LYS:HZ1	1.84	0.42
1:B:348:VAL:HG23	1:B:353:LYS:HG3	2.00	0.42
1:B:506:LYS:HD3	1:B:506:LYS:N	2.33	0.42
1:B:489:LEU:CD2	1:B:497:MET:CE	2.88	0.42
1:D:141:LEU:CD2	1:D:142:LEU:HD22	2.49	0.42
1:C:226:PHE:CZ	1:C:230:ILE:HD11	2.54	0.42
1:A:168:ARG:O	1:A:171:ASP:HB2	2.20	0.42
1:A:487:ILE:HD12	1:A:513:GLY:HA3	2.02	0.42
1:C:180:MET:HG2	1:C:202:CYS:HA	2.01	0.42
1:D:359:GLN:HG3	1:D:363:LYS:NZ	2.34	0.42
1:C:223:PHE:O	1:C:227:THR:HG23	2.20	0.42
1:D:409:ILE:HA	1:D:409:ILE:HD13	1.84	0.41
1:A:506:LYS:HA	1:A:506:LYS:HD2	1.87	0.41
1:C:162:LEU:HD21	1:C:174:LEU:HD13	2.01	0.41
1:D:262:VAL:HG13	1:D:497:MET:HE1	2.02	0.41
1:C:313:SER:HG	1:C:314:GLY:H	1.62	0.41
1:D:445:ARG:NH1	3:D:609:HOH:O	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:LEU:HA	1:A:410:LEU:HD23	1.92	0.41
1:A:277:THR:O	1:A:424:GLU:HG3	2.21	0.41
1:C:401:PRO:O	1:C:404:THR:OG1	2.35	0.41
1:A:536:ALA:HB2	1:C:449:PRO:HG2	2.02	0.41
1:B:269:GLY:O	1:B:271:ARG:HG2	2.20	0.41
1:B:356:TYR:HA	1:B:359:GLN:HE21	1.86	0.41
1:D:189:SER:HB2	1:D:190:ASP:H	1.62	0.41
1:D:410:LEU:HD23	1:D:410:LEU:HA	1.88	0.41
1:A:215:ARG:HB3	1:A:217:LYS:NZ	2.36	0.41
1:D:431:ALA:HB1	1:D:440:PRO:HG3	2.01	0.41
1:B:386:ARG:O	1:B:390:ILE:HG13	2.21	0.41
1:D:155:VAL:H	1:D:192:VAL:HG23	1.86	0.41
1:A:215:ARG:HA	1:A:215:ARG:HD3	1.78	0.40
1:A:317:PHE:CD1	1:C:316:ARG:HG3	2.56	0.40
1:D:180:MET:HG2	1:D:202:CYS:HA	2.02	0.40
1:A:378:GLN:O	1:A:381:ARG:HG2	2.21	0.40
1:D:312:PRO:HA	1:D:462:CYS:SG	2.62	0.40
1:A:143:PHE:CE1	1:A:196:LYS:HA	2.57	0.40
1:D:248:TYR:CE1	1:D:249:ILE:HG12	2.57	0.40
1:A:313:SER:OG	1:A:314:GLY:N	2.54	0.40
1:C:434:ALA:HB2	1:C:490:VAL:HG13	2.03	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	408/539 (76%)	379 (93%)	17 (4%)	12 (3%)	<b>6</b> <b>8</b>
1	B	408/539 (76%)	388 (95%)	18 (4%)	2 (0%)	34 55
1	C	408/539 (76%)	379 (93%)	22 (5%)	7 (2%)	<b>11</b> <b>19</b>
1	D	408/539 (76%)	386 (95%)	19 (5%)	3 (1%)	<b>26</b> <b>46</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1632/2156 (76%)	1532 (94%)	76 (5%)	24 (2%)	13	22

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	GLU
1	A	248	TYR
1	A	313	SER
1	A	316	ARG
1	A	544	GLU
1	C	148	GLU
1	C	313	SER
1	D	189	SER
1	D	318	ASN
1	A	195	ASP
1	A	196	LYS
1	A	315	LEU
1	B	313	SER
1	C	190	ASP
1	C	251	GLN
1	A	148	GLU
1	C	152	LYS
1	C	316	ARG
1	D	316	ARG
1	A	153	ILE
1	A	138	LEU
1	C	248	TYR
1	A	314	GLY
1	B	191	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	353/462 (76%)	345 (98%)	8 (2%)	58	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	353/462 (76%)	347 (98%)	6 (2%)	68	89
1	C	353/462 (76%)	345 (98%)	8 (2%)	58	83
1	D	353/462 (76%)	347 (98%)	6 (2%)	68	89
All	All	1412/1848 (76%)	1384 (98%)	28 (2%)	63	86

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	205	SER
1	A	248	TYR
1	A	317	PHE
1	A	360	PHE
1	A	383	SER
1	A	411	ASP
1	A	507	MET
1	A	537	LYS
1	B	137	SER
1	B	205	SER
1	B	287	VAL
1	B	316	ARG
1	B	350	ASN
1	B	360	PHE
1	C	190	ASP
1	C	196	LYS
1	C	215	ARG
1	C	244	LYS
1	C	317	PHE
1	C	360	PHE
1	C	386	ARG
1	C	411	ASP
1	D	137	SER
1	D	189	SER
1	D	215	ARG
1	D	241	SER
1	D	342	SER
1	D	360	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	435	ASN
1	B	270	GLN
1	B	359	GLN
1	B	493	ASN
1	C	251	GLN
1	C	297	ASN
1	C	329	HIS
1	D	251	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	5XZ	A	601	-	32,40,40	4.13	9 (28%)	33,54,54	1.15	2 (6%)
2	5XZ	C	601	-	32,40,40	4.12	9 (28%)	33,54,54	1.79	8 (24%)

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	5XZ	A	601	-	-	0/14/33/33	0/3/5/5
2	5XZ	C	601	-	-	0/14/33/33	0/3/5/5

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	5XZ	C12-C11	-13.24	1.30	1.53
2	C	601	5XZ	C12-C11	-13.13	1.30	1.53
2	A	601	5XZ	C09-N08	-11.02	1.30	1.47
2	C	601	5XZ	C09-N08	-10.57	1.31	1.47
2	C	601	5XZ	O13-C14	2.11	1.41	1.36
2	A	601	5XZ	O13-C14	2.19	1.41	1.36
2	C	601	5XZ	C02-N03	3.00	1.42	1.35
2	A	601	5XZ	C19-N18	3.00	1.42	1.35
2	A	601	5XZ	C02-N03	3.02	1.42	1.35
2	C	601	5XZ	C19-N18	3.18	1.43	1.35
2	A	601	5XZ	C17-N18	3.64	1.42	1.36
2	C	601	5XZ	C04-N03	3.78	1.42	1.36
2	A	601	5XZ	C04-N03	4.09	1.43	1.36
2	C	601	5XZ	C17-N18	4.17	1.43	1.36
2	A	601	5XZ	C07-N08	6.54	1.42	1.32
2	C	601	5XZ	C07-N08	6.87	1.43	1.32
2	A	601	5XZ	C12-N08	12.10	1.62	1.46
2	C	601	5XZ	C12-N08	12.22	1.62	1.46

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	5XZ	C14-O13-C11	-5.09	105.97	118.86
2	C	601	5XZ	O27-C19-N18	-3.87	116.98	123.77
2	A	601	5XZ	C14-O13-C11	-3.00	111.27	118.86
2	C	601	5XZ	C21-C20-C19	-2.31	105.55	112.86
2	C	601	5XZ	O27-C19-C20	-2.16	115.78	121.89
2	C	601	5XZ	C09-N08-C12	-2.00	106.38	111.54
2	C	601	5XZ	C11-C12-N08	2.34	105.72	102.92
2	C	601	5XZ	C10-C09-N08	3.53	107.94	103.35
2	A	601	5XZ	C11-C12-N08	3.88	107.56	102.92
2	C	601	5XZ	C20-C19-N18	4.38	127.24	114.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	5XZ	2	0
2	C	601	5XZ	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	410/539 (76%)	0.39	37 (9%) 12 12	23, 38, 95, 170	0
1	B	410/539 (76%)	0.26	34 (8%) 14 15	20, 38, 87, 155	0
1	C	410/539 (76%)	0.34	36 (8%) 12 13	22, 38, 88, 165	0
1	D	410/539 (76%)	0.26	26 (6%) 23 26	20, 36, 79, 141	0
All	All	1640/2156 (76%)	0.31	133 (8%) 15 16	20, 38, 89, 170	0

All (133) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	190	ASP	22.7
1	A	189	SER	14.1
1	D	314	GLY	10.5
1	B	191	GLY	9.5
1	A	191	GLY	9.3
1	C	314	GLY	9.2
1	B	190	ASP	9.0
1	B	316	ARG	8.8
1	D	315	LEU	8.6
1	B	317	PHE	8.2
1	D	136	PRO	8.0
1	A	152	LYS	7.2
1	D	317	PHE	7.1
1	B	144	TYR	7.0
1	D	143	PHE	6.7
1	C	251	GLN	6.7
1	C	313	SER	6.1
1	C	317	PHE	6.0
1	D	190	ASP	6.0
1	C	190	ASP	5.9
1	A	314	GLY	5.7

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Mol	Chain	Res	Type	RSRZ
1	D	191	GLY	5.6
1	A	144	TYR	5.6
1	A	317	PHE	5.6
1	D	318	ASN	5.6
1	B	141	LEU	5.5
1	A	136	PRO	5.5
1	D	137	SER	5.5
1	A	188	THR	5.5
1	B	136	PRO	5.3
1	B	314	GLY	5.2
1	C	252	LEU	5.1
1	C	191	GLY	5.0
1	A	147	ALA	4.9
1	D	313	SER	4.8
1	B	189	SER	4.8
1	B	148	GLU	4.7
1	A	318	ASN	4.5
1	C	138	LEU	4.4
1	A	248	TYR	4.4
1	C	149	GLY	4.3
1	C	143	PHE	4.3
1	A	250	PRO	4.1
1	B	147	ALA	4.1
1	B	187	THR	4.1
1	A	249	ILE	3.9
1	D	189	SER	3.9
1	D	316	ARG	3.9
1	A	149	GLY	3.9
1	C	248	TYR	3.9
1	C	255	PHE	3.8
1	B	199	PHE	3.8
1	B	143	PHE	3.8
1	A	315	LEU	3.7
1	C	141	LEU	3.7
1	A	251	GLN	3.7
1	C	315	LEU	3.7
1	C	192	VAL	3.7
1	B	140	ASP	3.6
1	A	148	GLU	3.6
1	A	316	ARG	3.6
1	C	148	GLU	3.6
1	C	142	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	194	LEU	3.6
1	A	142	LEU	3.5
1	A	146	ILE	3.4
1	B	149	GLY	3.4
1	D	149	GLY	3.4
1	A	254	LYS	3.4
1	C	144	TYR	3.3
1	B	196	LYS	3.3
1	D	147	ALA	3.3
1	D	199	PHE	3.2
1	D	144	TYR	3.2
1	B	313	SER	3.2
1	D	141	LEU	3.2
1	A	143	PHE	3.2
1	C	137	SER	3.1
1	D	192	VAL	3.1
1	C	318	ASN	3.0
1	C	140	ASP	3.0
1	D	148	GLU	3.0
1	C	205	SER	2.9
1	B	142	LEU	2.8
1	B	137	SER	2.8
1	B	151	GLU	2.8
1	C	201	LYS	2.8
1	A	195	ASP	2.8
1	C	136	PRO	2.8
1	A	196	LYS	2.7
1	C	194	LEU	2.7
1	A	199	PHE	2.7
1	A	212	GLN	2.7
1	A	145	THR	2.7
1	A	255	PHE	2.7
1	B	195	ASP	2.6
1	B	250	PRO	2.5
1	C	185	LEU	2.5
1	C	249	ILE	2.5
1	B	315	LEU	2.5
1	C	198	LEU	2.5
1	A	197	ASP	2.5
1	D	207	ILE	2.5
1	A	137	SER	2.5
1	B	212	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	159	ILE	2.4
1	D	545	GLY	2.4
1	D	155	VAL	2.4
1	C	146	ILE	2.4
1	B	159	ILE	2.4
1	B	192	VAL	2.3
1	B	207	ILE	2.3
1	B	185	LEU	2.3
1	D	198	LEU	2.3
1	D	138	LEU	2.3
1	C	196	LYS	2.3
1	A	537	LYS	2.3
1	C	316	ARG	2.2
1	A	545	GLY	2.2
1	A	187	THR	2.2
1	C	145	THR	2.2
1	D	140	ASP	2.2
1	B	545	GLY	2.2
1	A	141	LEU	2.2
1	C	151	GLU	2.2
1	A	313	SER	2.2
1	B	155	VAL	2.1
1	C	153	ILE	2.1
1	C	197	ASP	2.1
1	B	145	THR	2.1
1	B	211	THR	2.1
1	B	150	GLN	2.1
1	C	189	SER	2.1

## 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	5XZ	C	601	36/36	0.70	0.32	1.73	93,105,114,121	0
2	5XZ	A	601	36/36	0.75	0.28	1.01	82,97,117,119	0

## 6.5 Other polymers

There are no such residues in this entry.