



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 25, 2024 – 02:49 PM EST

PDB ID : 5FI6
Title : Crystal structure of human GAC in complex with inhibitor UPGL_00011: 2-phenyl- {N}-[5-[[[(3 {S})-1-[5-(2-phenylethanoylamino)-1,3,4-thiadiazol-2-yl]p yrrolidin-3-yl]amino]-1,3,4-thiadiazol-2-yl]ethanamide
Authors : Huang, Q.; Cerione, R.
Deposited on : 2015-12-22
Resolution : 2.52 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

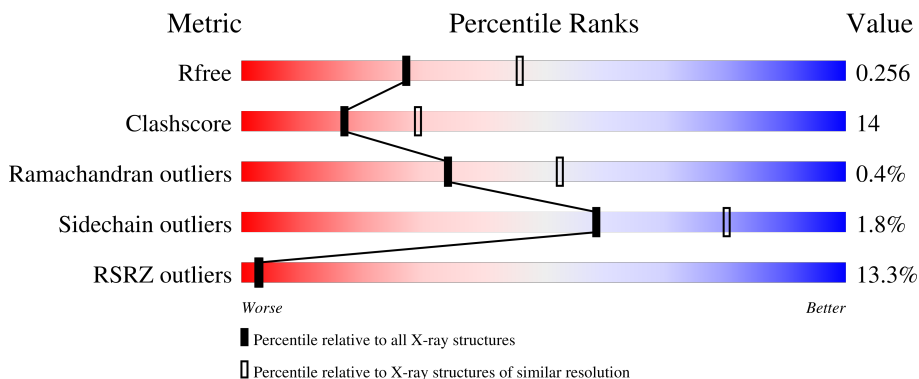
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.52 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}	130704	5743 (2.54-2.50)
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630 (2.54-2.50)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	
1	B	539	
1	C	539	
1	D	539	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13115 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
			Total	C	N	O	S			
1	A	410	3194	2036	540	590	28	1	0	0
1	B	410	3194	2036	540	590	28	1	0	0
1	C	410	3194	2036	540	590	28	1	0	0
1	D	410	3194	2036	540	590	28	1	0	0

There are 48 discrepancies between the modelled and reference sequences:

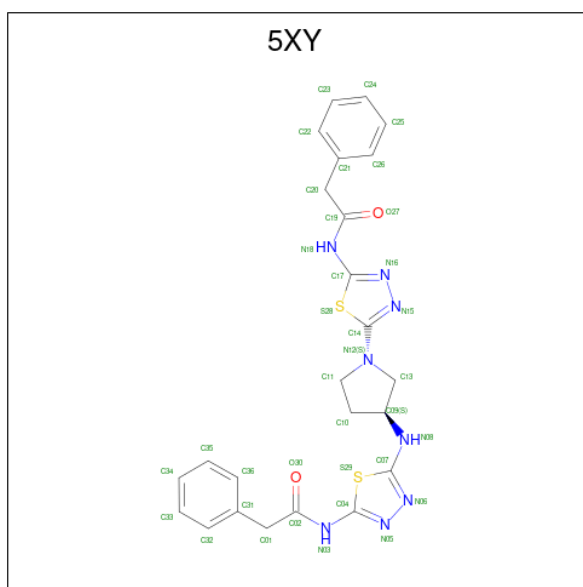
Chain	Residue	Modelled	Actual	Comment	Reference
A	59	MET	-	initiating methionine	UNP O94925
A	60	ARG	-	expression tag	UNP O94925
A	61	GLY	-	expression tag	UNP O94925
A	62	SER	-	expression tag	UNP O94925
A	63	HIS	-	expression tag	UNP O94925
A	64	HIS	-	expression tag	UNP O94925
A	65	HIS	-	expression tag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

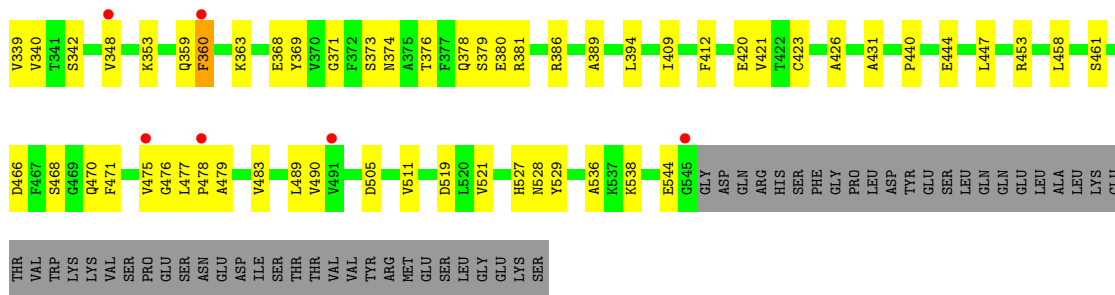
- Molecule 2 is 2-phenyl- {N}-[5-[(3 {S})-1-[5-(2-phenylethanoylamino)-1,3,4-thiadiazol-2-yl]pyrrolidin-3-yl]amino]-1,3,4-thiadiazol-2-yl]ethanamide (three-letter code: 5XY) (formula: C₂₄H₂₄N₈O₂S₂).



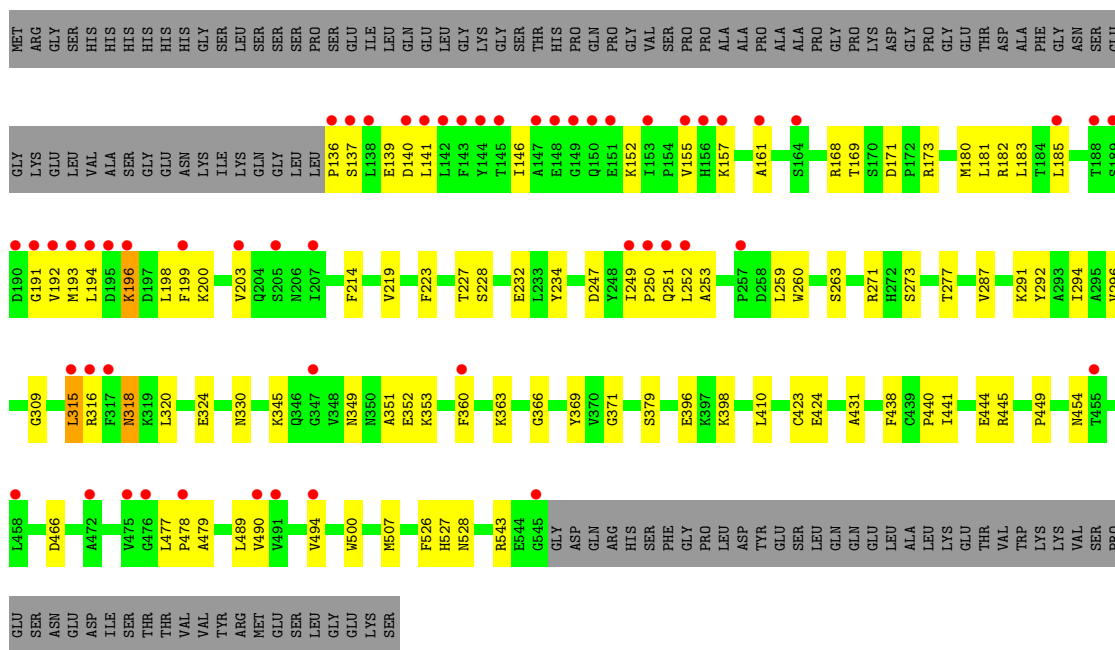
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	36	24	8	2	2	0	0
2	C	1	36	24	8	2	2	0	0

- Molecule 3 is water.

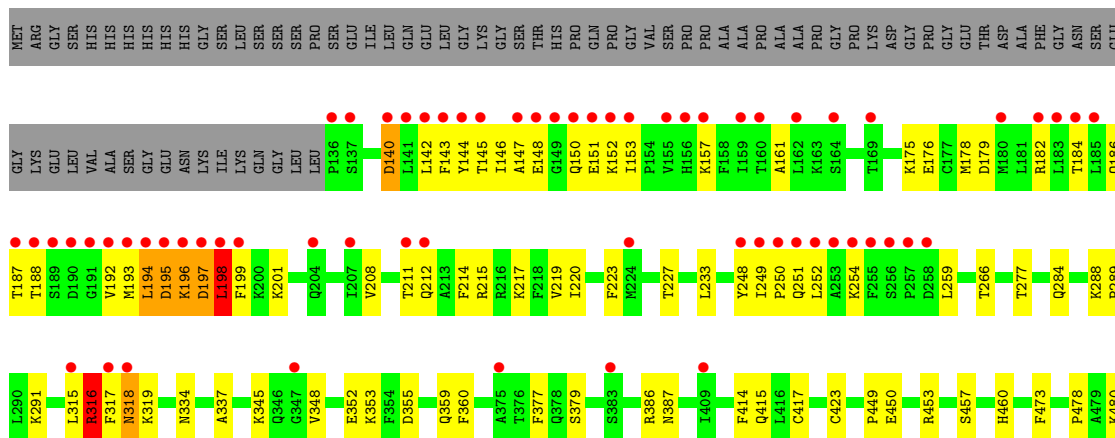
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	75	75	75	0	0
3	B	56	56	56	0	0
3	C	77	77	77	0	0
3	D	59	59	59	0	0

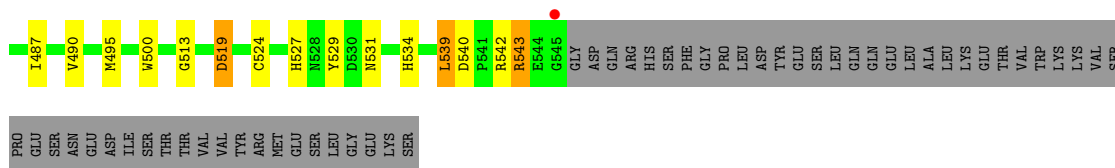


• Molecule 1: Glutaminase kidney isoform, mitochondrial



• Molecule 1: Glutaminase kidney isoform, mitochondrial





PRO
GLU
SER
ASN
GLU
ASP
ILE
SER
THR
VAL
VAL
TYR
ARG
MET
GLU
SER
LEU
GLY
GLU
LYS
SER

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.69Å 139.03Å 176.78Å 90.00° 95.56° 90.00°	Depositor
Resolution (Å)	47.30 – 2.52 47.43 – 2.52	Depositor EDS
% Data completeness (in resolution range)	97.3 (47.30-2.52) 97.4 (47.43-2.52)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 2.51Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.209 , 0.253 0.211 , 0.256	Depositor DCC
R_{free} test set	1996 reflections (2.48%)	wwPDB-VP
Wilson B-factor (Å ²)	41.9	Xtrriage
Anisotropy	0.733	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.024 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13115	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: 5XY

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	0.51	3/3266 (0.1%)	0.69	4/4408 (0.1%)
1	B	0.50	3/3266 (0.1%)	0.65	3/4408 (0.1%)
1	C	0.47	0/3266	0.62	1/4408 (0.0%)
1	D	0.57	6/3266 (0.2%)	0.65	4/4408 (0.1%)
All	All	0.51	12/13064 (0.1%)	0.65	12/17632 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	2
1	D	0	1
All	All	0	4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	316	ARG	CZ-NH1	-8.69	1.21	1.33
1	D	316	ARG	NE-CZ	-8.68	1.21	1.33
1	B	196	LYS	CD-CE	-7.38	1.32	1.51
1	D	316	ARG	CZ-NH2	-7.04	1.23	1.33
1	A	196	LYS	CD-CE	-6.71	1.34	1.51
1	D	176	GLU	CD-OE1	-6.16	1.18	1.25
1	D	176	GLU	CD-OE2	-6.13	1.19	1.25
1	B	196	LYS	CE-NZ	-5.62	1.35	1.49
1	D	316	ARG	CD-NE	-5.60	1.36	1.46
1	A	196	LYS	CB-CG	-5.29	1.38	1.52
1	B	190	ASP	CB-CG	-5.11	1.41	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	386	ARG	NE-CZ	5.09	1.39	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	140	ASP	CB-CG-OD1	9.44	126.80	118.30
1	A	193	MET	CG-SD-CE	7.77	112.63	100.20
1	A	193	MET	CB-CG-SD	7.55	135.05	112.40
1	C	196	LYS	CD-CE-NZ	-6.72	96.25	111.70
1	B	140	ASP	CB-CG-OD1	6.09	123.78	118.30
1	D	194	LEU	CA-CB-CG	5.90	128.88	115.30
1	D	539	LEU	CA-CB-CG	5.63	128.26	115.30
1	B	190	ASP	CB-CG-OD2	-5.46	113.39	118.30
1	B	173	ARG	NE-CZ-NH2	-5.43	117.59	120.30
1	A	152	LYS	CB-CG-CD	-5.38	97.61	111.60
1	D	195	ASP	CB-CG-OD1	5.25	123.03	118.30
1	D	198	LEU	CB-CG-CD1	5.19	119.83	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	317	PHE	Peptide
1	C	315	LEU	Peptide
1	C	316	ARG	Peptide
1	D	140	ASP	Peptide

5.2 Too-close contacts [\(i\)](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3194	0	3167	104	0
1	B	3194	0	3167	90	0
1	C	3194	0	3167	82	0
1	D	3194	0	3167	97	0
2	A	36	0	0	2	0
2	C	36	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	75	0	0	9	0
3	B	56	0	0	5	0
3	C	77	0	0	5	0
3	D	59	0	0	4	0
All	All	13115	0	12668	356	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 14.

All (356) 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:152:LYS:NZ	1:A:193:MET:HB3	1.52	1.24
1:C:249:ILE:CG2	1:C:252:LEU:HD12	1.71	1.19
1:A:152:LYS:NZ	1:A:193:MET:CB	2.14	1.10
1:D:195:ASP:H	1:D:198:LEU:HD21	1.16	1.09
1:A:152:LYS:HZ3	1:A:193:MET:CB	1.65	1.08
1:C:249:ILE:HG22	1:C:252:LEU:HD12	1.36	1.03
1:A:152:LYS:HZ1	1:A:193:MET:CG	1.72	1.03
1:C:249:ILE:HD11	1:C:379:SER:HB2	1.38	1.01
1:C:249:ILE:HD11	1:C:379:SER:CB	1.92	1.00
1:A:152:LYS:HZ3	1:A:193:MET:HB3	1.14	0.96
1:B:544:GLU:O	3:B:601:HOH:O	1.82	0.96
1:A:152:LYS:CE	1:A:193:MET:HB3	1.97	0.94
1:D:195:ASP:H	1:D:198:LEU:CD2	1.82	0.92
1:C:249:ILE:HG21	1:C:252:LEU:HD12	1.52	0.90
1:B:185:LEU:HD22	1:B:192:VAL:HG11	1.57	0.87
1:D:233:LEU:HD22	1:D:519:ASP:HB3	1.57	0.86
1:B:444:GLU:OE1	3:B:602:HOH:O	1.91	0.86
1:B:152:LYS:HE2	1:B:193:MET:SD	2.16	0.85
1:A:152:LYS:NZ	1:A:193:MET:CG	2.40	0.84
1:B:276:ASP:O	3:B:603:HOH:O	1.95	0.84
1:B:470:GLN:HG2	3:D:608:HOH:O	1.78	0.83
1:D:386:ARG:NH2	1:D:387:ASN:OD1	2.11	0.82
1:D:152:LYS:HZ3	1:D:193:MET:HB2	1.45	0.81
1:A:185:LEU:HD23	1:A:192:VAL:HG23	1.65	0.79
1:A:362:ASN:OD1	3:A:701:HOH:O	2.00	0.78
1:D:195:ASP:N	1:D:198:LEU:HD21	1.95	0.78
1:A:197:ASP:OD2	3:A:702:HOH:O	2.01	0.77
1:D:143:PHE:CE2	1:D:153:ILE:HG13	2.20	0.76
1:B:146:ILE:O	1:B:157:LYS:NZ	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:249:ILE:CD1	1:C:379:SER:HB2	2.16	0.75
1:B:216:ARG:NH2	1:B:544:GLU:OE2	2.18	0.75
1:A:233:LEU:HD22	1:A:519:ASP:HB3	1.69	0.74
1:C:351:ALA:O	3:C:701:HOH:O	2.05	0.74
1:A:450:GLU:OE1	3:A:703:HOH:O	2.05	0.73
1:C:140:ASP:HA	1:C:196:LYS:HZ1	1.54	0.72
1:A:249:ILE:HD11	1:A:379:SER:OG	1.91	0.70
1:A:444:GLU:OE1	3:A:704:HOH:O	2.07	0.70
1:C:139:GLU:HG3	1:C:200:LYS:HD2	1.74	0.69
1:D:186:GLN:O	3:D:602:HOH:O	2.10	0.69
1:C:140:ASP:HA	1:C:196:LYS:NZ	2.07	0.69
1:D:179:ASP:OD1	1:D:182:ARG:NH1	2.20	0.68
1:B:233:LEU:HD22	1:B:519:ASP:HB3	1.75	0.68
1:A:185:LEU:CD2	1:A:192:VAL:HG23	2.24	0.68
1:B:324:GLU:OE2	1:D:316:ARG:HB2	1.93	0.67
1:C:249:ILE:HG23	1:C:251:GLN:H	1.60	0.67
1:A:152:LYS:HZ3	1:A:193:MET:CA	2.07	0.66
1:C:161:ALA:HB1	1:C:214:PHE:HE1	1.61	0.66
1:B:368:GLU:OE1	3:B:604:HOH:O	2.13	0.66
1:D:143:PHE:O	1:D:153:ILE:HD11	1.96	0.65
1:D:540:ASP:O	1:D:543:ARG:HG3	1.96	0.65
1:A:152:LYS:HD2	1:A:153:ILE:N	2.12	0.65
1:A:188:THR:HG23	1:A:190:ASP:OD1	1.97	0.64
1:B:161:ALA:HB1	1:B:214:PHE:HE1	1.63	0.64
1:B:317:PHE:HE2	1:D:317:PHE:CD1	2.15	0.64
1:A:466:ASP:O	3:A:705:HOH:O	2.15	0.64
1:D:143:PHE:HB2	1:D:199:PHE:CD2	2.33	0.63
1:A:152:LYS:HB2	1:A:194:LEU:O	1.99	0.62
1:A:179:ASP:OD1	1:A:182:ARG:NH1	2.32	0.62
1:A:185:LEU:HD23	1:A:192:VAL:CG2	2.28	0.62
1:A:184:THR:O	1:A:187:THR:OG1	2.18	0.62
1:C:171:ASP:OD1	1:C:173:ARG:HD3	2.00	0.62
1:D:143:PHE:CD2	1:D:153:ILE:HD12	2.34	0.62
1:A:142:LEU:HD22	1:A:199:PHE:HZ	1.65	0.61
1:A:543:ARG:NH1	1:A:545:GLY:O	2.32	0.61
1:D:152:LYS:HZ3	1:D:193:MET:C	2.03	0.61
1:C:182:ARG:NH1	3:C:705:HOH:O	2.31	0.61
1:C:345:LYS:HB3	1:C:353:LYS:HG2	1.83	0.61
1:D:249:ILE:HB	1:D:252:LEU:HD12	1.83	0.60
1:B:479:ALA:HB2	1:B:489:LEU:HD12	1.84	0.60
1:B:316:ARG:HH22	1:B:319:LYS:HD3	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:152:LYS:NZ	1:D:193:MET:C	2.54	0.60
1:A:314:GLY:O	1:A:316:ARG:N	2.33	0.60
1:B:378:GLN:O	1:B:381:ARG:HG2	2.01	0.60
1:A:140:ASP:OD1	1:A:196:LYS:HE3	2.00	0.60
1:C:181:LEU:O	1:C:185:LEU:HG	2.02	0.60
1:C:277:THR:O	1:C:424:GLU:HG3	2.02	0.60
1:B:137:SER:OG	1:B:140:ASP:OD2	2.20	0.59
1:B:181:LEU:O	1:B:185:LEU:HG	2.01	0.59
1:B:374:ASN:N	3:B:606:HOH:O	2.35	0.59
1:C:137:SER:O	1:C:140:ASP:HB2	2.01	0.59
1:A:249:ILE:HG22	1:A:252:LEU:HB2	1.85	0.59
1:B:195:ASP:OD2	1:B:198:LEU:N	2.28	0.59
1:D:542:ARG:NH1	3:D:601:HOH:O	2.03	0.58
1:B:251:GLN:OE1	1:B:376:THR:HA	2.04	0.58
1:B:317:PHE:HE2	1:D:317:PHE:CG	2.21	0.58
1:C:168:ARG:NH2	1:C:424:GLU:OE2	2.30	0.58
1:D:377:PHE:CE1	1:D:415:GLN:HG3	2.37	0.58
1:C:155:VAL:HG21	1:C:185:LEU:HD21	1.85	0.58
1:A:316:ARG:HH22	2:A:601:5XY:C35	2.17	0.58
1:C:320:LEU:HD23	2:C:601:5XY:C17	2.32	0.58
1:D:387:ASN:HD22	1:D:414:PHE:HE1	1.52	0.58
1:B:141:LEU:O	1:B:145:THR:HG23	2.04	0.58
1:C:271:ARG:NH2	3:C:706:HOH:O	2.32	0.58
1:B:277:THR:HA	1:B:423:CYS:HB2	1.86	0.58
1:B:360:PHE:CE1	1:B:447:LEU:HD21	2.39	0.57
1:C:194:LEU:HD23	1:C:198:LEU:HD23	1.85	0.57
1:C:249:ILE:CG2	1:C:252:LEU:H	2.17	0.57
1:D:188:THR:HG22	1:D:192:VAL:HG12	1.85	0.57
1:A:374:ASN:OD1	3:A:706:HOH:O	2.17	0.57
1:C:152:LYS:HB2	1:C:193:MET:HE1	1.86	0.57
1:B:198:LEU:HD12	1:B:201:LYS:HD3	1.85	0.57
1:C:180:MET:HE3	1:C:183:LEU:HD23	1.87	0.57
1:A:137:SER:OG	1:A:140:ASP:OD2	2.18	0.57
1:A:152:LYS:HZ1	1:A:193:MET:CE	2.18	0.57
1:C:146:ILE:O	1:C:157:LYS:NZ	2.37	0.57
1:D:143:PHE:CD2	1:D:153:ILE:CD1	2.88	0.56
1:D:178:MET:O	1:D:182:ARG:HG3	2.04	0.56
1:D:140:ASP:OD1	1:D:143:PHE:HD1	1.88	0.56
1:A:215:ARG:O	1:A:216:ARG:HB2	2.05	0.56
1:A:528:ASN:HD21	1:C:528:ASN:ND2	2.04	0.56
1:D:318:ASN:OD1	1:D:318:ASN:N	2.29	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:TYR:HA	1:A:147:ALA:HB3	1.86	0.56
1:C:223:PHE:O	1:C:227:THR:HG23	2.06	0.56
1:B:273:SER:HB3	1:B:277:THR:HG21	1.87	0.56
1:D:140:ASP:OD2	1:D:144:TYR:N	2.39	0.56
1:B:527:HIS:CD2	1:D:453:ARG:HD2	2.40	0.56
1:C:431:ALA:HB1	1:C:440:PRO:HG2	1.88	0.56
1:D:147:ALA:HB1	1:D:150:GLN:O	2.05	0.56
1:D:161:ALA:HB1	1:D:214:PHE:HE1	1.70	0.56
1:C:249:ILE:HG21	1:C:252:LEU:CD1	2.32	0.55
1:A:536:ALA:HB2	1:C:449:PRO:HG2	1.87	0.55
1:D:184:THR:O	1:D:187:THR:HG22	2.07	0.55
1:D:152:LYS:HZ3	1:D:193:MET:CB	2.15	0.55
1:D:142:LEU:O	1:D:145:THR:HB	2.07	0.55
1:D:143:PHE:HB2	1:D:199:PHE:CE2	2.42	0.55
1:B:318:ASN:ND2	1:B:466:ASP:OD1	2.39	0.55
1:B:536:ALA:HB2	1:D:449:PRO:HG2	1.87	0.55
1:C:249:ILE:HG22	1:C:252:LEU:CD1	2.24	0.54
1:D:194:LEU:HD23	1:D:198:LEU:HG	1.89	0.54
1:A:226:PHE:CE2	1:A:495:MET:HE1	2.42	0.54
1:A:478:PRO:HD2	1:A:490:VAL:O	2.07	0.54
1:A:249:ILE:CD1	1:A:379:SER:OG	2.55	0.54
1:C:478:PRO:HD2	1:C:490:VAL:O	2.08	0.54
1:D:348:VAL:O	1:D:353:LYS:HE3	2.07	0.54
1:A:266:THR:HA	1:A:495:MET:HA	1.89	0.54
1:A:154:PRO:HB2	1:A:156:HIS:CD2	2.43	0.53
1:B:248:TYR:OH	1:B:380:GLU:OE2	2.23	0.53
1:C:318:ASN:OD1	1:C:318:ASN:N	2.40	0.53
1:A:194:LEU:HD23	1:A:198:LEU:HG	1.90	0.53
1:A:524:CYS:HA	1:A:539:LEU:O	2.09	0.53
1:A:226:PHE:HE2	1:A:495:MET:HE1	1.74	0.53
1:D:146:ILE:O	1:D:157:LYS:NZ	2.42	0.53
1:D:249:ILE:HD12	1:D:379:SER:HB3	1.90	0.53
1:B:155:VAL:HG21	1:B:185:LEU:HD21	1.88	0.53
1:B:331:PRO:HD2	1:B:458:LEU:HD13	1.90	0.53
1:A:289:PRO:HD3	1:A:480:LYS:HG2	1.90	0.53
1:D:249:ILE:HD12	1:D:379:SER:CB	2.39	0.53
1:A:377:PHE:CE1	1:A:415:GLN:HG3	2.44	0.53
1:D:195:ASP:OD1	1:D:198:LEU:HD22	2.09	0.53
1:A:152:LYS:CD	1:A:193:MET:HB3	2.39	0.52
1:B:150:GLN:HG3	1:B:151:GLU:H	1.74	0.52
1:B:431:ALA:HB1	1:B:440:PRO:HG2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:ARG:O	1:B:174:LEU:HD23	2.09	0.52
1:D:194:LEU:HD22	1:D:199:PHE:HA	1.90	0.52
1:A:148:GLU:CD	1:A:157:LYS:HZ1	2.13	0.52
1:A:453:ARG:HD2	1:C:527:HIS:CG	2.45	0.52
1:B:316:ARG:C	1:B:317:PHE:HD1	2.12	0.52
1:C:444:GLU:OE1	3:C:702:HOH:O	2.19	0.52
1:D:211:THR:O	1:D:215:ARG:HB2	2.10	0.52
1:D:266:THR:HA	1:D:495:MET:HA	1.92	0.52
1:B:194:LEU:HD23	1:B:198:LEU:HG	1.92	0.52
1:B:250:PRO:O	1:B:254:LYS:HD3	2.10	0.51
1:C:249:ILE:CD1	1:C:379:SER:CB	2.77	0.51
1:B:527:HIS:CG	1:D:453:ARG:HD2	2.45	0.51
1:D:142:LEU:HA	1:D:215:ARG:HH12	1.75	0.51
1:A:171:ASP:OD1	1:A:173:ARG:HD3	2.10	0.51
1:A:529:TYR:CE1	1:C:478:PRO:HG3	2.46	0.51
1:B:140:ASP:OD2	1:B:140:ASP:N	2.41	0.51
1:D:140:ASP:HA	1:D:143:PHE:H	1.75	0.51
1:B:373:SER:OG	1:B:376:THR:HG23	2.11	0.51
1:D:195:ASP:OD1	1:D:198:LEU:CD2	2.59	0.51
1:C:249:ILE:HD11	1:C:379:SER:C	2.32	0.50
1:C:315:LEU:HD23	1:C:315:LEU:O	2.10	0.50
1:A:152:LYS:HZ1	1:A:193:MET:CB	1.99	0.50
1:B:190:ASP:OD2	1:B:190:ASP:N	2.41	0.50
1:D:198:LEU:HD23	1:D:199:PHE:N	2.26	0.50
1:A:249:ILE:CG1	1:A:379:SER:OG	2.59	0.50
1:A:229:HIS:ND1	1:A:523:LEU:HD21	2.27	0.50
1:D:348:VAL:HG12	1:D:352:GLU:HB2	1.93	0.50
1:A:152:LYS:HD2	1:A:152:LYS:C	2.32	0.50
1:B:453:ARG:HD2	1:D:527:HIS:CG	2.47	0.50
1:B:521:VAL:O	1:B:538:LYS:NZ	2.25	0.50
1:C:294:ILE:HG12	1:C:360:PHE:HD2	1.77	0.50
1:D:144:TYR:HA	1:D:147:ALA:HB3	1.94	0.50
1:D:288:LYS:HE3	1:D:337:ALA:HB2	1.94	0.50
1:D:140:ASP:CG	1:D:143:PHE:HB3	2.32	0.49
1:A:142:LEU:HD23	1:A:146:ILE:HG13	1.95	0.49
1:D:144:TYR:OH	1:D:196:LYS:HD3	2.12	0.49
1:D:277:THR:HA	1:D:423:CYS:HB2	1.93	0.49
1:B:200:LYS:HE2	1:B:204:GLN:HB2	1.93	0.49
1:B:145:THR:O	1:B:148:GLU:HG3	2.13	0.49
1:D:198:LEU:HD23	1:D:199:PHE:H	1.78	0.49
1:A:342:SER:HA	1:A:409:ILE:HD12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:345:LYS:HB3	1:D:353:LYS:HG2	1.95	0.49
1:B:150:GLN:NE2	1:B:152:LYS:NZ	2.60	0.49
1:D:251:GLN:HA	1:D:254:LYS:HE3	1.93	0.49
1:B:142:LEU:HD23	1:B:199:PHE:HZ	1.78	0.48
1:C:287:VAL:O	1:C:291:LYS:HG2	2.13	0.48
1:D:531:ASN:HB3	1:D:534:HIS:O	2.12	0.48
1:C:466:ASP:HB2	1:C:507:MET:HE2	1.96	0.48
1:A:377:PHE:HZ	1:A:411:ASP:OD1	1.97	0.48
1:A:426:ALA:HB3	1:A:498:MET:HG2	1.96	0.48
1:C:349:ASN:OD1	1:C:352:GLU:HG3	2.14	0.48
1:D:151:GLU:OE1	1:D:151:GLU:HA	2.14	0.48
2:A:601:5XY:O27	1:B:319:LYS:HE3	2.14	0.48
1:D:259:LEU:HD13	1:D:500:TRP:CH2	2.49	0.48
1:A:453:ARG:HD2	1:C:527:HIS:CD2	2.49	0.48
1:B:309:GLY:O	1:B:330:ASN:HA	2.13	0.48
1:D:223:PHE:O	1:D:227:THR:HG23	2.14	0.48
1:B:353:LYS:HB3	1:B:412:PHE:CE2	2.49	0.48
1:B:189:SER:O	1:B:191:GLY:N	2.46	0.47
1:B:478:PRO:HG3	1:D:529:TYR:CE1	2.48	0.47
1:C:277:THR:HA	1:C:423:CYS:HB2	1.96	0.47
1:D:188:THR:CG2	1:D:192:VAL:HG12	2.44	0.47
1:A:316:ARG:HD3	2:C:601:5XY:C24	2.44	0.47
1:B:316:ARG:NH2	1:B:319:LYS:HD3	2.29	0.47
1:B:359:GLN:O	1:B:363:LYS:HG3	2.15	0.47
1:A:143:PHE:HZ	1:A:152:LYS:HA	1.79	0.47
1:A:215:ARG:HB3	1:A:217:LYS:HE3	1.96	0.47
1:C:259:LEU:HD13	1:C:500:TRP:CH2	2.50	0.47
1:B:223:PHE:O	1:B:227:THR:HG23	2.14	0.47
1:B:310:LYS:HD2	1:D:473:PHE:CD2	2.50	0.47
1:A:331:PRO:CD	1:A:458:LEU:HD13	2.45	0.47
1:D:259:LEU:HD13	1:D:500:TRP:HH2	1.80	0.47
1:B:152:LYS:HG2	1:B:193:MET:HG2	1.96	0.46
1:B:317:PHE:N	1:B:317:PHE:CD1	2.83	0.46
1:D:145:THR:OG1	1:D:215:ARG:NH2	2.49	0.46
1:C:292:TYR:OH	1:C:454:ASN:HB3	2.15	0.46
1:D:248:TYR:CE2	1:D:249:ILE:HG12	2.49	0.46
1:B:363:LYS:HD3	1:B:444:GLU:OE2	2.14	0.46
1:A:161:ALA:HB1	1:A:214:PHE:HE1	1.79	0.46
1:C:431:ALA:CB	1:C:440:PRO:HG2	2.45	0.46
1:D:208:VAL:O	1:D:212:GLN:HG3	2.15	0.46
1:D:284:GLN:OE1	1:D:417:CYS:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:GLY:C	1:A:316:ARG:H	2.19	0.46
1:C:137:SER:O	1:C:141:LEU:HG	2.15	0.46
1:A:152:LYS:NZ	1:A:193:MET:CE	2.79	0.46
1:A:223:PHE:O	1:A:227:THR:HG23	2.16	0.46
1:A:512:LYS:HG3	3:A:744:HOH:O	2.16	0.46
1:B:142:LEU:HD23	1:B:199:PHE:CZ	2.50	0.46
1:D:143:PHE:O	1:D:147:ALA:N	2.49	0.46
1:A:152:LYS:HD3	1:A:193:MET:HB3	1.98	0.46
1:B:284:GLN:HG3	1:B:483:VAL:HG12	1.98	0.46
1:C:194:LEU:HA	1:C:198:LEU:HD23	1.98	0.46
1:C:249:ILE:HD11	1:C:379:SER:HB3	1.90	0.46
1:A:316:ARG:HG3	1:C:324:GLU:CD	2.37	0.45
1:A:277:THR:HA	1:A:423:CYS:HB2	1.97	0.45
1:C:260:TRP:HE3	1:C:500:TRP:O	1.99	0.45
1:C:479:ALA:HB2	1:C:489:LEU:HD12	1.98	0.45
1:D:195:ASP:O	1:D:197:ASP:N	2.49	0.45
1:D:316:ARG:NH1	1:D:319:LYS:HE3	2.30	0.45
1:B:342:SER:HA	1:B:409:ILE:HD12	1.99	0.45
1:B:373:SER:HB2	1:B:420:GLU:OE2	2.17	0.45
1:A:249:ILE:HG13	1:A:379:SER:OG	2.15	0.45
1:B:317:PHE:HD1	1:B:317:PHE:N	2.15	0.45
1:A:348:VAL:O	1:A:353:LYS:HE3	2.16	0.45
1:B:212:GLN:H	1:B:212:GLN:HG3	1.55	0.45
1:C:309:GLY:O	1:C:330:ASN:HA	2.17	0.45
1:A:471:PHE:CE1	1:A:475:VAL:HG21	2.52	0.45
1:D:457:SER:O	1:D:460:HIS:HB3	2.16	0.45
1:A:185:LEU:HD23	1:A:185:LEU:HA	1.64	0.45
1:A:208:VAL:O	1:A:212:GLN:HG3	2.17	0.44
1:D:148:GLU:O	1:D:150:GLN:N	2.46	0.44
1:B:285:SER:HB3	1:B:288:LYS:HD2	2.00	0.44
1:A:155:VAL:HG22	1:A:194:LEU:HD11	1.99	0.44
1:D:175:LYS:O	1:D:179:ASP:N	2.46	0.44
1:C:410:LEU:HD23	1:C:410:LEU:HA	1.85	0.44
1:A:140:ASP:HB3	1:A:196:LYS:NZ	2.32	0.44
1:A:528:ASN:HD21	1:C:528:ASN:CG	2.20	0.44
1:B:249:ILE:HD11	1:B:379:SER:HB3	1.98	0.44
1:A:180:MET:HG2	1:A:202:CYS:HA	2.00	0.44
1:A:191:GLY:HA3	1:A:192:VAL:HA	1.76	0.44
1:A:315:LEU:HD23	1:A:315:LEU:HA	1.84	0.44
1:D:524:CYS:HA	1:D:539:LEU:O	2.17	0.44
1:A:152:LYS:NZ	1:A:193:MET:HE3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:VAL:O	1:A:291:LYS:HG2	2.18	0.44
1:B:461:SER:O	1:B:468:SER:HB3	2.18	0.44
1:C:396:GLU:O	1:C:398:LYS:HE2	2.18	0.44
1:B:360:PHE:CE1	1:B:447:LEU:CD2	3.00	0.43
1:A:375:ALA:O	1:A:379:SER:HB3	2.18	0.43
1:B:152:LYS:HG2	1:B:193:MET:CG	2.49	0.43
1:B:316:ARG:HA	1:B:316:ARG:HD2	1.42	0.43
1:C:249:ILE:CG1	1:C:379:SER:HB2	2.48	0.43
1:A:307:TYR:HB3	1:A:339:VAL:HG11	2.00	0.43
1:C:296:VAL:HG11	1:C:454:ASN:HD22	1.84	0.43
1:B:250:PRO:HG2	1:B:251:GLN:NE2	2.33	0.43
1:C:191:GLY:HA3	1:C:192:VAL:HA	1.77	0.43
1:D:288:LYS:HE3	1:D:337:ALA:CB	2.49	0.43
1:A:249:ILE:HG13	1:A:379:SER:HG	1.83	0.43
1:B:505:ASP:HB3	1:B:511:VAL:HG22	2.01	0.43
1:D:152:LYS:NZ	1:D:193:MET:HB2	2.23	0.43
1:D:288:LYS:HA	1:D:291:LYS:HE2	2.01	0.43
1:D:450:GLU:OE1	3:D:603:HOH:O	2.19	0.43
1:B:369:TYR:CZ	1:B:371:GLY:HA3	2.54	0.43
1:B:529:TYR:CE1	1:D:478:PRO:HG3	2.53	0.43
1:A:148:GLU:OE2	1:A:157:LYS:NZ	2.52	0.42
1:D:355:ASP:O	1:D:359:GLN:HG3	2.19	0.42
1:B:292:TYR:HA	1:B:340:VAL:HG11	2.01	0.42
1:B:339:VAL:HG23	1:B:394:LEU:HD13	2.00	0.42
1:B:348:VAL:O	1:B:353:LYS:HE3	2.19	0.42
1:C:228:SER:O	1:C:232:GLU:HG3	2.18	0.42
1:D:334:ASN:ND2	1:D:386:ARG:NH2	2.67	0.42
1:C:369:TYR:CZ	1:C:371:GLY:HA3	2.54	0.42
1:D:250:PRO:O	1:D:254:LYS:HG3	2.20	0.42
1:A:140:ASP:HB3	1:A:196:LYS:HZ2	1.83	0.42
1:A:217:LYS:HA	1:A:217:LYS:HD3	1.91	0.42
1:A:182:ARG:O	1:A:186:GLN:HG2	2.20	0.42
1:C:136:PRO:HB2	1:C:141:LEU:HD21	2.01	0.42
1:B:471:PHE:CZ	1:B:475:VAL:HG11	2.55	0.42
1:D:289:PRO:HD3	1:D:480:LYS:HG2	2.02	0.42
1:D:487:ILE:HD12	1:D:513:GLY:HA3	2.02	0.42
1:A:168:ARG:HD2	3:A:713:HOH:O	2.19	0.42
1:A:195:ASP:OD2	3:A:707:HOH:O	2.21	0.42
1:A:318:ASN:ND2	1:A:466:ASP:OD2	2.52	0.42
1:B:478:PRO:HD2	1:B:490:VAL:O	2.20	0.42
1:D:478:PRO:HD2	1:D:490:VAL:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:LYS:O	1:A:204:GLN:HB3	2.20	0.42
1:A:259:LEU:HD13	1:A:500:TRP:CH2	2.54	0.41
1:B:150:GLN:HG3	1:B:151:GLU:N	2.35	0.41
1:B:150:GLN:HG2	1:B:152:LYS:HD3	2.01	0.41
1:B:421:VAL:HG21	1:B:426:ALA:HB2	2.00	0.41
1:C:363:LYS:HG2	3:C:728:HOH:O	2.19	0.41
1:C:366:GLY:HA3	1:C:441:ILE:HD11	2.02	0.41
1:B:476:GLY:O	1:B:528:ASN:HB2	2.20	0.41
1:A:152:LYS:HZ3	1:A:193:MET:HA	1.82	0.41
1:D:249:ILE:HG22	1:D:252:LEU:H	1.85	0.41
1:A:142:LEU:HD22	1:A:199:PHE:CZ	2.51	0.41
1:A:316:ARG:O	1:A:317:PHE:HD1	2.03	0.41
1:C:234:TYR:CE1	1:C:260:TRP:CD1	3.08	0.41
1:A:289:PRO:CD	1:A:480:LYS:HG2	2.50	0.41
1:C:249:ILE:HG13	1:C:250:PRO:HD2	2.02	0.41
1:D:215:ARG:HB3	1:D:217:LYS:HE2	2.02	0.41
1:B:141:LEU:HD12	1:B:141:LEU:HA	1.89	0.41
1:C:247:ASP:HA	1:C:253:ALA:HB2	2.03	0.41
1:D:198:LEU:HA	1:D:201:LYS:HB2	2.03	0.41
1:A:217:LYS:HE2	1:A:217:LYS:N	2.36	0.41
1:C:219:VAL:HG21	1:C:494:VAL:HA	2.01	0.41
1:C:273:SER:HB3	1:C:277:THR:HG21	2.03	0.41
1:C:363:LYS:HD3	1:C:444:GLU:OE2	2.19	0.41
1:B:386:ARG:O	1:B:389:ALA:HB3	2.20	0.41
1:C:263:SER:OG	1:C:424:GLU:HG2	2.21	0.41
1:C:438:PHE:CE2	1:C:445:ARG:HB2	2.56	0.41
1:C:199:PHE:O	1:C:203:VAL:HG22	2.21	0.40
1:C:296:VAL:HG11	1:C:454:ASN:ND2	2.36	0.40
1:A:497:MET:CE	1:A:516:PHE:CE1	3.04	0.40
1:C:477:LEU:HD21	1:C:526:PHE:O	2.22	0.40
1:D:315:LEU:HD12	1:D:315:LEU:HA	1.89	0.40
1:C:249:ILE:HG23	1:C:252:LEU:H	1.86	0.40
1:A:139:GLU:H	1:A:139:GLU:HG2	1.12	0.40
1:B:288:LYS:N	1:B:289:PRO:HD2	2.36	0.40
1:B:477:LEU:HD23	1:B:477:LEU:HA	1.89	0.40
1:C:139:GLU:HG3	1:C:200:LYS:CD	2.47	0.40
1:C:466:ASP:CB	1:C:507:MET:HE2	2.52	0.40
1:D:198:LEU:HD23	1:D:198:LEU:N	2.35	0.40
1:D:215:ARG:HB3	1:D:217:LYS:CE	2.51	0.40
1:D:219:VAL:HG13	1:D:220:ILE:HG13	2.02	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%)	390 (96%)	14 (3%)	4 (1%)	15	27
1	B	408/539 (76%)	385 (94%)	22 (5%)	1 (0%)	47	67
1	C	408/539 (76%)	390 (96%)	18 (4%)	0	100	100
1	D	408/539 (76%)	385 (94%)	22 (5%)	1 (0%)	47	67
All	All	1632/2156 (76%)	1550 (95%)	76 (5%)	6 (0%)	34	53

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	187	THR
1	A	318	ASN
1	B	190	ASP
1	A	315	LEU
1	D	196	LYS
1	A	216	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	353/462 (76%)	345 (98%)	8 (2%)	50	74
1	B	353/462 (76%)	346 (98%)	7 (2%)	55	78
1	C	353/462 (76%)	350 (99%)	3 (1%)	81	92
1	D	353/462 (76%)	346 (98%)	7 (2%)	55	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1412/1848 (76%)	1387 (98%)	25 (2%)	59 80

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	GLU
1	A	140	ASP
1	A	152	LYS
1	A	169	THR
1	A	241	SER
1	A	360	PHE
1	A	379	SER
1	A	519	ASP
1	B	140	ASP
1	B	150	GLN
1	B	152	LYS
1	B	169	THR
1	B	216	ARG
1	B	318	ASN
1	B	360	PHE
1	C	169	THR
1	C	318	ASN
1	C	543	ARG
1	D	197	ASP
1	D	198	LEU
1	D	316	ARG
1	D	318	ASN
1	D	360	PHE
1	D	519	ASP
1	D	543	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	240	GLN
1	A	528	ASN
1	B	150	GLN
1	B	240	GLN
1	D	515	HIS
1	D	528	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	5XY	C	601	-	31,40,40	3.83	9 (29%)	34,54,54	1.37	4 (11%)
2	5XY	A	601	-	31,40,40	3.73	9 (29%)	34,54,54	1.42	4 (11%)

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	5XY	C	601	-	-	3/14/33/33	0/5/5/5
2	5XY	A	601	-	-	1/14/33/33	0/5/5/5

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	5XY	C13-N12	12.45	1.62	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	5XY	C13-N12	12.07	1.62	1.46
2	A	601	5XY	C11-N12	-10.00	1.31	1.47
2	C	601	5XY	C13-C09	-9.88	1.34	1.53
2	C	601	5XY	C11-N12	-9.73	1.32	1.47
2	A	601	5XY	C13-C09	-9.51	1.35	1.53
2	C	601	5XY	C14-N12	6.46	1.42	1.32
2	A	601	5XY	C14-N12	6.37	1.42	1.32
2	C	601	5XY	C04-N03	4.19	1.44	1.36
2	C	601	5XY	C02-N03	3.61	1.43	1.35
2	C	601	5XY	C17-N18	3.48	1.42	1.36
2	A	601	5XY	C17-N18	3.29	1.42	1.36
2	A	601	5XY	C04-N03	3.26	1.42	1.36
2	A	601	5XY	C19-N18	3.13	1.42	1.35
2	A	601	5XY	C02-N03	2.98	1.42	1.35
2	C	601	5XY	C19-N18	2.92	1.42	1.35
2	C	601	5XY	C10-C11	2.60	1.57	1.52
2	A	601	5XY	C10-C11	2.56	1.57	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	5XY	C11-N12-C13	-4.15	100.82	111.55
2	C	601	5XY	C17-N18-C19	-3.02	121.38	129.54
2	C	601	5XY	C01-C02-N03	2.90	120.76	114.77
2	C	601	5XY	C20-C19-N18	2.86	120.69	114.77
2	A	601	5XY	C04-N03-C02	-2.74	122.15	129.54
2	C	601	5XY	O27-C19-N18	-2.69	118.73	123.63
2	A	601	5XY	C20-C19-N18	2.65	120.25	114.77
2	A	601	5XY	C11-N12-C14	2.02	129.33	123.54

There are no chirality outliers.

All (4) torsion outliers are listed below:

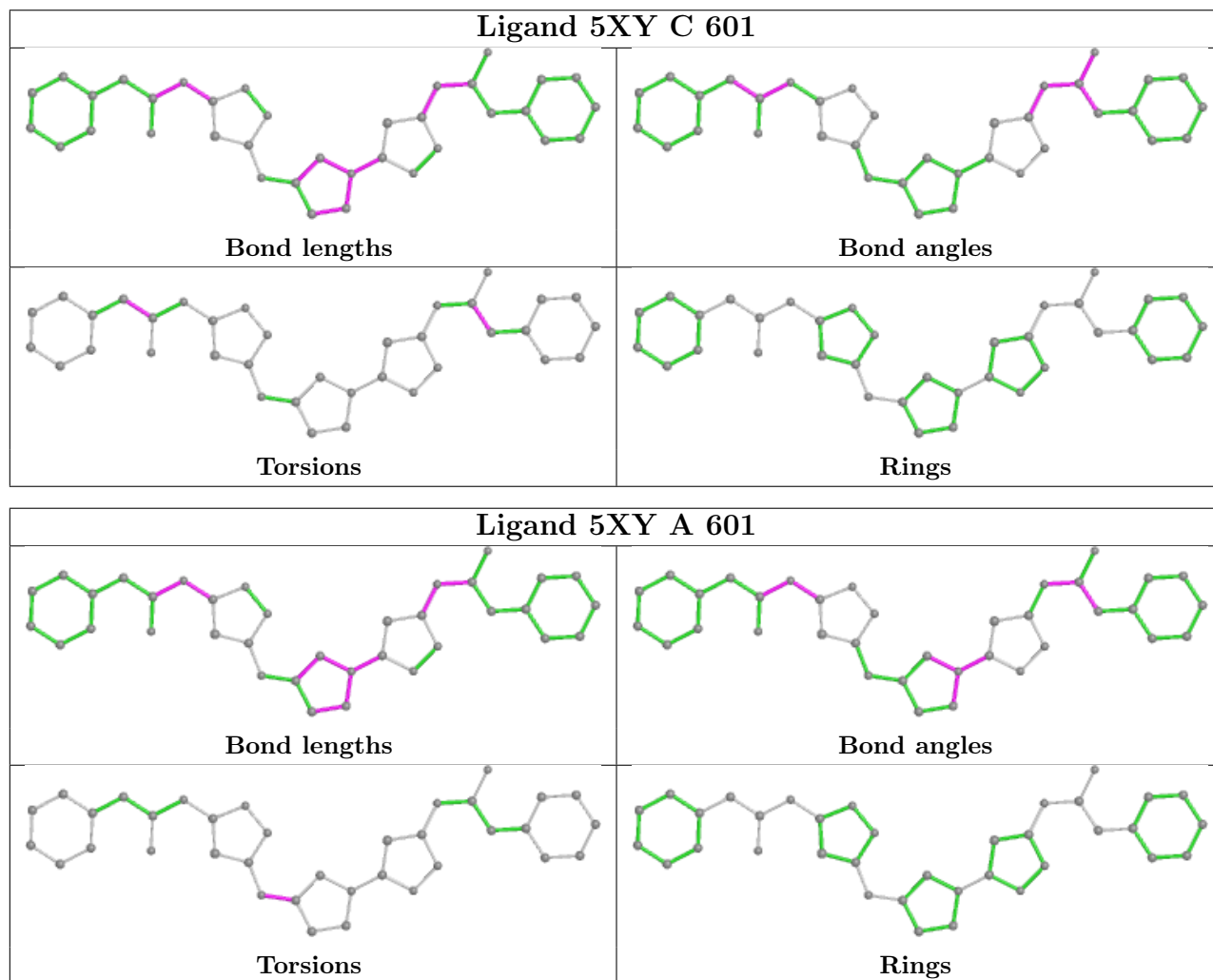
Mol	Chain	Res	Type	Atoms
2	A	601	5XY	C13-C09-N08-C07
2	C	601	5XY	O27-C19-C20-C21
2	C	601	5XY	N18-C19-C20-C21
2	C	601	5XY	C31-C01-C02-O30

There are no ring outliers.

2 monomers are involved in 4 short contacts:

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

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	410/539 (76%)	0.92	52 (12%) 3 3	30, 44, 79, 114	0
1	B	410/539 (76%)	0.80	47 (11%) 4 5	33, 48, 80, 98	0
1	C	410/539 (76%)	0.87	54 (13%) 3 3	31, 44, 80, 95	0
1	D	410/539 (76%)	0.99	65 (15%) 1 1	34, 47, 87, 111	0
All	All	1640/2156 (76%)	0.90	218 (13%) 3 3	30, 46, 81, 114	0

All (218) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	317	PHE	12.7
1	A	188	THR	12.3
1	A	190	ASP	9.3
1	D	188	THR	8.9
1	D	194	LEU	8.4
1	B	143	PHE	7.9
1	D	251	GLN	7.9
1	B	316	ARG	7.6
1	D	148	GLU	7.5
1	C	317	PHE	7.5
1	A	147	ALA	7.3
1	D	140	ASP	7.1
1	D	190	ASP	7.1
1	C	191	GLY	6.9
1	D	149	GLY	6.6
1	C	143	PHE	6.6
1	D	155	VAL	6.5
1	A	153	ILE	6.4
1	D	145	THR	6.4
1	D	151	GLU	6.2
1	D	144	TYR	6.2

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Mol	Chain	Res	Type	RSRZ
1	A	148	GLU	6.1
1	A	149	GLY	6.0
1	C	149	GLY	6.0
1	A	199	PHE	6.0
1	A	317	PHE	6.0
1	A	143	PHE	5.8
1	A	194	LEU	5.8
1	D	199	PHE	5.8
1	D	143	PHE	5.6
1	D	250	PRO	5.5
1	A	144	TYR	5.4
1	B	137	SER	5.4
1	B	190	ASP	5.3
1	B	317	PHE	5.3
1	C	251	GLN	5.3
1	D	196	LYS	5.3
1	B	199	PHE	5.2
1	B	149	GLY	5.1
1	A	155	VAL	5.1
1	D	249	ILE	5.1
1	A	145	THR	5.0
1	B	136	PRO	5.0
1	A	151	GLU	4.9
1	B	192	VAL	4.8
1	D	152	LYS	4.8
1	C	190	ASP	4.8
1	A	250	PRO	4.7
1	C	136	PRO	4.7
1	A	191	GLY	4.7
1	B	138	LEU	4.7
1	C	249	ILE	4.7
1	B	189	SER	4.7
1	A	150	GLN	4.7
1	A	136	PRO	4.6
1	D	195	ASP	4.6
1	C	199	PHE	4.5
1	C	155	VAL	4.4
1	D	248	TYR	4.4
1	C	161	ALA	4.4
1	A	152	LYS	4.4
1	D	136	PRO	4.3
1	D	255	PHE	4.3

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Mol	Chain	Res	Type	RSRZ
1	D	141	LEU	4.3
1	D	315	LEU	4.3
1	A	187	THR	4.3
1	A	248	TYR	4.3
1	D	187	THR	4.3
1	B	194	LEU	4.3
1	B	205	SER	4.2
1	D	192	VAL	4.2
1	C	147	ALA	4.2
1	B	144	TYR	4.2
1	A	545	GLY	4.1
1	B	147	ALA	4.1
1	D	142	LEU	4.1
1	A	251	GLN	4.1
1	C	250	PRO	4.1
1	B	140	ASP	4.0
1	B	148	GLU	4.0
1	C	194	LEU	4.0
1	C	137	SER	3.9
1	A	146	ILE	3.9
1	A	159	ILE	3.9
1	C	142	LEU	3.9
1	D	147	ALA	3.9
1	D	257	PRO	3.9
1	A	249	ILE	3.8
1	D	191	GLY	3.8
1	C	192	VAL	3.8
1	A	316	ARG	3.8
1	D	212	GLN	3.8
1	B	193	MET	3.7
1	D	211	THR	3.7
1	A	140	ASP	3.7
1	C	150	GLN	3.7
1	A	185	LEU	3.7
1	C	196	LYS	3.7
1	D	253	ALA	3.7
1	D	254	LYS	3.6
1	A	141	LEU	3.6
1	A	195	ASP	3.6
1	A	154	PRO	3.6
1	C	148	GLU	3.6
1	D	157	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	142	LEU	3.6
1	C	545	GLY	3.6
1	A	383	SER	3.5
1	B	195	ASP	3.5
1	B	150	GLN	3.4
1	A	196	LYS	3.4
1	C	195	ASP	3.4
1	D	153	ILE	3.3
1	D	256	SER	3.3
1	D	347	GLY	3.2
1	A	224	MET	3.2
1	B	141	LEU	3.2
1	C	156	HIS	3.2
1	D	159	ILE	3.2
1	B	153	ILE	3.1
1	D	156	HIS	3.1
1	D	150	GLN	3.1
1	A	193	MET	3.1
1	D	185	LEU	3.1
1	B	155	VAL	3.1
1	C	478	PRO	3.1
1	B	318	ASN	3.1
1	C	157	LYS	3.1
1	C	188	THR	3.0
1	A	189	SER	3.0
1	B	156	HIS	2.9
1	A	253	ALA	2.9
1	C	315	LEU	2.9
1	C	475	VAL	2.9
1	A	137	SER	2.9
1	B	360	PHE	2.9
1	D	184	THR	2.8
1	D	193	MET	2.8
1	B	478	PRO	2.8
1	A	255	PHE	2.8
1	B	251	GLN	2.8
1	D	383	SER	2.8
1	C	140	ASP	2.7
1	C	138	LEU	2.7
1	D	198	LEU	2.7
1	A	156	HIS	2.7
1	D	545	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	162	LEU	2.6
1	A	192	VAL	2.6
1	B	475	VAL	2.6
1	A	204	GLN	2.6
1	A	254	LYS	2.6
1	D	137	SER	2.6
1	B	252	LEU	2.6
1	C	476	GLY	2.6
1	C	144	TYR	2.6
1	C	189	SER	2.5
1	D	169	THR	2.5
1	C	252	LEU	2.5
1	D	197	ASP	2.5
1	B	250	PRO	2.5
1	D	189	SER	2.5
1	D	160	THR	2.5
1	C	164	SER	2.5
1	B	151	GLU	2.5
1	A	160	THR	2.4
1	A	212	GLN	2.4
1	B	348	VAL	2.4
1	C	494	VAL	2.4
1	D	409	ILE	2.4
1	B	315	LEU	2.4
1	B	145	THR	2.4
1	C	458	LEU	2.4
1	C	360	PHE	2.3
1	C	207	ILE	2.3
1	D	207	ILE	2.3
1	C	257	PRO	2.3
1	C	491	VAL	2.3
1	C	193	MET	2.3
1	A	211	THR	2.3
1	C	141	LEU	2.3
1	C	151	GLU	2.3
1	A	157	LYS	2.3
1	B	249	ILE	2.3
1	B	545	GLY	2.2
1	B	160	THR	2.2
1	D	182	ARG	2.2
1	C	205	SER	2.2
1	C	316	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	184	THR	2.2
1	C	455	THR	2.2
1	B	196	LYS	2.2
1	D	164	SER	2.2
1	B	142	LEU	2.2
1	D	258	ASP	2.2
1	D	204	GLN	2.2
1	C	490	VAL	2.2
1	C	185	LEU	2.2
1	A	529	TYR	2.1
1	B	491	VAL	2.1
1	D	318	ASN	2.1
1	D	183	LEU	2.1
1	C	472	ALA	2.1
1	D	252	LEU	2.1
1	B	204	GLN	2.1
1	B	183	LEU	2.1
1	C	153	ILE	2.1
1	B	191	GLY	2.1
1	A	216	ARG	2.1
1	C	145	THR	2.0
1	C	203	VAL	2.0
1	D	224	MET	2.0
1	B	154	PRO	2.0
1	D	375	ALA	2.0
1	D	180	MET	2.0
1	B	152	LYS	2.0
1	C	347	GLY	2.0
1	B	178	MET	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](#)

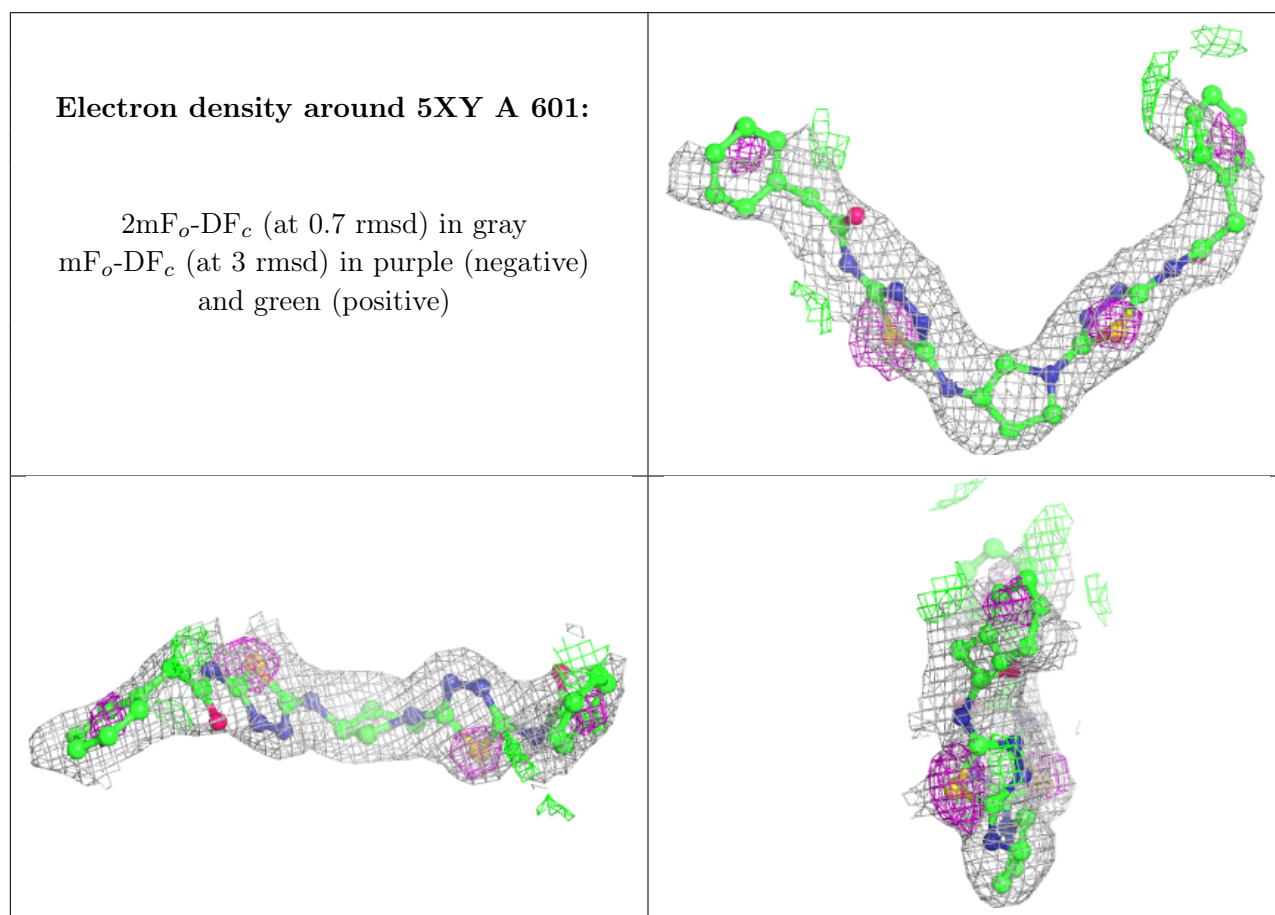
There are no monosaccharides in this entry.

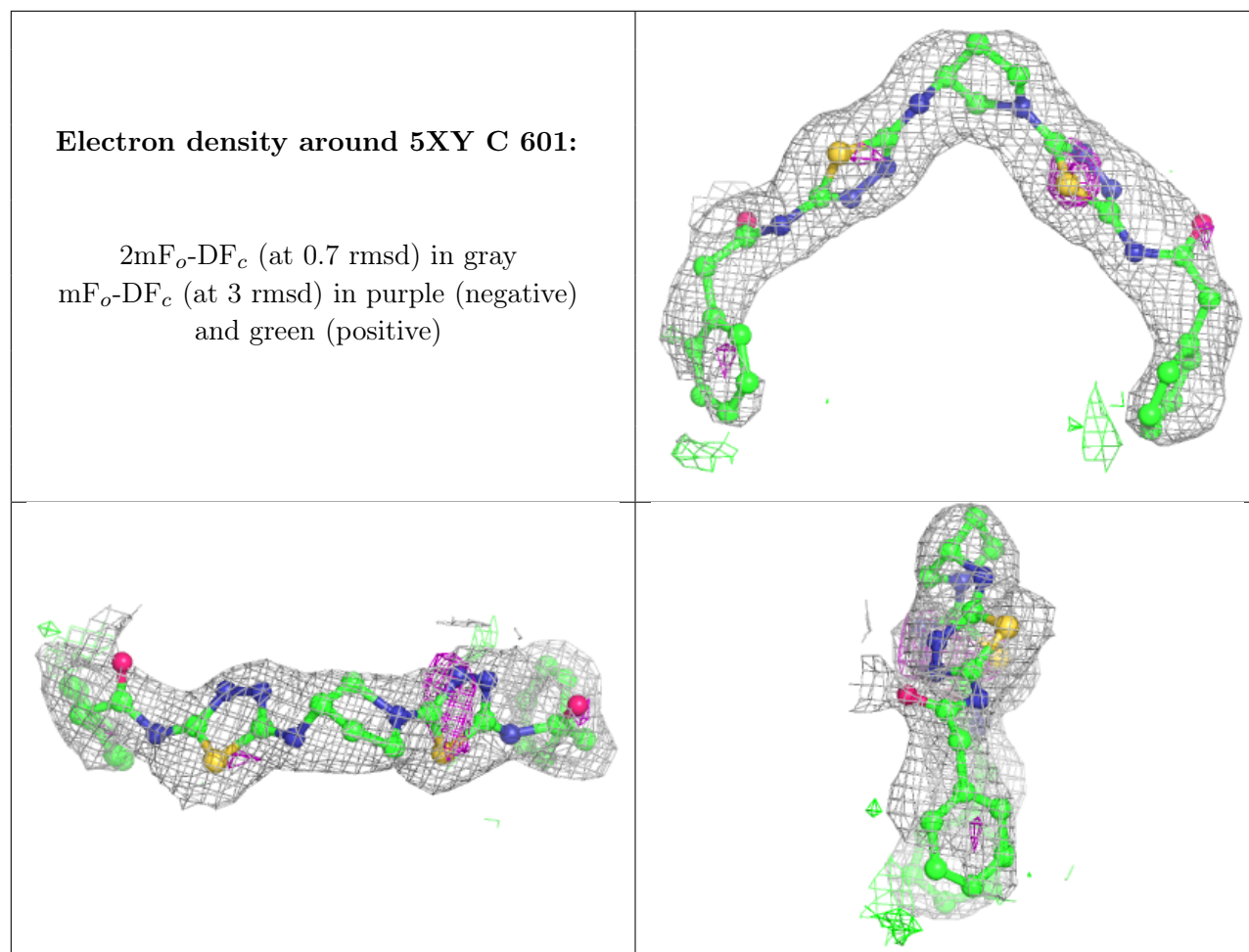
6.4 Ligands [i](#)

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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	5XY	A	601	36/36	0.87	0.26	48,65,82,85	0
2	5XY	C	601	36/36	0.89	0.23	52,67,83,84	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.