



## Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2024 – 04:36 PM EDT

PDB ID : 5J87  
Title : Discovery of N-(3-(5-((3-acrylamido-4-(morpholine-4-carbonyl)phenyl)amino)-1-methyl-6-oxo-1,6-dihydropyridin-3-yl)-2-methylphenyl)-4-(tert-butyl)benzamide (CHMFL-BTK-01) as a Highly Selective Irreversible BTK Kinase Inhibitor  
Authors : Yun, C.H.; Zhang, S.  
Deposited on : 2016-04-07  
Resolution : 1.59 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

<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>.

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The following versions of software and data (see [references](#) ①) were used in the production of this report:

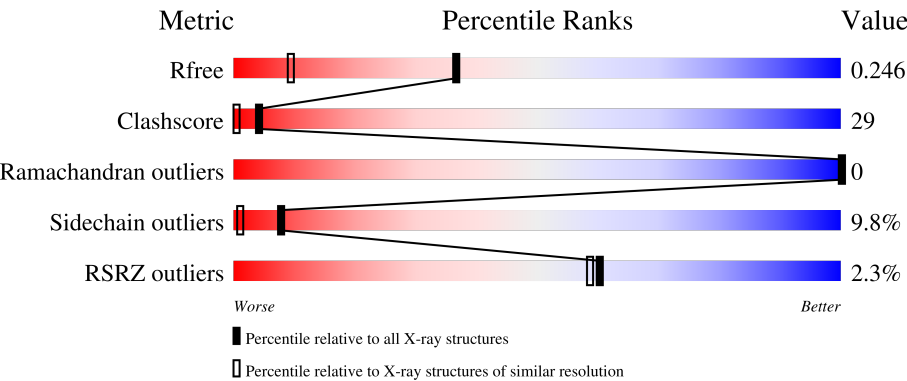
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.59 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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  $\geq 3$ , 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	274	<div><div>%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>67%26%. .</div></div>
1	B	274	<div><div></div><div></div><div></div><div></div><div></div></div> <div>73%24%. .</div>
1	C	274	<div><div>4%</div><div></div><div></div><div></div><div></div><div></div></div> <div>49%39%7%5%</div>
1	D	274	<div><div>3%</div><div></div><div></div><div></div><div></div><div></div></div> <div>50%38%8%. .</div>

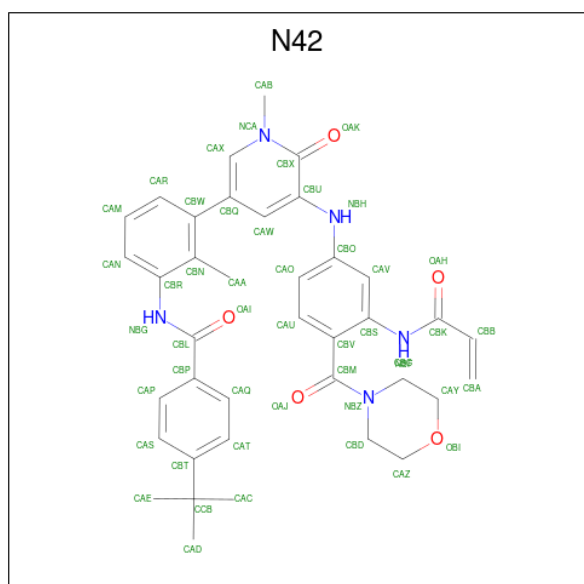


In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tyrosine-protein kinase BTK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total 2158	C 1385	N 352	O 402	S 19	0	2	0
1	B	274	Total 2239	C 1433	N 368	O 420	S 18	0	3	0
1	C	261	Total 2127	C 1365	N 349	O 394	S 19	0	1	0
1	D	263	Total 2141	C 1374	N 348	O 400	S 19	0	1	0

- Molecule 2 is N-[3-(5-{[3-(acryloylamino)-4-(morpholine-4-carbonyl)phenyl]amino}-1-methyl-6-oxo-1,6-dihydropyridin-3-yl)-2-methylphenyl]-4-tert-butylbenzamide (three-letter code: N42) (formula: C<sub>38</sub>H<sub>41</sub>N<sub>5</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			48	38	5	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			48	38	5	5		
2	C	1	Total	C	N	O	0	0
			48	38	5	5		
2	D	1	Total	C	N	O	0	0
			48	38	5	5		

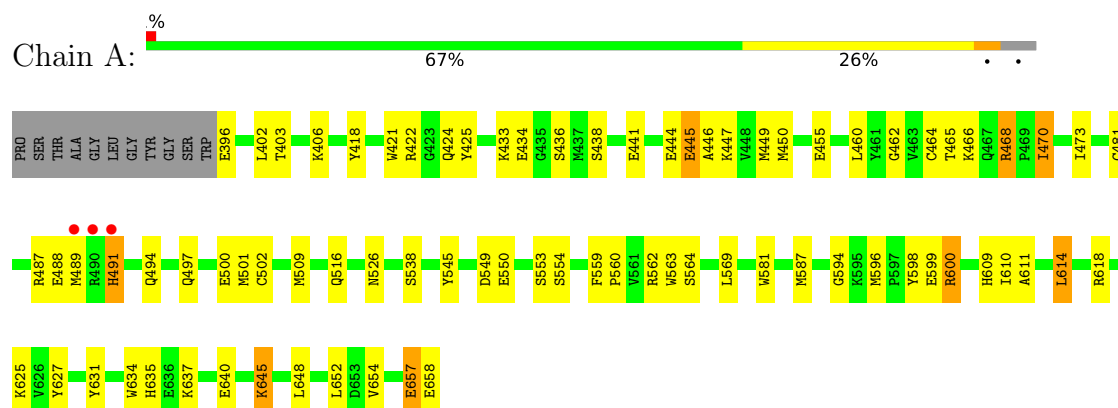
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	221	Total	O	0	0
			221	221		
3	B	235	Total	O	0	0
			235	235		
3	C	165	Total	O	0	0
			165	165		
3	D	243	Total	O	0	0
			243	243		

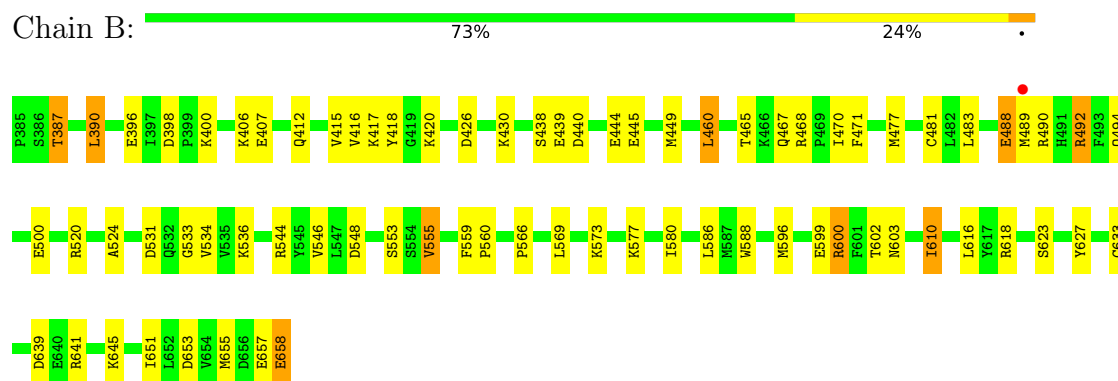
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

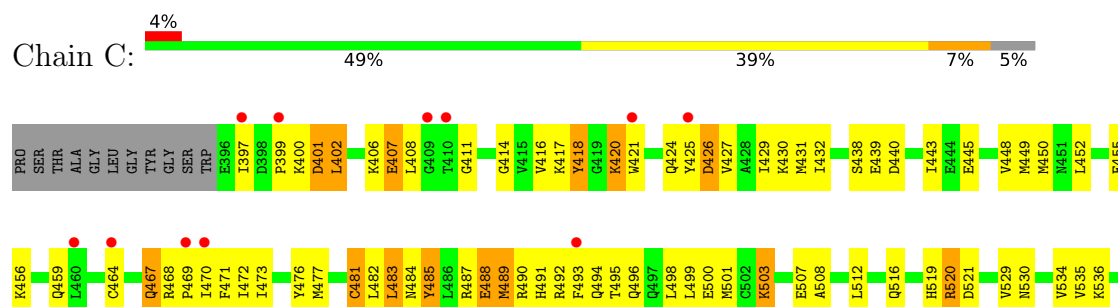
#### • Molecule 1: Tyrosine-protein kinase BTK

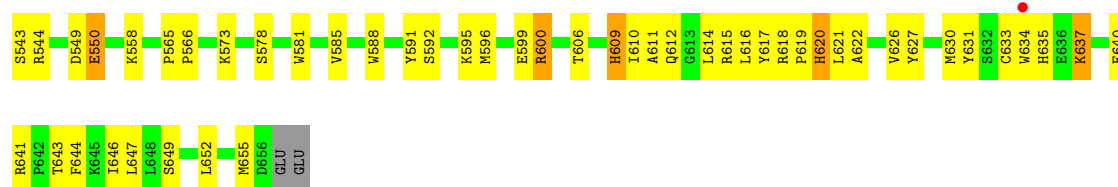


#### • Molecule 1: Tyrosine-protein kinase BTK

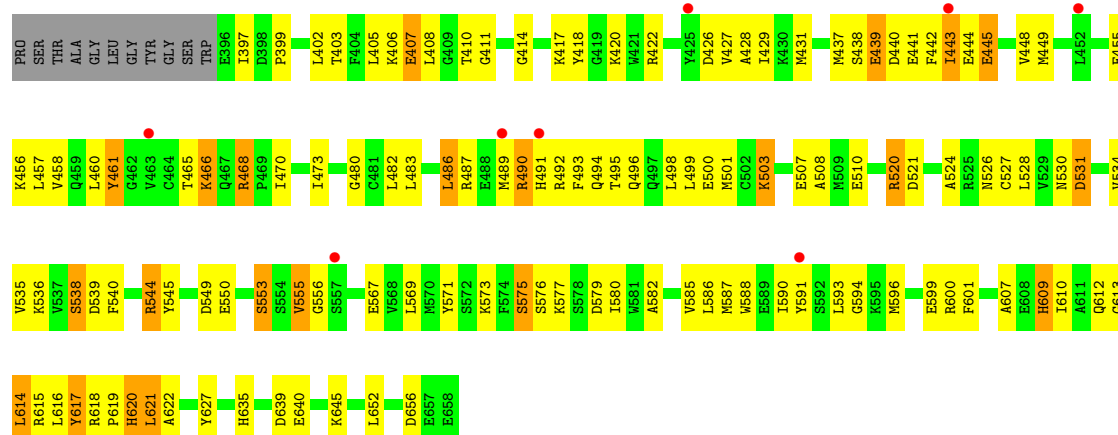


#### • Molecule 1: Tyrosine-protein kinase BTK





● Molecule 1: Tyrosine-protein kinase BTK



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.76Å 93.55Å 145.89Å 90.00° 89.94° 90.00°	Depositor
Resolution (Å)	48.63 – 1.59 48.63 – 1.58	Depositor EDS
% Data completeness (in resolution range)	90.1 (48.63-1.59) 90.1 (48.63-1.58)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 1.58Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, $R_{free}$	0.216 , 0.248 0.218 , 0.246	Depositor DCC
$R_{free}$ test set	6882 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.8	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 52.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.458 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9721	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.70% 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, 0.333 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: N42

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	1.19	0/2213	0.82	0/2982
1	B	1.24	0/2294	0.81	0/3094
1	C	1.07	0/2179	0.92	0/2938
1	D	0.89	0/2193	0.85	0/2957
All	All	1.11	0/8879	0.85	0/11971

There are no bond length outliers.

There are no bond angle outliers.

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	2158	0	2129	59	0
1	B	2239	0	2188	75	0
1	C	2127	0	2091	204	0
1	D	2141	0	2096	231	0
2	A	48	0	0	3	0
2	B	48	0	0	1	0
2	C	48	0	0	5	0
2	D	48	0	0	2	0
3	A	221	0	0	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	235	0	0	24	0
3	C	165	0	0	44	0
3	D	243	0	0	41	0
All	All	9721	0	8504	511	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 29.

All (511) 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:620:HIS:N	1:D:617:TYR:HB3	1.21	1.46
1:C:618:ARG:CB	1:D:618:ARG:HG2	1.60	1.30
1:B:492:ARG:HH21	1:B:492:ARG:HG3	1.01	1.17
1:C:455:GLU:O	1:C:536:LYS:HE2	1.43	1.16
1:C:489:MET:HG3	3:C:866:HOH:O	1.40	1.15
1:D:490:ARG:HB2	1:D:490:ARG:NH2	1.61	1.14
1:D:429:ILE:HG13	3:D:889:HOH:O	1.48	1.13
1:D:499:LEU:HD22	3:D:820:HOH:O	1.47	1.11
1:C:618:ARG:HB3	1:D:618:ARG:HG2	1.27	1.11
1:D:620:HIS:HB3	1:D:621:LEU:HD12	1.32	1.11
1:D:486:LEU:HD23	3:D:881:HOH:O	1.51	1.11
1:C:620:HIS:N	1:D:617:TYR:CB	2.14	1.09
1:C:618:ARG:HB2	1:D:618:ARG:HG2	1.35	1.06
1:C:620:HIS:CA	1:D:617:TYR:HB3	1.86	1.05
1:D:490:ARG:HB2	1:D:490:ARG:CZ	1.85	1.04
1:A:614:LEU:HD12	1:A:614:LEU:O	1.57	1.04
1:A:614:LEU:HD12	1:A:614:LEU:C	1.79	1.01
1:D:620:HIS:HB3	1:D:621:LEU:CD1	1.92	1.00
1:D:486:LEU:HD11	1:D:590:ILE:HA	1.44	0.98
1:D:486:LEU:HA	3:D:881:HOH:O	1.61	0.97
1:C:616:LEU:HD23	1:D:620:HIS:HE1	1.27	0.97
1:C:617:TYR:HB3	1:D:620:HIS:N	1.79	0.96
1:C:618:ARG:HB3	1:D:618:ARG:CG	1.97	0.95
1:C:529:VAL:HG22	1:C:535:VAL:HG22	1.45	0.94
1:C:616:LEU:HA	1:D:620:HIS:CE1	2.03	0.93
1:C:477:MET:HG2	3:C:807:HOH:O	1.67	0.93
1:C:620:HIS:HA	1:D:617:TYR:CA	1.99	0.92
1:C:620:HIS:H	1:D:617:TYR:HB3	1.34	0.91
1:C:581:TRP:HE3	1:C:641:ARG:NH1	1.69	0.90
1:C:464:CYS:HB2	1:C:471:PHE:HB2	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:618:ARG:NH2	1:D:627:TYR:CE1	2.40	0.89
1:D:490:ARG:NH2	1:D:490:ARG:CB	2.36	0.88
1:B:492:ARG:HG3	1:B:492:ARG:NH2	1.80	0.88
1:C:429:ILE:HG23	3:C:902:HOH:O	1.71	0.87
1:C:620:HIS:HA	1:D:617:TYR:N	1.90	0.87
1:D:621:LEU:CD1	1:D:621:LEU:N	2.38	0.87
1:C:615:ARG:HD2	1:C:634:TRP:HE3	1.38	0.87
1:C:616:LEU:HD23	1:D:620:HIS:CE1	2.11	0.86
1:A:614:LEU:C	1:A:614:LEU:CD1	2.44	0.85
1:C:619:PRO:C	1:D:617:TYR:HB3	1.96	0.85
1:C:485:TYR:CE2	1:C:491:HIS:CE1	2.65	0.84
1:D:440:ASP:O	1:D:444:GLU:HG3	1.77	0.83
1:D:618:ARG:CB	1:D:627:TYR:CD1	2.62	0.82
1:B:600:ARG:HG3	1:D:407:GLU:OE2	1.79	0.82
1:A:598:TYR:CE2	1:A:614:LEU:HD11	2.14	0.82
1:C:491:HIS:ND1	1:C:493:PHE:CE2	2.47	0.81
1:A:445:GLU:HG2	1:A:545:TYR:OH	1.79	0.81
1:C:476:TYR:CD2	3:C:834:HOH:O	2.33	0.81
1:C:501:MET:SD	3:C:940:HOH:O	2.38	0.81
1:C:617:TYR:HB3	1:D:620:HIS:CA	2.10	0.81
1:B:534:VAL:HA	3:B:807:HOH:O	1.80	0.80
1:D:490:ARG:CG	1:D:490:ARG:HH21	1.95	0.80
1:B:494:GLN:HG2	3:B:860:HOH:O	1.80	0.79
1:C:592:SER:HB2	3:C:839:HOH:O	1.82	0.79
1:D:405:LEU:HD12	1:D:418:TYR:CE2	2.17	0.79
1:C:491:HIS:HD1	1:C:493:PHE:HE2	1.29	0.79
1:D:549:ASP:O	1:D:553:SER:HB3	1.82	0.79
1:D:490:ARG:CZ	1:D:490:ARG:CB	2.60	0.79
1:D:417:LYS:NZ	1:D:431:MET:SD	2.56	0.79
1:D:503:LYS:HE3	1:D:507:GLU:OE1	1.82	0.79
1:C:581:TRP:HB2	1:C:641:ARG:NH1	1.97	0.78
1:C:618:ARG:HH21	1:D:627:TYR:HE1	1.31	0.78
1:D:465:THR:HA	1:D:470:ILE:HG12	1.65	0.78
1:C:615:ARG:HD2	1:C:634:TRP:CE3	2.17	0.78
1:C:631:TYR:HA	3:C:894:HOH:O	1.84	0.78
1:C:611:ALA:HB2	3:C:877:HOH:O	1.84	0.77
1:C:485:TYR:HB3	3:C:855:HOH:O	1.84	0.77
1:B:460:LEU:HD12	3:B:862:HOH:O	1.84	0.77
1:C:530:ASN:HB2	3:C:808:HOH:O	1.84	0.77
1:C:406:LYS:HG2	1:C:418:TYR:HD2	1.50	0.76
1:C:498:LEU:HD12	3:C:884:HOH:O	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:641:ARG:HD2	3:B:856:HOH:O	1.86	0.75
1:D:621:LEU:HD12	1:D:621:LEU:N	1.99	0.75
1:C:617:TYR:HB3	1:D:619:PRO:C	2.06	0.75
1:D:618:ARG:HB3	1:D:627:TYR:CD1	2.21	0.75
1:C:473:ILE:HG13	3:C:902:HOH:O	1.87	0.75
1:B:610:ILE:HD12	3:B:849:HOH:O	1.87	0.74
1:C:618:ARG:O	1:D:617:TYR:HB2	1.88	0.74
1:B:488:GLU:OE1	1:B:490:ARG:HD3	1.87	0.74
1:C:503:LYS:O	1:C:507:GLU:HG3	1.87	0.74
1:C:618:ARG:HG3	1:C:627:TYR:HB2	1.69	0.74
1:C:581:TRP:CE3	1:C:641:ARG:NH1	2.55	0.74
1:C:489:MET:HG2	3:C:889:HOH:O	1.86	0.73
1:D:439:GLU:OE2	1:D:470:ILE:HD12	1.87	0.73
1:D:403:THR:HB	3:D:802:HOH:O	1.87	0.73
1:D:618:ARG:HB2	1:D:627:TYR:CD1	2.24	0.72
1:C:617:TYR:HB2	1:D:618:ARG:O	1.90	0.72
1:C:618:ARG:NH2	1:D:618:ARG:H	1.88	0.72
1:A:509:MET:SD	3:A:919:HOH:O	2.48	0.72
1:D:486:LEU:HA	1:D:493:PHE:HE2	1.55	0.72
1:C:617:TYR:CA	1:D:620:HIS:HA	2.20	0.71
1:C:620:HIS:CA	1:D:617:TYR:CB	2.66	0.71
1:D:420:LYS:HG2	1:D:426:ASP:OD1	1.89	0.71
1:C:617:TYR:HB3	1:D:620:HIS:HA	1.71	0.71
1:A:402:LEU:HB3	3:A:823:HOH:O	1.90	0.70
1:C:620:HIS:ND1	1:D:617:TYR:CD2	2.58	0.70
1:C:401:ASP:HB2	1:C:421:TRP:HD1	1.55	0.70
1:C:408:LEU:HD21	1:C:418:TYR:HB3	1.72	0.70
1:D:442:PHE:HD2	1:D:443:ILE:HD13	1.57	0.70
1:C:635:HIS:CD2	1:C:637:LYS:HG3	2.27	0.70
1:D:455:GLU:HG2	1:D:456:LYS:HG2	1.74	0.69
1:C:619:PRO:C	1:D:617:TYR:CB	2.56	0.69
1:B:398:ASP:OD1	1:B:400:LYS:HB2	1.92	0.69
1:C:418:TYR:CD1	3:C:834:HOH:O	2.46	0.69
1:C:585:VAL:HG22	1:C:634:TRP:HZ2	1.58	0.69
1:D:501:MET:SD	3:D:994:HOH:O	2.50	0.69
1:D:620:HIS:CB	1:D:621:LEU:CD1	2.70	0.69
1:D:490:ARG:HH21	1:D:490:ARG:HG3	1.56	0.69
1:C:491:HIS:HB2	1:C:493:PHE:CD2	2.28	0.68
1:C:618:ARG:NE	1:D:618:ARG:HB3	2.08	0.68
1:B:534:VAL:CA	3:B:807:HOH:O	2.37	0.68
1:D:473:ILE:HG22	3:D:832:HOH:O	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:618:ARG:HB3	1:D:618:ARG:CB	2.23	0.68
1:D:618:ARG:CD	1:D:622:ALA:HB3	2.24	0.68
1:C:464:CYS:SG	3:C:933:HOH:O	2.53	0.67
1:D:483:LEU:O	1:D:487:ARG:HG3	1.95	0.67
1:B:470:ILE:HD11	3:B:801:HOH:O	1.93	0.67
1:A:434:GLU:HB2	3:A:991:HOH:O	1.96	0.66
1:A:450:MET:HE1	1:A:462:GLY:HA2	1.77	0.66
1:D:418:TYR:HE1	1:D:426:ASP:HB3	1.60	0.66
1:D:621:LEU:HD13	1:D:621:LEU:H	1.61	0.65
1:C:430:LYS:HB2	1:C:472:ILE:HB	1.78	0.65
1:D:441:GLU:O	1:D:545:TYR:CE1	2.50	0.65
1:C:620:HIS:HA	1:D:617:TYR:HA	1.78	0.65
1:B:412:GLN:HG3	3:B:876:HOH:O	1.96	0.65
1:D:427:VAL:HG23	3:D:889:HOH:O	1.97	0.65
1:D:569:LEU:CD1	1:D:610:ILE:HD11	2.26	0.65
1:D:534:VAL:HG13	3:D:828:HOH:O	1.96	0.65
1:C:618:ARG:CZ	1:D:618:ARG:H	2.10	0.65
1:C:482:LEU:HD12	3:C:855:HOH:O	1.97	0.64
1:C:503:LYS:HD3	3:C:864:HOH:O	1.97	0.64
1:C:635:HIS:HD2	1:C:637:LYS:HG3	1.62	0.64
1:C:476:TYR:CG	3:C:834:HOH:O	2.47	0.64
1:D:582:ALA:HA	3:D:856:HOH:O	1.98	0.64
1:C:618:ARG:NH1	1:C:619:PRO:O	2.31	0.64
1:D:495:THR:HG22	1:D:621:LEU:HB3	1.80	0.64
1:C:477:MET:HE3	1:C:530:ASN:HB3	1.80	0.63
1:B:468:ARG:NH2	3:B:801:HOH:O	2.32	0.63
1:C:407:GLU:HG2	1:C:416:VAL:O	1.98	0.63
1:D:455:GLU:CG	1:D:456:LYS:HG2	2.28	0.63
1:C:418:TYR:HD1	3:C:834:HOH:O	1.82	0.63
1:D:596:MET:CE	1:D:599:GLU:HA	2.29	0.63
1:D:618:ARG:CD	1:D:622:ALA:CB	2.77	0.63
1:C:406:LYS:HG2	1:C:418:TYR:CD2	2.33	0.63
1:C:618:ARG:NH1	1:C:622:ALA:O	2.32	0.63
1:D:618:ARG:HB2	1:D:627:TYR:HD1	1.62	0.63
1:B:449:MET:HG2	1:B:460:LEU:HD11	1.81	0.62
1:C:620:HIS:CD2	3:C:860:HOH:O	2.52	0.62
1:D:635:HIS:CG	1:D:640:GLU:HB2	2.35	0.62
1:C:618:ARG:HE	1:D:618:ARG:HB3	1.62	0.62
1:C:616:LEU:CD2	1:D:620:HIS:HE1	2.09	0.62
1:D:573:LYS:NZ	1:D:575:SER:OG	2.33	0.62
1:D:613:GLY:HA3	3:D:807:HOH:O	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:617:TYR:CB	1:D:620:HIS:HA	2.29	0.61
1:A:494:GLN:HG3	1:A:497:GLN:HG3	1.82	0.61
1:D:503:LYS:HE3	1:D:507:GLU:CD	2.20	0.61
1:C:618:ARG:NH2	1:D:618:ARG:N	2.49	0.61
1:D:490:ARG:NE	3:D:809:HOH:O	2.34	0.61
1:C:520:ARG:HH11	1:C:544:ARG:HD3	1.66	0.61
1:D:468:ARG:NH1	1:D:470:ILE:HG13	2.16	0.61
1:C:618:ARG:CB	1:D:618:ARG:CG	2.53	0.61
1:C:618:ARG:NE	1:D:627:TYR:CE1	2.69	0.61
1:C:599:GLU:OE1	1:C:600:ARG:NH2	2.34	0.60
1:A:433:LYS:HE2	1:A:436:SER:HB3	1.82	0.60
1:B:618:ARG:HH11	1:B:618:ARG:HG2	1.65	0.60
1:D:482:LEU:HD12	1:D:527:CYS:HB2	1.82	0.60
1:C:620:HIS:HA	1:D:617:TYR:CB	2.29	0.60
1:D:569:LEU:HD11	1:D:610:ILE:HD11	1.83	0.60
1:A:481:CYS:HB2	3:A:821:HOH:O	2.01	0.60
1:C:616:LEU:HD12	1:C:634:TRP:CH2	2.37	0.60
1:D:550:GLU:O	1:D:556:GLY:HA3	2.01	0.60
1:B:449:MET:HG2	1:B:460:LEU:CD1	2.32	0.60
1:C:616:LEU:HA	1:D:620:HIS:ND1	2.17	0.60
1:C:585:VAL:HG22	1:C:634:TRP:CZ2	2.36	0.60
1:D:397:ILE:HD12	1:D:473:ILE:HG13	1.84	0.60
1:D:490:ARG:CB	1:D:490:ARG:HH21	2.13	0.60
1:C:618:ARG:NH2	1:D:616:LEU:O	2.32	0.59
1:A:465:THR:HA	1:A:470:ILE:HG12	1.84	0.59
1:C:467:GLN:HB2	1:C:469:PRO:O	2.03	0.59
2:C:701:N42:CAA	2:C:701:N42:CAX	2.80	0.59
1:C:530:ASN:HD21	1:C:534:VAL:HB	1.67	0.59
1:C:618:ARG:NE	1:D:627:TYR:CZ	2.70	0.59
1:B:544:ARG:HD2	3:B:866:HOH:O	2.03	0.59
1:C:455:GLU:O	1:C:536:LYS:CE	2.34	0.59
1:A:406:LYS:HB3	1:A:418:TYR:HB3	1.85	0.59
1:D:499:LEU:HB2	3:D:820:HOH:O	2.01	0.59
1:D:456:LYS:NZ	1:D:507:GLU:OE2	2.32	0.59
1:C:565:PRO:HB3	1:C:641:ARG:HH12	1.68	0.59
1:D:455:GLU:HG3	1:D:456:LYS:HE3	1.84	0.58
1:C:588:TRP:HA	3:C:870:HOH:O	2.01	0.58
1:C:401:ASP:HB2	1:C:421:TRP:CD1	2.37	0.58
1:C:600:ARG:NE	3:C:806:HOH:O	2.34	0.58
1:D:422:ARG:NH2	3:D:816:HOH:O	2.36	0.58
1:D:442:PHE:CD2	1:D:443:ILE:HD13	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:519:HIS:CE1	1:C:521:ASP:O	2.56	0.58
1:B:524:ALA:N	1:B:586[A]:LEU:HD13	2.18	0.58
1:B:534:VAL:N	3:B:807:HOH:O	2.37	0.58
1:C:618:ARG:NH2	1:D:627:TYR:CZ	2.72	0.58
1:C:620:HIS:ND1	1:D:617:TYR:CG	2.61	0.58
1:A:609:HIS:ND1	3:A:805:HOH:O	2.33	0.58
1:D:500:GLU:HB3	3:D:867:HOH:O	2.04	0.58
1:D:596:MET:HE3	1:D:599:GLU:HA	1.84	0.58
1:B:600:ARG:NH1	3:B:804:HOH:O	2.36	0.57
1:C:516:GLN:NE2	3:C:801:HOH:O	2.31	0.57
1:C:424:GLN:HG2	1:C:425:TYR:CD2	2.39	0.57
1:D:544:ARG:NH2	1:D:545:TYR:OH	2.34	0.57
1:D:621:LEU:CD1	1:D:621:LEU:H	2.12	0.57
1:A:645:LYS:NZ	3:A:801:HOH:O	2.31	0.57
1:B:599:GLU:HG3	1:D:407:GLU:OE2	2.04	0.57
1:C:618:ARG:CZ	1:D:627:TYR:CE1	2.88	0.57
1:D:406:LYS:HG2	1:D:418:TYR:HD2	1.69	0.57
1:D:496:GLN:NE2	3:D:819:HOH:O	2.37	0.57
1:C:485:TYR:HE2	1:C:491:HIS:CE1	2.19	0.57
1:C:417:LYS:O	1:C:429:ILE:N	2.38	0.56
1:C:618:ARG:CZ	1:D:627:TYR:CZ	2.88	0.56
1:D:618:ARG:O	1:D:618:ARG:HG3	2.03	0.56
1:D:635:HIS:CD2	1:D:640:GLU:HB2	2.41	0.56
1:A:424:GLN:HG2	1:A:425:TYR:N	2.20	0.56
1:C:617:TYR:N	1:D:620:HIS:ND1	2.53	0.56
1:C:630:MET:SD	3:C:870:HOH:O	2.58	0.56
2:C:701:N42:CAB	3:C:807:HOH:O	2.53	0.56
1:D:618:ARG:CD	1:D:627:TYR:HB2	2.36	0.56
1:B:477:MET:HE2	1:B:536:LYS:HB2	1.87	0.56
1:C:401:ASP:N	1:C:401:ASP:OD2	2.38	0.56
1:D:571:TYR:HB2	3:D:823:HOH:O	2.05	0.56
1:D:427:VAL:CG2	3:D:889:HOH:O	2.52	0.56
1:A:625:LYS:HE2	1:A:654:VAL:HG22	1.88	0.56
1:D:483:LEU:HD13	1:D:524:ALA:HB3	1.87	0.55
1:C:445:GLU:O	1:C:448:VAL:N	2.39	0.55
1:D:591:TYR:HB3	1:D:619:PRO:HB2	1.88	0.55
1:C:581:TRP:HB2	1:C:641:ARG:HH12	1.70	0.55
1:D:486:LEU:HA	1:D:493:PHE:CE2	2.38	0.55
1:B:651:ILE:O	1:B:655:MET:HG3	2.06	0.55
1:D:487:ARG:HE	1:D:594:GLY:HA3	1.71	0.54
1:A:598:TYR:HE2	1:A:614:LEU:HD11	1.67	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:595:LYS:NZ	1:D:617:TYR:CD2	2.75	0.54
1:D:540:PHE:HD1	3:D:874:HOH:O	1.89	0.54
1:C:609:HIS:CD2	3:C:814:HOH:O	2.59	0.54
1:C:617:TYR:CB	1:D:619:PRO:C	2.75	0.54
1:D:521:ASP:O	1:D:526:ASN:ND2	2.36	0.54
1:C:618:ARG:HG3	1:C:627:TYR:CD1	2.43	0.54
1:C:620:HIS:ND1	1:D:617:TYR:N	2.52	0.53
1:B:580:ILE:HB	3:B:856:HOH:O	2.08	0.53
1:D:510:GLU:OE1	1:D:645:LYS:HA	2.08	0.53
1:C:618:ARG:HB3	1:D:618:ARG:HB3	1.90	0.53
1:D:508:ALA:CB	3:D:830:HOH:O	2.56	0.53
1:D:620:HIS:CB	1:D:621:LEU:HD12	2.23	0.53
1:A:635:HIS:NE2	1:A:640:GLU:OE1	2.41	0.53
1:C:581:TRP:HB2	1:C:641:ARG:HH11	1.74	0.53
1:C:599:GLU:HG3	1:C:600:ARG:HG2	1.91	0.53
1:C:592:SER:HB3	1:C:595:LYS:HB2	1.90	0.53
1:C:617:TYR:N	1:D:620:HIS:HA	2.23	0.53
1:D:482:LEU:HD12	1:D:527:CYS:CB	2.38	0.53
1:C:489:MET:SD	3:C:954:HOH:O	2.59	0.53
1:A:635:HIS:HB2	3:A:944:HOH:O	2.08	0.53
1:C:618:ARG:HG2	1:C:618:ARG:HH11	1.74	0.53
1:D:555:VAL:CG2	3:D:843:HOH:O	2.57	0.53
1:C:615:ARG:HB3	1:C:634:TRP:CZ3	2.44	0.53
1:C:620:HIS:HD1	1:D:617:TYR:CB	2.21	0.53
1:D:493:PHE:HB3	1:D:498:LEU:HD21	1.90	0.53
1:D:588:TRP:NE1	1:D:617:TYR:O	2.42	0.53
2:C:701:N42:CAU	2:C:701:N42:CBD	2.88	0.52
2:C:701:N42:CAV	2:C:701:N42:CAW	2.86	0.52
1:D:586:LEU:HD23	1:D:586:LEU:O	2.09	0.52
1:C:445:GLU:CD	1:C:544:ARG:HH22	2.12	0.52
1:D:585:VAL:HB	3:D:856:HOH:O	2.08	0.52
1:C:616:LEU:HD12	1:C:634:TRP:HH2	1.74	0.52
1:D:486:LEU:CA	3:D:881:HOH:O	2.37	0.52
1:A:600:ARG:HG2	1:A:600:ARG:HH21	1.75	0.52
1:B:492:ARG:NH2	1:B:492:ARG:CG	2.62	0.52
1:C:620:HIS:HD2	3:C:860:HOH:O	1.88	0.52
1:D:461:TYR:HD2	1:D:461:TYR:N	2.07	0.52
1:C:606:THR:O	1:C:610:ILE:HG23	2.10	0.52
1:B:407:GLU:HG2	3:B:883:HOH:O	2.09	0.52
1:C:609:HIS:HE1	3:C:881:HOH:O	1.93	0.52
1:D:599:GLU:HG3	1:D:600:ARG:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:439:GLU:OE2	1:C:468:ARG:CZ	2.58	0.52
1:C:464:CYS:CB	1:C:471:PHE:HB2	2.33	0.52
1:C:520:ARG:NH1	1:C:544:ARG:HD3	2.25	0.52
1:C:615:ARG:HB3	1:C:634:TRP:CE3	2.45	0.52
1:D:458:VAL:HB	1:D:538:SER:OG	2.10	0.51
1:B:420:LYS:NZ	1:B:426:ASP:OD1	2.43	0.51
1:C:445:GLU:OE2	1:C:544:ARG:NH2	2.44	0.51
1:C:596:MET:CE	1:C:599:GLU:HA	2.40	0.51
1:D:591:TYR:CB	1:D:619:PRO:HG2	2.41	0.51
1:A:549:ASP:O	1:A:553:SER:HB3	2.11	0.51
1:C:476:TYR:HA	3:C:807:HOH:O	2.09	0.51
1:D:455:GLU:O	1:D:536:LYS:HE2	2.10	0.51
1:C:489:MET:O	1:C:492:ARG:N	2.44	0.51
1:B:416:VAL:HG22	1:B:430:LYS:HG2	1.93	0.51
1:B:488:GLU:HG3	1:B:490:ARG:HG2	1.92	0.51
1:C:424:GLN:HG2	1:C:425:TYR:CE2	2.46	0.51
1:C:609:HIS:HA	1:C:612:GLN:HB2	1.93	0.50
1:D:461:TYR:N	1:D:461:TYR:CD2	2.79	0.50
1:D:490:ARG:HD3	3:D:824:HOH:O	2.11	0.50
1:D:491:HIS:HB3	1:D:493:PHE:CE1	2.45	0.50
1:D:486:LEU:O	1:D:493:PHE:CE2	2.65	0.50
1:B:553:SER:OG	1:B:555:VAL:HG23	2.11	0.50
1:D:612:GLN:NE2	3:D:825:HOH:O	2.45	0.50
1:B:600:ARG:H	1:B:600:ARG:NE	2.09	0.50
1:B:600:ARG:H	1:B:600:ARG:CD	2.25	0.50
1:C:611:ALA:CB	3:C:877:HOH:O	2.51	0.50
1:C:635:HIS:CD2	1:C:640:GLU:HB2	2.47	0.49
1:A:550:GLU:HA	1:A:550:GLU:OE1	2.12	0.49
1:A:610:ILE:C	1:A:610:ILE:HD12	2.31	0.49
1:B:618:ARG:HG2	1:B:618:ARG:NH1	2.27	0.49
1:C:550:GLU:HB2	1:C:558:LYS:HD2	1.93	0.49
1:C:477:MET:CE	1:C:530:ASN:HB3	2.40	0.49
1:A:637:LYS:HG2	1:A:640:GLU:HG3	1.94	0.49
1:D:456:LYS:C	3:D:830:HOH:O	2.50	0.49
1:C:439:GLU:OE2	1:C:468:ARG:NE	2.46	0.49
1:B:439:GLU:HB3	3:B:801:HOH:O	2.13	0.49
1:B:467:GLN:O	1:B:468:ARG:HD3	2.13	0.49
1:D:443:ILE:HG21	1:D:465:THR:HG21	1.95	0.49
1:A:403:THR:N	3:A:823:HOH:O	2.46	0.49
1:C:431:MET:HE2	3:C:810:HOH:O	2.13	0.49
1:D:457:LEU:HG	3:D:830:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:466:LYS:NZ	3:D:826:HOH:O	2.45	0.49
1:A:562:ARG:HB2	1:A:563:TRP:CZ3	2.48	0.48
1:C:616:LEU:H	1:C:634:TRP:HZ3	1.60	0.48
1:C:397:ILE:HD12	1:C:473:ILE:HG21	1.96	0.48
1:B:602:THR:HG22	1:D:410:THR:HG21	1.94	0.48
1:C:617:TYR:HA	1:D:620:HIS:HA	1.95	0.48
1:C:500:GLU:OE2	1:C:503:LYS:NZ	2.47	0.48
1:C:508:ALA:O	1:C:512:LEU:HG	2.13	0.48
1:C:620:HIS:CA	1:D:617:TYR:CA	2.82	0.48
1:D:535:VAL:N	3:D:828:HOH:O	2.47	0.48
1:D:571:TYR:HD1	3:D:823:HOH:O	1.94	0.48
1:C:635:HIS:NE2	1:C:637:LYS:HE2	2.28	0.48
1:D:402:LEU:HD22	1:D:473:ILE:HD12	1.95	0.48
1:D:406:LYS:HG2	1:D:418:TYR:CD2	2.49	0.48
1:A:488:GLU:O	1:A:491:HIS:O	2.32	0.48
1:C:530:ASN:ND2	1:C:534:VAL:HB	2.29	0.48
1:A:421:TRP:CD1	1:A:422:ARG:HG3	2.49	0.48
1:A:516:GLN:HG2	3:A:969:HOH:O	2.12	0.48
1:D:609:HIS:HE1	1:D:614:LEU:HB3	1.79	0.48
1:C:643:THR:H	1:C:646:ILE:HD12	1.78	0.47
1:D:528:LEU:HB3	3:D:884:HOH:O	2.14	0.47
1:D:530:ASN:OD1	1:D:534:VAL:HB	2.13	0.47
1:C:489:MET:HA	3:C:889:HOH:O	2.14	0.47
1:B:546:VAL:HG12	1:B:548:ASP:H	1.80	0.47
2:A:701:N42:CBM	2:A:701:N42:CBK	2.92	0.47
1:C:421:TRP:HB3	1:C:427:VAL:HG11	1.97	0.47
1:C:485:TYR:CE2	1:C:491:HIS:HE1	2.27	0.47
1:D:449:MET:HG2	1:D:460:LEU:HD12	1.96	0.47
1:D:482:LEU:CD1	1:D:527:CYS:HB2	2.45	0.47
1:C:493:PHE:HD2	1:C:493:PHE:H	1.62	0.47
1:A:500:GLU:O	1:A:500:GLU:HG3	2.14	0.47
1:A:657:GLU:OE2	1:A:658:GLU:HG3	2.15	0.47
1:C:619:PRO:HG2	3:C:870:HOH:O	2.14	0.47
1:D:618:ARG:HB2	1:D:627:TYR:HB2	1.96	0.47
1:C:591:TYR:CZ	1:C:626:VAL:HG11	2.49	0.46
1:C:620:HIS:HD1	1:D:617:TYR:H	1.61	0.46
1:D:420:LYS:N	3:D:802:HOH:O	2.31	0.46
1:A:473:ILE:N	1:A:473:ILE:HD12	2.30	0.46
2:A:701:N42:CAX	2:A:701:N42:CAA	2.90	0.46
1:C:483:LEU:O	1:C:487:ARG:HG3	2.16	0.46
1:A:610:ILE:HD12	1:A:611:ALA:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:477:MET:N	3:C:807:HOH:O	2.48	0.46
1:D:457:LEU:N	3:D:830:HOH:O	2.48	0.46
1:A:487:ARG:NH2	1:A:594:GLY:O	2.41	0.46
1:C:618:ARG:HG3	1:C:627:TYR:CB	2.43	0.46
1:D:456:LYS:HB2	1:D:508:ALA:HB2	1.96	0.46
1:A:600:ARG:HD2	3:A:942:HOH:O	2.15	0.46
2:B:701:N42:CAA	2:B:701:N42:CAX	2.93	0.46
1:A:560:PRO:O	1:A:564:SER:OG	2.33	0.46
1:D:445:GLU:O	1:D:445:GLU:HG3	2.01	0.46
1:B:481:CYS:HB3	3:B:926:HOH:O	2.16	0.46
1:B:520:ARG:NH2	3:B:821:HOH:O	2.48	0.46
1:B:533:GLY:C	3:B:807:HOH:O	2.53	0.46
1:D:492:ARG:HA	3:D:957:HOH:O	2.15	0.46
1:D:569:LEU:HD12	1:D:610:ILE:HD11	1.96	0.46
1:B:406:LYS:HB2	3:B:943:HOH:O	2.16	0.46
1:B:633:CYS:O	1:B:641:ARG:HD3	2.15	0.46
1:C:449:MET:HA	1:C:452:LEU:HD12	1.97	0.46
1:B:387:THR:HG21	1:B:396:GLU:HB2	1.97	0.46
1:A:502:CYS:SG	1:A:587:MET:HG2	2.57	0.45
1:C:485:TYR:CE2	1:C:491:HIS:NE2	2.84	0.45
1:D:599:GLU:HG3	1:D:600:ARG:N	2.31	0.45
1:A:468:ARG:NH2	3:A:809:HOH:O	2.34	0.45
1:A:559:PHE:CG	1:A:560:PRO:HD2	2.51	0.45
1:D:576:SER:HA	1:D:579:ASP:HB2	1.98	0.45
1:B:489:MET:HA	1:B:492:ARG:HE	1.81	0.45
1:D:615:ARG:NH2	3:D:827:HOH:O	2.45	0.45
1:C:425:TYR:O	1:C:427:VAL:HG13	2.16	0.45
1:C:477:MET:HE1	1:C:530:ASN:HD22	1.82	0.45
1:D:406:LYS:HE2	1:D:408:LEU:CD2	2.46	0.45
1:D:538:SER:O	1:D:539:ASP:HB2	2.17	0.45
1:B:618:ARG:HG3	1:B:627:TYR:HB2	1.98	0.45
1:C:614:LEU:CD2	1:C:615:ARG:H	2.30	0.45
1:D:482:LEU:HD22	1:D:524:ALA:HB1	1.97	0.45
1:D:531:ASP:OD1	1:D:531:ASP:N	2.42	0.45
1:B:599:GLU:HG3	1:D:407:GLU:HG2	1.99	0.45
1:D:411:GLY:N	1:D:414:GLY:O	2.39	0.45
1:D:486:LEU:CG	3:D:881:HOH:O	2.61	0.45
1:D:567:GLU:HB2	3:D:823:HOH:O	2.16	0.45
1:D:569:LEU:HD13	1:D:607:ALA:HA	1.98	0.45
1:A:446:ALA:O	1:A:450:MET:HG2	2.17	0.45
1:B:387:THR:HB	1:B:465:THR:OG1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:439:GLU:HG2	1:C:470:ILE:HD12	1.99	0.45
1:D:486:LEU:CA	1:D:493:PHE:HE2	2.27	0.45
1:D:495:THR:HB	3:D:806:HOH:O	2.16	0.45
1:C:476:TYR:CB	3:C:834:HOH:O	2.65	0.44
1:C:484:ASN:O	1:C:488:GLU:HG2	2.17	0.44
1:D:621:LEU:N	1:D:621:LEU:HD13	2.19	0.44
1:A:581:TRP:CD1	1:A:581:TRP:C	2.89	0.44
1:A:618:ARG:HG3	1:A:627:TYR:HB2	1.99	0.44
1:B:577:LYS:HB3	3:B:856:HOH:O	2.17	0.44
1:C:470:ILE:CG2	1:C:471:PHE:N	2.80	0.44
1:D:486:LEU:O	1:D:493:PHE:HE2	1.99	0.44
1:A:438:SER:OG	1:A:441:GLU:OE1	2.35	0.44
1:B:599:GLU:H	1:B:600:ARG:HH11	1.64	0.44
1:C:619:PRO:C	1:D:617:TYR:HB2	2.38	0.44
1:D:503:LYS:CE	1:D:507:GLU:CD	2.85	0.44
2:D:701:N42:CAX	2:D:701:N42:CAA	2.93	0.44
1:B:488:GLU:HG3	1:B:490:ARG:CG	2.48	0.44
1:C:495:THR:HG22	3:C:884:HOH:O	2.18	0.44
1:C:618:ARG:NH1	1:C:618:ARG:HG2	2.32	0.44
1:D:439:GLU:HG2	1:D:468:ARG:NH2	2.32	0.44
1:D:493:PHE:HD2	1:D:593:LEU:HD22	1.82	0.44
1:A:631:TYR:HA	1:A:634:TRP:CE3	2.53	0.44
1:C:481:CYS:HB2	2:C:701:N42:OAH	2.18	0.44
1:C:565:PRO:HG3	1:C:578:SER:HA	2.00	0.44
1:D:428:ALA:HB3	2:D:701:N42:CAB	2.48	0.43
1:D:480:GLY:HA2	3:D:884:HOH:O	2.18	0.43
1:C:581:TRP:HE3	1:C:641:ARG:CZ	2.29	0.43
1:D:576:SER:O	1:D:580:ILE:N	2.51	0.43
1:B:417:LYS:NZ	1:C:600:ARG:O	2.46	0.43
1:B:488:GLU:CG	1:B:490:ARG:HG2	2.47	0.43
1:B:406:LYS:HG2	1:B:418:TYR:HD2	1.83	0.43
1:B:602:THR:HG22	1:D:410:THR:CG2	2.49	0.43
1:C:644:PHE:HA	1:C:647:LEU:HD12	2.00	0.43
1:D:635:HIS:CE1	1:D:640:GLU:HG3	2.54	0.43
1:A:406:LYS:O	1:A:418:TYR:N	2.43	0.43
1:B:653:ASP:O	1:B:657:GLU:HG3	2.18	0.43
1:D:587:MET:HG2	3:D:952:HOH:O	2.18	0.43
1:D:449:MET:HG2	1:D:460:LEU:CD1	2.49	0.43
1:A:466:LYS:HA	1:A:466:LYS:HD3	1.90	0.43
1:A:600:ARG:NH2	3:A:829:HOH:O	2.52	0.43
1:B:603:ASN:HA	3:B:814:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:390:LEU:HD12	1:B:390:LEU:HA	1.87	0.43
1:C:432:ILE:O	1:C:469:PRO:HB3	2.18	0.43
1:C:482:LEU:HD11	3:C:901:HOH:O	2.18	0.43
1:C:618:ARG:HG3	1:C:627:TYR:CG	2.54	0.43
1:D:445:GLU:OE1	1:D:448:VAL:HB	2.19	0.43
1:D:588:TRP:CD1	1:D:616:LEU:HB3	2.54	0.43
1:A:494:GLN:HG3	1:A:497:GLN:CG	2.48	0.42
1:C:618:ARG:O	1:D:618:ARG:O	2.37	0.42
1:D:520:ARG:HB2	1:D:520:ARG:NH1	2.33	0.42
1:C:456:LYS:HA	1:C:536:LYS:HG2	2.00	0.42
1:B:596:MET:HG3	3:B:1001:HOH:O	2.19	0.42
1:D:399:PRO:HA	1:D:402:LEU:HD12	2.01	0.42
1:A:598:TYR:HE2	1:A:614:LEU:CD1	2.31	0.42
1:B:430:LYS:O	1:B:471:PHE:HA	2.19	0.42
1:C:420:LYS:HD2	3:C:909:HOH:O	2.19	0.42
1:C:618:ARG:NE	1:D:627:TYR:CE2	2.88	0.42
1:B:488:GLU:OE1	1:B:490:ARG:CD	2.63	0.42
1:B:559:PHE:CD1	1:B:560:PRO:HD2	2.54	0.42
1:C:481:CYS:HB3	1:C:484:ASN:H	1.84	0.42
1:D:408:LEU:HD11	1:D:418:TYR:HB2	2.01	0.42
1:C:418:TYR:HE1	1:C:426:ASP:OD2	2.03	0.42
1:D:470:ILE:HD11	3:D:900:HOH:O	2.20	0.42
1:D:569:LEU:HD23	1:D:569:LEU:HA	1.76	0.42
1:D:652:LEU:O	1:D:656:ASP:N	2.53	0.42
1:A:449:MET:HG2	1:A:460:LEU:HD13	2.00	0.42
1:B:524:ALA:HB2	1:B:586[A]:LEU:CD1	2.49	0.42
1:B:559:PHE:CG	1:B:560:PRO:HD2	2.55	0.42
1:B:588:TRP:CE2	1:B:616:LEU:HD22	2.55	0.42
1:B:602:THR:HA	1:D:410:THR:HG21	2.02	0.42
1:D:586:LEU:HD23	1:D:586:LEU:C	2.40	0.42
1:B:524:ALA:HA	1:B:586[A]:LEU:HD11	2.01	0.42
1:A:569:LEU:HD12	1:A:610:ILE:HD11	2.02	0.41
1:A:600:ARG:HD2	1:A:600:ARG:H	1.85	0.41
1:D:577:LYS:HD3	1:D:580:ILE:HG13	2.02	0.41
1:B:623:SER:N	3:B:826:HOH:O	2.54	0.41
2:A:701:N42:CAU	2:A:701:N42:CBD	2.98	0.41
1:D:468:ARG:HD3	1:D:468:ARG:HA	1.84	0.41
1:B:569:LEU:HD11	1:B:610:ILE:CD1	2.51	0.41
1:D:486:LEU:HD13	1:D:593:LEU:HA	2.01	0.41
1:D:618:ARG:HA	1:D:619:PRO:HD3	1.75	0.41
1:B:534:VAL:CG2	3:B:807:HOH:O	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:430:LYS:N	3:C:832:HOH:O	2.53	0.41
1:C:618:ARG:H	1:D:618:ARG:HG3	1.85	0.41
1:A:497:GLN:O	1:A:501:MET:HG3	2.21	0.41
1:C:430:LYS:HG3	3:C:832:HOH:O	2.19	0.41
1:C:652:LEU:HD23	1:C:652:LEU:HA	1.89	0.41
1:B:599:GLU:OE1	1:D:407:GLU:HB3	2.20	0.41
1:D:397:ILE:HG21	1:D:402:LEU:HD21	2.03	0.41
1:D:468:ARG:HH12	1:D:470:ILE:HG13	1.86	0.41
1:D:491:HIS:CB	1:D:493:PHE:CE1	3.04	0.41
1:D:617:TYR:O	1:D:617:TYR:HD1	2.03	0.41
1:A:396:GLU:OE1	1:A:464:CYS:HA	2.21	0.41
1:B:445:GLU:O	1:B:445:GLU:HG3	2.21	0.41
1:B:488:GLU:OE2	1:B:488:GLU:HA	2.18	0.41
1:C:411:GLY:N	1:C:414:GLY:O	2.52	0.41
1:C:543:SER:HB3	3:C:822:HOH:O	2.21	0.41
1:D:437:MET:HG2	1:D:438:SER:N	2.36	0.41
1:A:526:ASN:O	1:A:538[A]:SER:OG	2.33	0.40
1:C:499:LEU:HB3	3:C:850:HOH:O	2.21	0.40
1:C:591:TYR:HB2	3:C:870:HOH:O	2.21	0.40
1:D:618:ARG:CD	1:D:622:ALA:HB1	2.51	0.40
1:A:648:LEU:O	1:A:652:LEU:HG	2.21	0.40
1:B:658:GLU:C	1:B:658:GLU:CD	2.80	0.40
1:D:620:HIS:C	1:D:621:LEU:HD12	2.42	0.40
1:C:610:ILE:HG13	1:C:611:ALA:H	1.86	0.40
1:C:633:CYS:O	1:C:641:ARG:HD3	2.21	0.40
1:A:596:MET:HB3	1:A:596:MET:HE2	1.96	0.40
1:D:482:LEU:HB3	1:D:524:ALA:O	2.22	0.40
1:C:399:PRO:HA	1:C:402:LEU:HB2	2.04	0.40
1:C:456:LYS:HA	1:C:456:LYS:HD3	2.00	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	263/274 (96%)	259 (98%)	4 (2%)	0	100	100
1	B	275/274 (100%)	272 (99%)	3 (1%)	0	100	100
1	C	260/274 (95%)	253 (97%)	7 (3%)	0	100	100
1	D	262/274 (96%)	253 (97%)	9 (3%)	0	100	100
All	All	1060/1096 (97%)	1037 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	239/245 (98%)	225 (94%)	14 (6%)	19	4
1	B	245/245 (100%)	226 (92%)	19 (8%)	12	2
1	C	234/245 (96%)	200 (86%)	34 (14%)	3	0
1	D	235/245 (96%)	209 (89%)	26 (11%)	6	0
All	All	953/980 (97%)	860 (90%)	93 (10%)	8	1

All (93) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	444	GLU
1	A	445	GLU
1	A	447	LYS
1	A	455	GLU
1	A	468	ARG
1	A	470	ILE
1	A	489	MET
1	A	491	HIS
1	A	554	SER
1	A	599	GLU
1	A	600	ARG
1	A	614	LEU
1	A	645	LYS

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Mol	Chain	Res	Type
1	A	657	GLU
1	B	387	THR
1	B	390	LEU
1	B	415	VAL
1	B	438	SER
1	B	440	ASP
1	B	444	GLU
1	B	460	LEU
1	B	483	LEU
1	B	488	GLU
1	B	492	ARG
1	B	500	GLU
1	B	531	ASP
1	B	555	VAL
1	B	566	PRO
1	B	573	LYS
1	B	600	ARG
1	B	610	ILE
1	B	645	LYS
1	B	658	GLU
1	C	400	LYS
1	C	401	ASP
1	C	402	LEU
1	C	407	GLU
1	C	418	TYR
1	C	420	LYS
1	C	426	ASP
1	C	438	SER
1	C	440	ASP
1	C	443	ILE
1	C	450	MET
1	C	459	GLN
1	C	467	GLN
1	C	481	CYS
1	C	483	LEU
1	C	485	TYR
1	C	488	GLU
1	C	489	MET
1	C	490	ARG
1	C	494	GLN
1	C	496	GLN
1	C	503	LYS

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Mol	Chain	Res	Type
1	C	520	ARG
1	C	549	ASP
1	C	550	GLU
1	C	566	PRO
1	C	573	LYS
1	C	600	ARG
1	C	609	HIS
1	C	620	HIS
1	C	621	LEU
1	C	637	LYS
1	C	649	SER
1	C	655	MET
1	D	407	GLU
1	D	439	GLU
1	D	443	ILE
1	D	445	GLU
1	D	461	TYR
1	D	466	LYS
1	D	468	ARG
1	D	486	LEU
1	D	489	MET
1	D	490	ARG
1	D	494	GLN
1	D	503	LYS
1	D	520	ARG
1	D	531	ASP
1	D	538	SER
1	D	544	ARG
1	D	553	SER
1	D	555	VAL
1	D	575	SER
1	D	601	PHE
1	D	609	HIS
1	D	614	LEU
1	D	617	TYR
1	D	620	HIS
1	D	621	LEU
1	D	639	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	491	HIS
1	B	491	HIS
1	D	609	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

4 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	N42	D	701	1	52,52,52	2.46	13 (25%)	73,75,75	1.93	12 (16%)
2	N42	A	701	1	52,52,52	2.36	13 (25%)	73,75,75	2.39	13 (17%)
2	N42	C	701	1	52,52,52	2.59	13 (25%)	73,75,75	1.75	10 (13%)
2	N42	B	701	1	52,52,52	2.37	12 (23%)	73,75,75	1.91	13 (17%)

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	N42	D	701	1	-	6/36/44/44	0/5/5/5
2	N42	A	701	1	-	6/36/44/44	0/5/5/5
2	N42	C	701	1	-	7/36/44/44	0/5/5/5
2	N42	B	701	1	-	6/36/44/44	0/5/5/5

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	701	N42	CAA-CBN	-7.81	1.35	1.51
2	C	701	N42	CCB-CBT	-7.37	1.38	1.53
2	D	701	N42	CBV-CBM	-7.18	1.39	1.50
2	C	701	N42	CBV-CBM	-6.83	1.40	1.50
2	A	701	N42	CBV-CBM	-6.72	1.40	1.50
2	A	701	N42	CCB-CBT	-6.66	1.40	1.53
2	B	701	N42	CBW-CBQ	-6.62	1.40	1.48
2	B	701	N42	CBV-CBM	-6.51	1.40	1.50
2	A	701	N42	CAA-CBN	-6.43	1.38	1.51
2	D	701	N42	CCB-CBT	-6.43	1.40	1.53
2	D	701	N42	CBW-CBQ	-6.39	1.41	1.48
2	B	701	N42	CAA-CBN	-6.24	1.38	1.51
2	D	701	N42	CAA-CBN	-5.90	1.39	1.51
2	C	701	N42	CBX-NCA	-5.82	1.31	1.39
2	B	701	N42	CCB-CBT	-5.82	1.41	1.53
2	C	701	N42	CBP-CBL	-5.81	1.38	1.50
2	C	701	N42	CBW-CBQ	-5.28	1.42	1.48
2	C	701	N42	CBA-CBB	5.27	1.56	1.30
2	A	701	N42	CBW-CBQ	-5.14	1.42	1.48
2	A	701	N42	CBA-CBB	4.84	1.54	1.30
2	D	701	N42	CBA-CBB	4.82	1.54	1.30
2	A	701	N42	CBP-CBL	-4.78	1.40	1.50
2	B	701	N42	CBA-CBB	4.49	1.52	1.30
2	B	701	N42	CBS-NBF	-4.42	1.33	1.41
2	D	701	N42	CBO-NBH	-4.37	1.32	1.41
2	A	701	N42	CBS-NBF	-4.18	1.33	1.41
2	A	701	N42	CBX-NCA	-4.15	1.33	1.39
2	B	701	N42	CBP-CBL	-4.11	1.41	1.50
2	D	701	N42	CBP-CBL	-4.07	1.41	1.50
2	D	701	N42	CBS-NBF	-3.83	1.34	1.41
2	B	701	N42	CBR-NBG	-3.81	1.34	1.41
2	D	701	N42	CBB-CBK	3.77	1.54	1.48
2	B	701	N42	CBX-NCA	-3.75	1.34	1.39
2	D	701	N42	CBR-NBG	-3.72	1.34	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	N42	CBU-CBX	-3.70	1.38	1.47
2	D	701	N42	CBX-NCA	-3.68	1.34	1.39
2	A	701	N42	CBU-CBX	-3.57	1.39	1.47
2	D	701	N42	CBU-CBX	-3.45	1.39	1.47
2	B	701	N42	CBO-NBH	-3.34	1.34	1.41
2	C	701	N42	CBU-CBX	-3.11	1.40	1.47
2	A	701	N42	CBO-NBH	-2.95	1.35	1.41
2	C	701	N42	CBR-NBG	-2.93	1.36	1.41
2	C	701	N42	CBS-NBF	-2.86	1.36	1.41
2	A	701	N42	CBR-NBG	-2.85	1.36	1.41
2	B	701	N42	CBB-CBK	2.74	1.52	1.48
2	C	701	N42	CBO-NBH	-2.68	1.36	1.41
2	A	701	N42	CBB-CBK	2.49	1.52	1.48
2	C	701	N42	CBB-CBK	2.44	1.52	1.48
2	D	701	N42	CAW-CBU	2.33	1.41	1.36
2	A	701	N42	CAW-CBU	2.26	1.41	1.36
2	C	701	N42	OAI-CBL	-2.07	1.19	1.23

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	N42	CBA-CBB-CBK	-14.95	105.17	122.27
2	D	701	N42	CBA-CBB-CBK	-11.19	109.48	122.27
2	B	701	N42	CBA-CBB-CBK	-10.17	110.64	122.27
2	A	701	N42	CBW-CBN-CBR	5.60	121.54	117.15
2	C	701	N42	CBW-CBN-CBR	5.41	121.39	117.15
2	C	701	N42	CBA-CBB-CBK	-5.39	116.10	122.27
2	C	701	N42	CBU-CBX-NCA	5.26	121.17	116.39
2	D	701	N42	CBW-CBN-CBR	5.23	121.25	117.15
2	B	701	N42	CBW-CBN-CBR	5.16	121.19	117.15
2	A	701	N42	CBU-CBX-NCA	4.69	120.65	116.39
2	C	701	N42	CBX-CBU-NBH	4.54	116.53	112.34
2	A	701	N42	CAR-CBW-CBN	-4.37	117.59	120.72
2	B	701	N42	CAR-CBW-CBN	-4.35	117.60	120.72
2	C	701	N42	CBB-CBK-NBF	4.22	116.62	113.84
2	D	701	N42	CAR-CBW-CBN	-4.09	117.78	120.72
2	B	701	N42	CBU-CBX-NCA	3.76	119.80	116.39
2	C	701	N42	CAR-CBW-CBN	-3.62	118.12	120.72
2	D	701	N42	CBU-CBX-NCA	3.59	119.65	116.39
2	A	701	N42	OAH-CBK-NBF	3.54	127.11	123.05
2	A	701	N42	CBD-NBZ-CBC	3.47	119.31	112.62
2	B	701	N42	CAU-CAO-CBO	3.33	124.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	701	N42	CBS-CBV-CBM	3.26	125.30	120.69
2	D	701	N42	CBS-NBF-CBK	-3.18	119.82	127.15
2	C	701	N42	CAW-CBU-CBX	-3.16	118.20	120.22
2	D	701	N42	CBB-CBK-NBF	3.08	115.87	113.84
2	C	701	N42	OAH-CBK-CBB	-3.00	117.93	122.72
2	A	701	N42	CBV-CBM-NBZ	2.68	122.57	118.28
2	B	701	N42	CBS-NBF-CBK	-2.59	121.17	127.15
2	B	701	N42	CBV-CBM-NBZ	2.58	122.41	118.28
2	D	701	N42	CBD-NBZ-CBC	2.55	117.52	112.62
2	D	701	N42	CBS-CBV-CBM	2.49	124.21	120.69
2	A	701	N42	CBN-CBW-CBQ	2.38	125.00	121.98
2	A	701	N42	CAW-CBU-CBX	-2.36	118.71	120.22
2	D	701	N42	CAA-CBN-CBW	-2.35	118.91	122.31
2	B	701	N42	CAV-CBS-CBV	2.34	122.23	118.89
2	A	701	N42	CBB-CBK-NBF	-2.29	112.33	113.84
2	B	701	N42	CBR-NBG-CBL	-2.28	120.68	126.93
2	B	701	N42	OAK-CBX-CBU	-2.28	119.64	122.29
2	D	701	N42	CBR-NBG-CBL	-2.24	120.78	126.93
2	C	701	N42	CAA-CBN-CBW	-2.24	119.08	122.31
2	A	701	N42	CAU-CAO-CBO	2.21	122.86	120.30
2	D	701	N42	CAB-NCA-CBX	2.17	120.21	117.12
2	C	701	N42	CBV-CBM-NBZ	2.16	121.74	118.28
2	A	701	N42	CAO-CBO-CAV	-2.12	117.14	119.65
2	B	701	N42	OAH-CBK-NBF	2.06	125.41	123.05
2	A	701	N42	OAK-CBX-CBU	-2.05	119.90	122.29
2	D	701	N42	OBI-CAY-CBC	-2.03	107.33	111.80
2	B	701	N42	CAO-CBO-CAV	-2.01	117.27	119.65

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	N42	CBA-CBB-CBK-OAH
2	A	701	N42	CBA-CBB-CBK-NBF
2	B	701	N42	CBA-CBB-CBK-OAH
2	B	701	N42	CBA-CBB-CBK-NBF
2	C	701	N42	CBA-CBB-CBK-OAH
2	D	701	N42	CBA-CBB-CBK-OAH
2	D	701	N42	CBA-CBB-CBK-NBF
2	B	701	N42	CAN-CBR-NBG-CBL
2	A	701	N42	CAN-CBR-NBG-CBL
2	C	701	N42	CAN-CBR-NBG-CBL

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Mol	Chain	Res	Type	Atoms
2	D	701	N42	CAN-CBR-NBG-CBL
2	C	701	N42	CBN-CBR-NBG-CBL
2	D	701	N42	CBN-CBR-NBG-CBL
2	B	701	N42	CBN-CBR-NBG-CBL
2	A	701	N42	CBN-CBR-NBG-CBL
2	A	701	N42	CAW-CBQ-CBW-CBN
2	C	701	N42	CAW-CBQ-CBW-CBN
2	A	701	N42	CBV-CBS-NBF-CBK
2	B	701	N42	CBV-CBS-NBF-CBK
2	D	701	N42	CBV-CBS-NBF-CBK
2	D	701	N42	CAW-CBQ-CBW-CAR
2	C	701	N42	CAX-CBQ-CBW-CAR
2	C	701	N42	CAV-CBS-NBF-CBK
2	C	701	N42	CBV-CBS-NBF-CBK
2	B	701	N42	CAW-CBQ-CBW-CBN

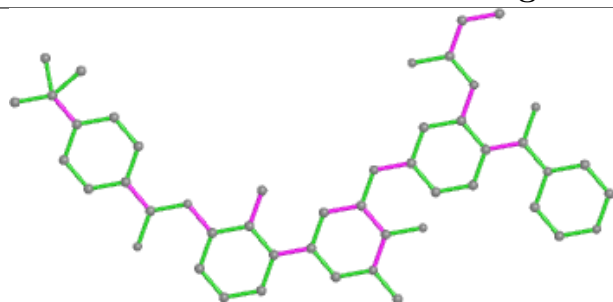
There are no ring outliers.

4 monomers are involved in 11 short contacts:

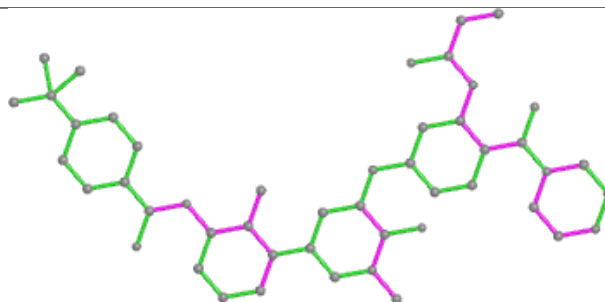
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	701	N42	2	0
2	A	701	N42	3	0
2	C	701	N42	5	0
2	B	701	N42	1	0

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.

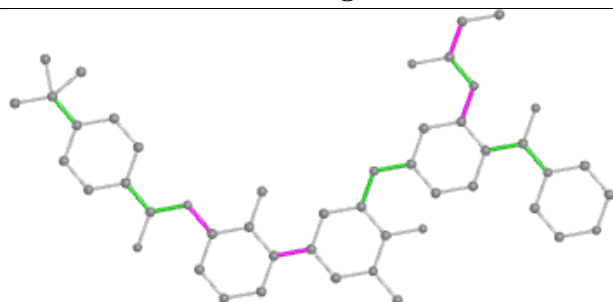
## Ligand N42 D 701



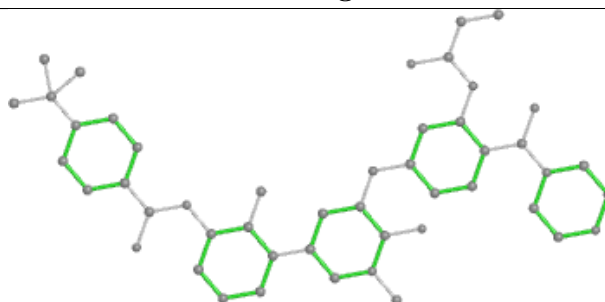
Bond lengths



Bond angles

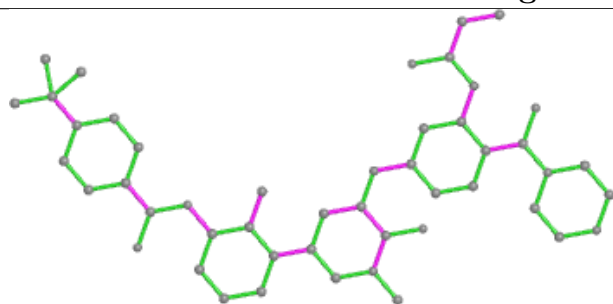


Torsions

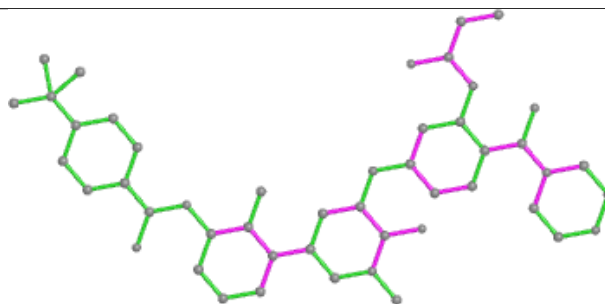


Rings

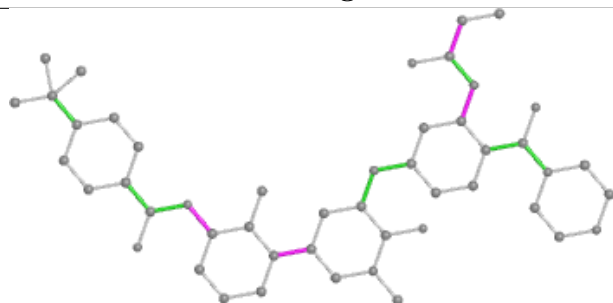
## Ligand N42 A 701



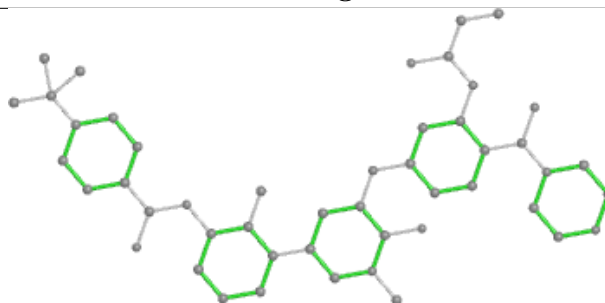
Bond lengths



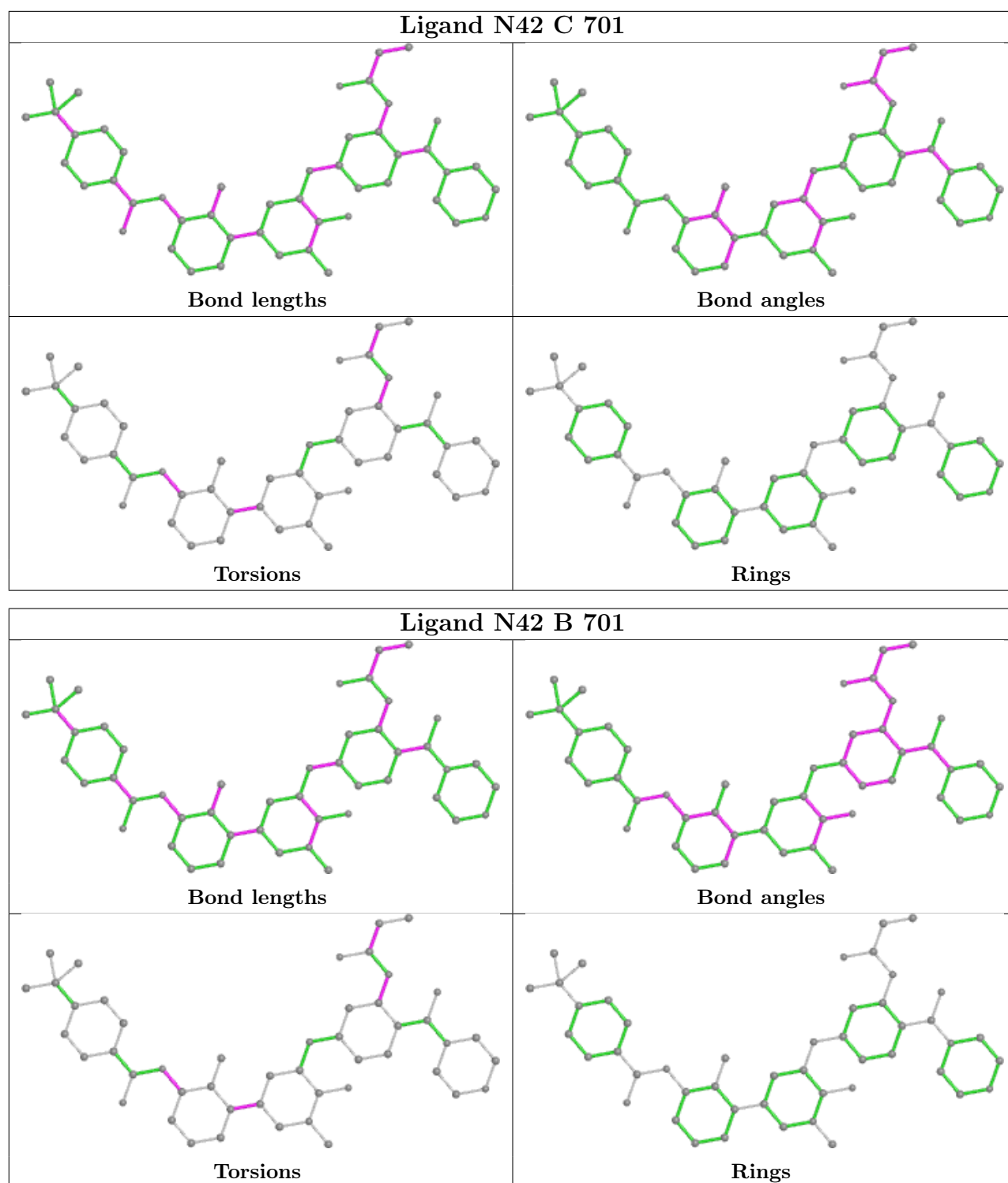
Bond angles



Torsions



Rings



## 5.7 Other polymers [i](#)

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	263/274 (95%)	-0.22	3 (1%) 80 80	4, 10, 19, 37	0
1	B	274/274 (100%)	-0.25	1 (0%) 92 92	4, 9, 18, 40	0
1	C	261/274 (95%)	0.48	12 (4%) 32 29	13, 19, 29, 36	0
1	D	263/274 (95%)	0.37	8 (3%) 50 48	11, 19, 27, 33	0
All	All	1061/1096 (96%)	0.09	24 (2%) 60 59	4, 15, 27, 40	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	443	ILE	5.5
1	B	489	MET	5.0
1	D	489	MET	3.8
1	C	421	TRP	3.7
1	D	425	TYR	3.3
1	C	493	PHE	3.3
1	C	460	LEU	3.2
1	C	464	CYS	3.0
1	C	410	THR	3.0
1	C	425	TYR	2.7
1	C	469	PRO	2.6
1	D	463	VAL	2.6
1	C	470	ILE	2.5
1	D	452	LEU	2.4
1	C	399	PRO	2.4
1	D	591	TYR	2.4
1	C	634	TRP	2.4
1	C	397	ILE	2.4
1	A	489	MET	2.3
1	C	409	GLY	2.3
1	A	491	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	557	SER	2.1
1	A	490	ARG	2.1
1	D	491	HIS	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](#)

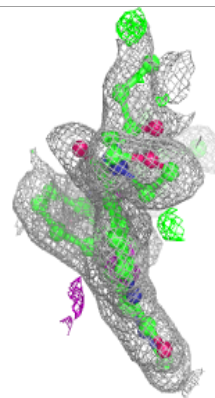
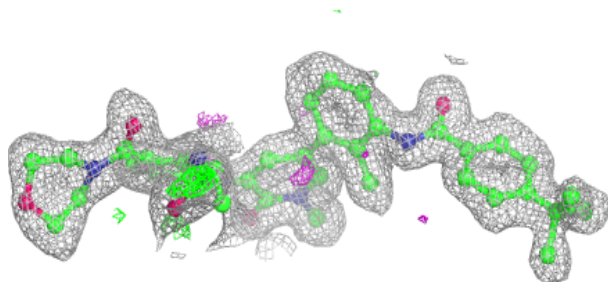
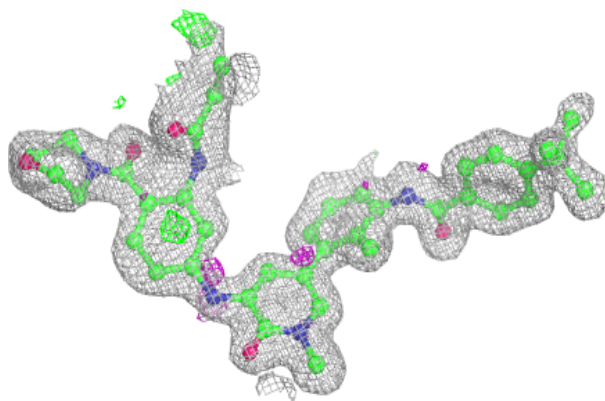
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	N42	C	701	48/48	0.88	0.11	13,18,28,33	0
2	N42	D	701	48/48	0.90	0.11	10,18,34,37	0
2	N42	A	701	48/48	0.95	0.08	6,9,17,21	0
2	N42	B	701	48/48	0.95	0.08	5,9,13,20	0

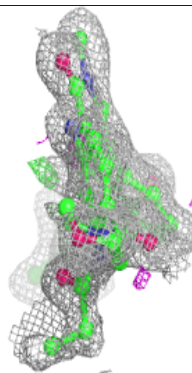
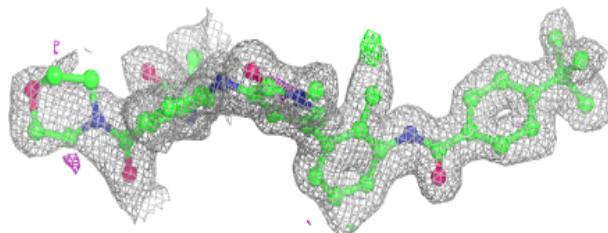
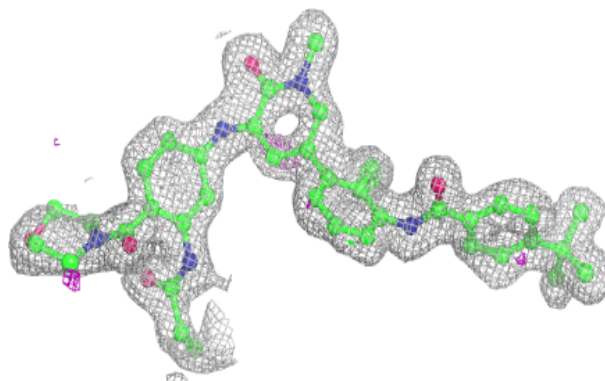
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around N42 C 701:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

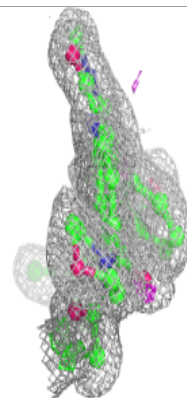
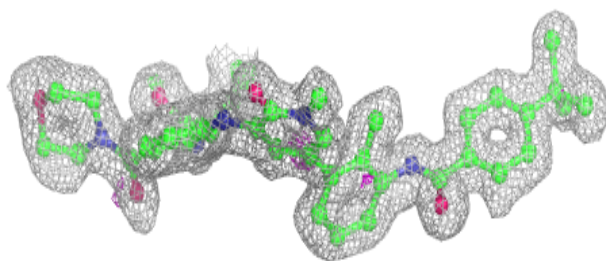
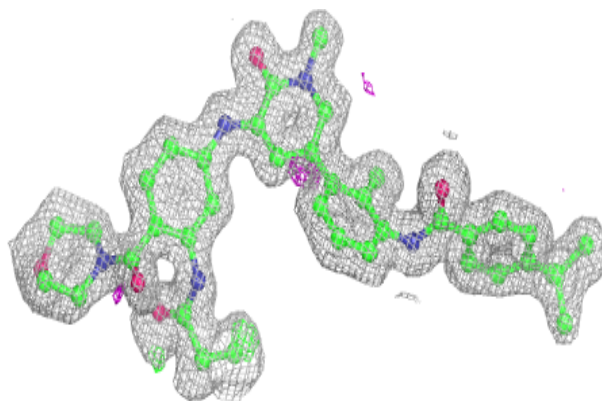
**Electron density around N42 D 701:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

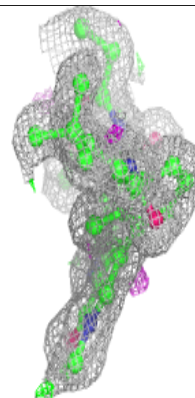
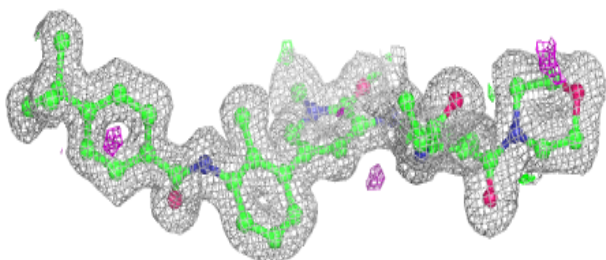
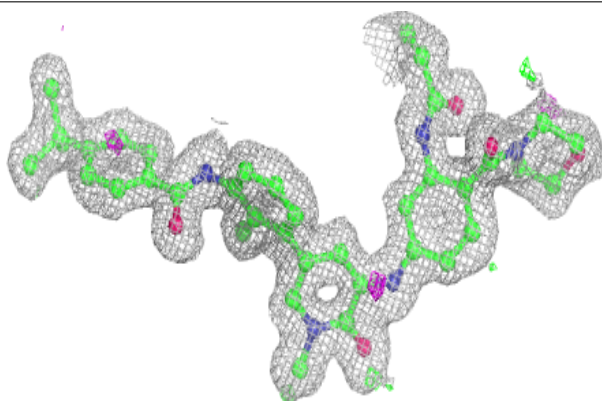


**Electron density around N42 A 701:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around N42 B 701:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.