



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 07:08 pm BST

PDB ID : 6AIT
Title : Crystal structure of E. coli BepA
Authors : Umar, M.S.M.; Tanaka, Y.; Kamikubo, H.; Tsukazaki, T.
Deposited on : 2018-08-24
Resolution : 2.60 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 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 : 2.11
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) : 2.11

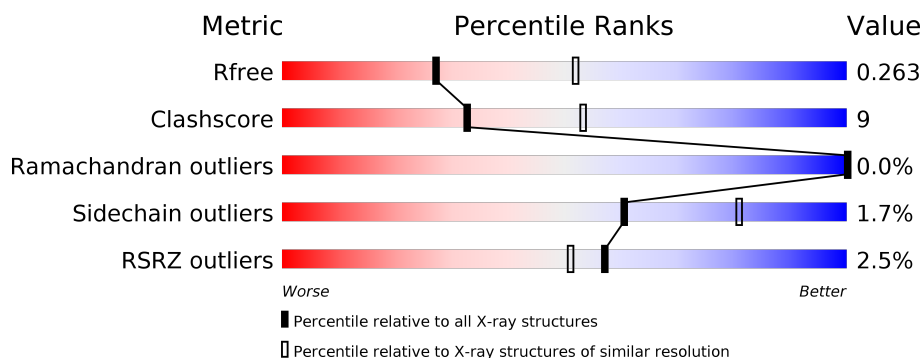
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 on 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	439	<div> <div>0%</div> <div> <div></div> <div>82%</div> <div>12%</div> <div>• 5%</div> </div> </div>
1	B	439	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>18%</div> <div>• 5%</div> </div> </div>
1	C	439	<div> <div>3%</div> <div> <div></div> <div>78%</div> <div>16%</div> <div>5%</div> </div> </div>
1	D	439	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>18%</div> <div>• 5%</div> </div> </div>
1	E	439	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>17%</div> <div>7%</div> </div> </div>
1	F	439	<div> <div>4%</div> <div> <div></div> <div>68%</div> <div>24%</div> <div>• 8%</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 19732 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Beta-barrel assembly-enhancing protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	418	Total	C	N	O	S	0	0	0
			3297	2046	608	631	12			
1	B	418	Total	C	N	O	S	0	0	0
			3288	2041	606	629	12			
1	C	415	Total	C	N	O	S	0	0	0
			3272	2032	603	625	12			
1	D	416	Total	C	N	O	S	0	0	0
			3279	2035	604	628	12			
1	E	410	Total	C	N	O	S	0	0	0
			3235	2009	596	619	11			
1	F	406	Total	C	N	O	S	0	0	0
			3197	1982	588	615	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	44	GLY	-	see sequence details	UNP P66948
B	44	GLY	-	see sequence details	UNP P66948
C	44	GLY	-	see sequence details	UNP P66948
D	44	GLY	-	see sequence details	UNP P66948
E	44	GLY	-	see sequence details	UNP P66948
F	44	GLY	-	see sequence details	UNP P66948

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	B	1	Total	C	N	O	0	0
			8	4	1	3		
3	C	1	Total	C	N	O	0	0
			8	4	1	3		
3	D	1	Total	C	N	O	0	0
			8	4	1	3		
3	E	1	Total	C	N	O	0	0
			8	4	1	3		
3	F	1	Total	C	N	O	0	0
			8	4	1	3		

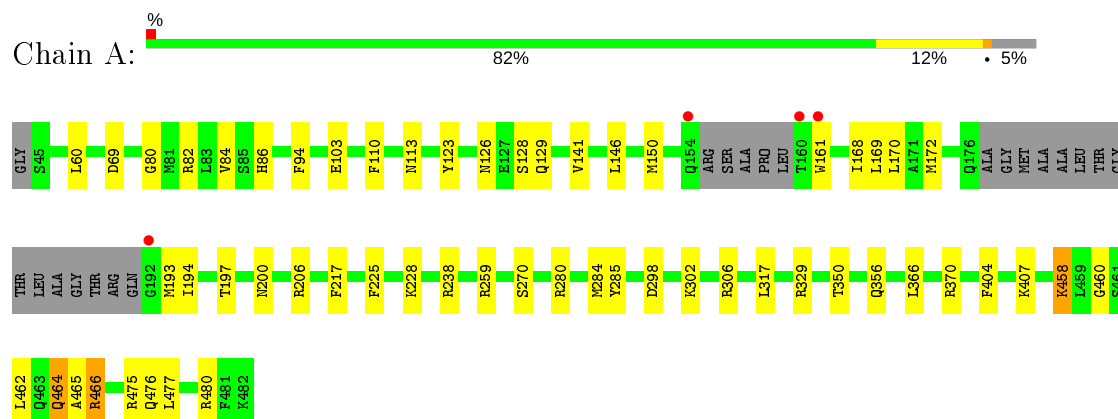
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	35	Total 35	O 35	0	0
4	B	15	Total 15	O 15	0	0
4	C	14	Total 14	O 14	0	0
4	D	17	Total 17	O 17	0	0
4	E	16	Total 16	O 16	0	0
4	F	13	Total 13	O 13	0	0

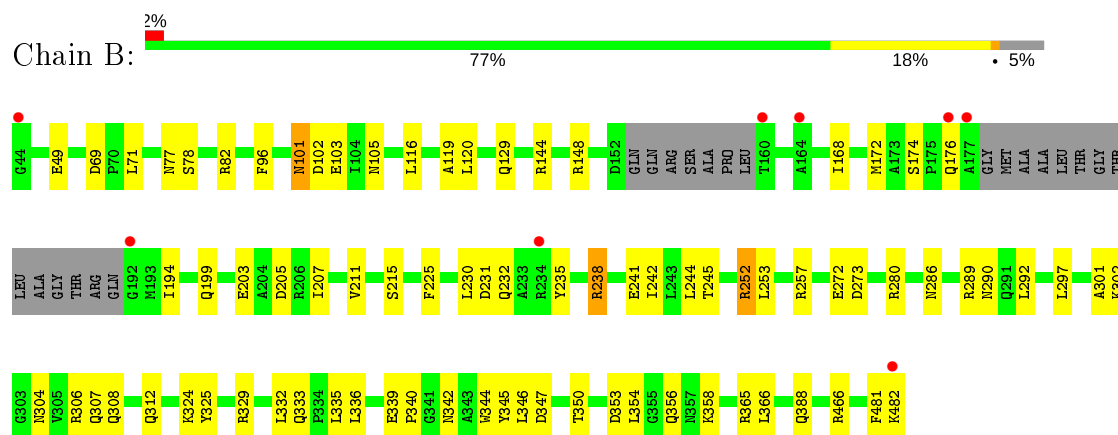
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

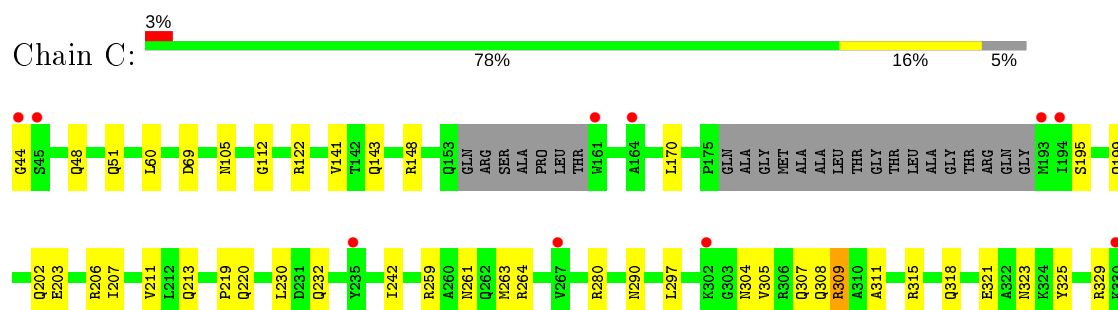
- Molecule 1: Beta-barrel assembly-enhancing protease



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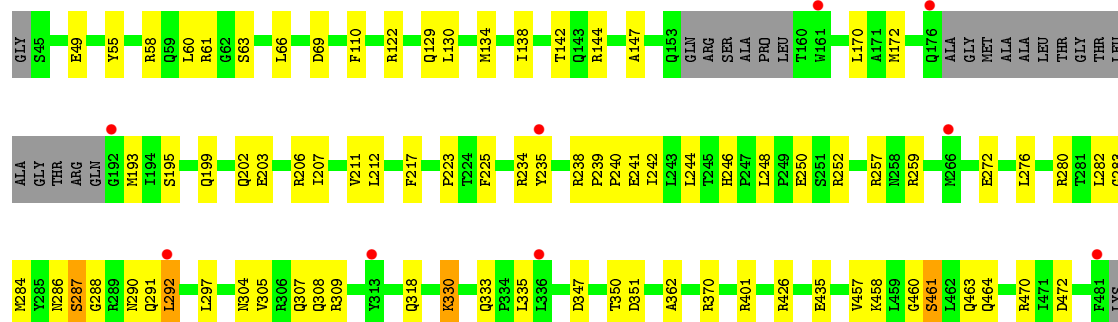
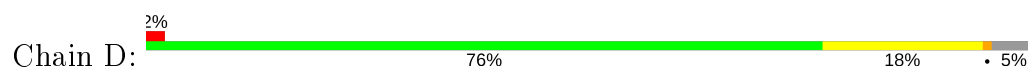


- Molecule 1: Beta-barrel assembly-enhancing protease

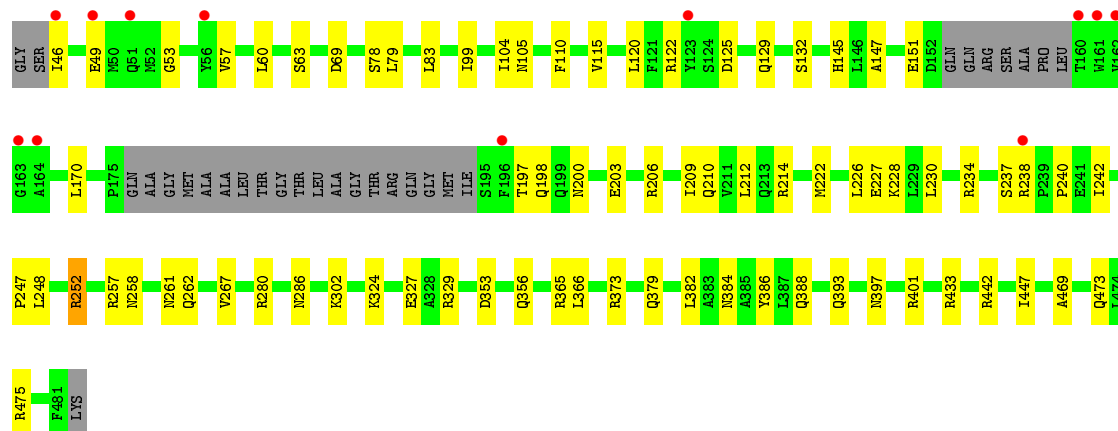
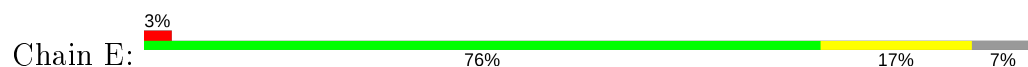




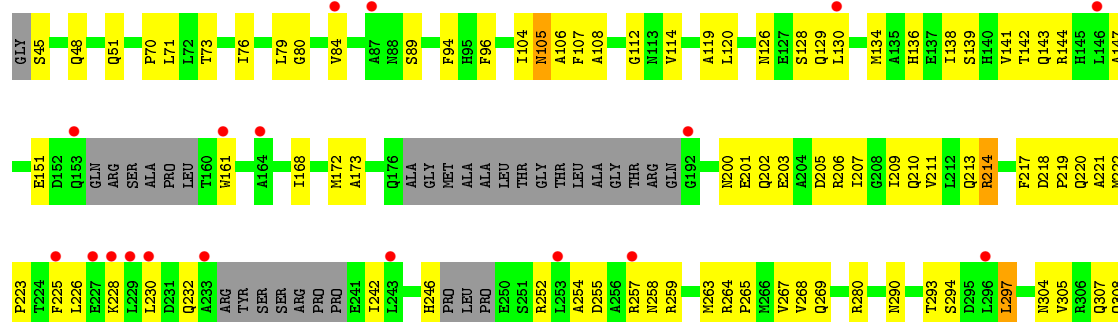
- Molecule 1: Beta-barrel assembly-enhancing protease



- Molecule 1: Beta-barrel assembly-enhancing protease



- Molecule 1: Beta-barrel assembly-enhancing protease





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	85.84Å 104.67Å 104.97Å 113.61° 105.84° 104.03°	Depositor
Resolution (Å)	48.59 – 2.60 48.59 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.2 (48.59-2.60) 98.2 (48.59-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.206 , 0.263 0.206 , 0.263	Depositor DCC
R_{free} test set	2016 reflections (2.25%)	wwPDB-VP
Wilson B-factor (Å ²)	62.5	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for h,l,-h-k-l 0.000 for h,-h-k-l,k 0.000 for -h,-l,-k 0.000 for -h,-k,h+k+l 0.000 for -h,h+k+l,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19732	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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: ZN, TRS

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	0.27	0/3351	0.42	0/4530
1	B	0.27	0/3342	0.43	0/4518
1	C	0.29	0/3326	0.44	0/4496
1	D	0.26	0/3333	0.44	1/4507 (0.0%)
1	E	0.28	0/3289	0.45	0/4449
1	F	0.28	0/3244	0.47	1/4380 (0.0%)
All	All	0.27	0/19885	0.44	2/26880 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	292	LEU	CA-CB-CG	5.73	128.48	115.30
1	F	297	LEU	CB-CG-CD1	5.40	120.18	111.00

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	3297	0	3234	37	0
1	B	3288	0	3226	51	0
1	C	3272	0	3211	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3279	0	3213	59	0
1	E	3235	0	3169	55	0
1	F	3197	0	3127	81	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	8	0	12	0	0
3	B	8	0	12	0	0
3	C	8	0	12	0	0
3	D	8	0	12	1	0
3	E	8	0	12	0	0
3	F	8	0	12	2	0
4	A	35	0	0	2	0
4	B	15	0	0	0	0
4	C	14	0	0	0	0
4	D	17	0	0	1	0
4	E	16	0	0	1	0
4	F	13	0	0	0	0
All	All	19732	0	19252	337	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 9.

All (337) 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:475:ARG:O	1:C:479:GLU:OE2	1.80	0.97
1:B:253:LEU:HD21	1:B:257:ARG:HD2	1.52	0.90
1:C:373:ARG:NE	1:C:373:ARG:O	2.06	0.89
1:D:283:GLY:HA2	1:D:292:LEU:HD22	1.57	0.87
1:D:282:LEU:HB3	1:D:292:LEU:HB3	1.59	0.84
1:E:324:LYS:HG3	1:E:327:GLU:HB3	1.61	0.82
1:F:202:GLN:HE21	1:F:206:ARG:HH12	1.28	0.81
1:F:297:LEU:HD12	1:F:315:ARG:HG2	1.62	0.80
1:C:373:ARG:HH11	1:C:401:ARG:NH2	1.80	0.79
1:E:209:ILE:HD11	1:E:222:MET:SD	2.22	0.78
1:B:253:LEU:CD2	1:B:257:ARG:HD2	2.13	0.78
1:F:51:GLN:HB3	1:F:480:ARG:HH22	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:297:LEU:HD11	1:C:311:ALA:O	1.84	0.76
1:E:329:ARG:NH2	1:E:356:GLN:OE1	2.18	0.76
1:F:205:ASP:OD2	1:F:252:ARG:NH1	2.20	0.74
1:F:108:ALA:HB2	1:F:114:VAL:HG23	1.70	0.72
1:B:272:GLU:HB3	1:B:306:ARG:HD3	1.71	0.71
1:A:197:THR:HG23	1:A:200:ASN:H	1.56	0.70
1:C:202:GLN:HE21	1:C:206:ARG:HH12	1.39	0.70
1:F:223:PRO:HB3	1:F:257:ARG:HG2	1.73	0.70
1:E:49:GLU:HB2	1:E:110:PHE:HB3	1.72	0.70
1:F:294:SER:HA	1:F:297:LEU:CD2	2.22	0.69
1:A:169:LEU:HA	1:A:172:MET:HE2	1.75	0.69
1:F:294:SER:HA	1:F:297:LEU:HD21	1.75	0.69
1:D:304:ASN:H	1:D:307:GLN:HE21	1.40	0.69
1:F:347:ASP:OD1	3:F:502:TRS:O3	2.10	0.69
1:B:103:GLU:HG2	1:B:289:ARG:HH22	1.57	0.68
1:C:206:ARG:HE	1:C:259:ARG:CZ	2.05	0.68
1:C:332:LEU:HD13	1:C:336:LEU:HB2	1.74	0.68
1:C:259:ARG:HB2	1:C:259:ARG:NH2	2.09	0.67
1:D:457:VAL:O	1:E:433:ARG:NH2	2.25	0.66
1:C:297:LEU:HD22	1:C:315:ARG:CZ	2.25	0.66
1:E:210:GLN:O	1:E:214:ARG:HG3	1.95	0.65
1:B:332:LEU:HD21	1:B:345:TYR:HB3	1.78	0.64
1:C:213:GLN:HB2	1:C:219:PRO:HG3	1.79	0.64
1:E:99:ILE:CD1	1:E:115:VAL:HG13	2.28	0.64
1:F:51:GLN:CB	1:F:480:ARG:HH22	2.09	0.64
1:D:234:ARG:NH1	1:D:250:GLU:OE2	2.32	0.62
1:E:198:GLN:NE2	1:E:247:PRO:O	2.31	0.62
1:F:119:ALA:HA	1:F:290:ASN:HD21	1.63	0.62
1:C:325:TYR:HD2	1:C:356:GLN:HG3	1.64	0.62
1:E:99:ILE:HD11	1:E:115:VAL:HG13	1.81	0.62
1:F:144:ARG:HG2	1:F:147:ALA:HB3	1.81	0.62
1:B:49:GLU:OE2	1:B:144:ARG:NH2	2.33	0.61
1:D:238:ARG:HE	1:D:239:PRO:HD2	1.63	0.61
1:B:353:ASP:OD2	1:B:365:ARG:NH2	2.34	0.61
1:D:49:GLU:HB2	1:D:110:PHE:HB3	1.82	0.61
1:F:218:ASP:HB3	1:F:221:ALA:HB2	1.83	0.60
1:F:201:GLU:OE1	1:F:246:HIS:ND1	2.27	0.60
1:A:329:ARG:NH2	1:A:356:GLN:OE1	2.34	0.60
1:C:263:MET:HG3	1:C:264:ARG:H	1.66	0.60
1:F:297:LEU:HD12	1:F:315:ARG:CG	2.31	0.60
1:F:89:SER:O	1:F:89:SER:OG	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:267:VAL:O	1:E:267:VAL:HG13	2.02	0.59
1:F:134:MET:O	1:F:138:ILE:HG22	2.03	0.59
1:B:238:ARG:HD2	1:B:238:ARG:H	1.68	0.59
1:C:202:GLN:NE2	1:C:206:ARG:HH12	2.01	0.59
1:D:286:ASN:OD1	1:D:291:GLN:NE2	2.35	0.59
1:A:69:ASP:OD1	1:A:280:ARG:NH1	2.36	0.58
1:A:103:GLU:OE2	1:A:238:ARG:NH2	2.37	0.58
1:F:267:VAL:HG12	1:F:269:GLN:OE1	2.03	0.58
1:D:199:GLN:O	1:D:203:GLU:HG3	2.03	0.58
1:A:404:PHE:HA	1:A:407:LYS:HE3	1.86	0.58
1:C:472:ASP:O	1:C:476:GLN:HG2	2.03	0.58
1:B:77:ASN:HD21	1:B:96:PHE:H	1.50	0.58
1:C:105:ASN:HA	1:C:242:ILE:HB	1.86	0.57
1:D:304:ASN:O	1:D:308:GLN:HG3	2.04	0.57
1:B:253:LEU:O	1:B:257:ARG:HG3	2.05	0.57
1:F:304:ASN:H	1:F:307:GLN:HE21	1.52	0.57
1:F:213:GLN:HG3	1:F:214:ARG:HD3	1.87	0.56
1:D:238:ARG:HA	1:D:238:ARG:NE	2.20	0.56
1:D:238:ARG:HE	1:D:238:ARG:HA	1.69	0.56
1:C:259:ARG:CZ	1:C:259:ARG:HB2	2.36	0.56
1:D:280:ARG:NH2	1:D:347:ASP:OD1	2.38	0.56
1:F:457:VAL:HG21	1:F:463:GLN:HB2	1.88	0.56
1:B:280:ARG:NH2	1:B:347:ASP:OD1	2.39	0.56
1:D:248:LEU:HD12	1:D:252:ARG:HG2	1.89	0.55
1:C:206:ARG:HH21	1:C:259:ARG:HH12	1.52	0.55
1:D:60:LEU:HD23	1:D:170:LEU:HD12	1.89	0.55
1:C:329:ARG:HH22	1:C:358:LYS:HE3	1.72	0.55
1:F:104:ILE:HD11	1:F:225:PHE:HZ	1.71	0.55
1:C:323:ASN:HB3	1:F:305:VAL:HG21	1.89	0.54
1:D:350:THR:HG23	1:D:362:ALA:HB1	1.89	0.54
1:D:460:GLY:N	1:D:464:GLN:OE1	2.37	0.54
1:F:96:PHE:CD2	1:F:114:VAL:HG11	2.42	0.54
1:E:104:ILE:HD11	1:E:120:LEU:HD23	1.90	0.54
1:E:104:ILE:HG23	1:E:242:ILE:HG22	1.88	0.54
1:F:144:ARG:NH1	1:F:151:GLU:OE1	2.35	0.54
1:F:84:VAL:HG22	1:F:138:ILE:HD12	1.89	0.54
1:F:254:ALA:O	1:F:258:ASN:HB2	2.07	0.54
1:D:282:LEU:HB3	1:D:292:LEU:CB	2.36	0.53
1:F:80:GLY:O	1:F:84:VAL:HG23	2.09	0.53
1:D:297:LEU:HD11	1:D:318:GLN:HE22	1.73	0.53
1:F:94:PHE:CZ	1:F:138:ILE:HG13	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:305:VAL:O	1:D:309:ARG:HG3	2.09	0.53
1:E:145:HIS:CD2	1:E:200:ASN:HB3	2.43	0.53
1:A:146:LEU:O	1:A:146:LEU:HD13	2.09	0.52
1:B:329:ARG:HH22	1:B:358:LYS:HD2	1.74	0.52
1:F:264:ARG:NH2	1:F:265:PRO:O	2.42	0.52
1:A:458:LYS:HE2	1:A:458:LYS:H	1.75	0.52
1:B:230:LEU:HD12	1:B:253:LEU:HD13	1.92	0.52
1:B:101:ASN:HD22	1:B:102:ASP:N	2.07	0.52
1:C:371:ASP:HB3	1:C:374:THR:OG1	2.09	0.52
1:E:53:GLY:O	1:E:57:VAL:HG13	2.09	0.52
1:C:352:ILE:HD12	1:C:353:ASP:N	2.24	0.52
1:D:122:ARG:NH1	1:D:290:ASN:OD1	2.43	0.52
1:E:69:ASP:OD1	1:E:280:ARG:NH1	2.42	0.52
1:F:107:PHE:HZ	1:F:173:ALA:HB2	1.74	0.52
1:F:209:ILE:HD11	1:F:219:PRO:HA	1.91	0.52
1:B:312:GLN:HB2	1:B:335:LEU:HD11	1.91	0.52
1:D:69:ASP:OD1	1:D:280:ARG:NH1	2.43	0.52
1:B:329:ARG:NH1	1:B:353:ASP:OD1	2.44	0.51
1:F:304:ASN:H	1:F:307:GLN:NE2	2.08	0.51
1:F:139:SER:HA	1:F:142:THR:HG22	1.92	0.51
1:E:104:ILE:CD1	1:E:120:LEU:HA	2.40	0.51
1:F:219:PRO:HB3	1:F:263:MET:SD	2.50	0.51
1:C:44:GLY:O	1:C:48:GLN:HG3	2.10	0.51
1:F:293:THR:O	1:F:297:LEU:HD22	2.10	0.51
1:E:379:GLN:HE22	1:E:401:ARG:HH21	1.57	0.51
1:E:197:THR:HG22	1:E:200:ASN:HD21	1.74	0.51
1:F:407:LYS:HE2	1:F:407:LYS:H	1.75	0.51
1:B:231:ASP:O	1:B:235:TYR:HB2	2.10	0.51
1:C:335:LEU:HG	1:C:345:TYR:CZ	2.46	0.51
1:A:475:ARG:NH1	4:A:601:HOH:O	2.44	0.50
1:E:393:GLN:HE21	1:E:397:ASN:HD21	1.57	0.50
1:F:375:ASN:O	1:F:379:GLN:HG3	2.11	0.50
1:C:220:GLN:HE22	1:C:261:ASN:HD22	1.57	0.50
1:F:120:LEU:HD21	1:F:130:LEU:HG	1.93	0.50
1:F:210:GLN:HA	1:F:213:GLN:HG2	1.94	0.50
1:D:234:ARG:HD2	1:D:235:TYR:HE1	1.77	0.50
1:F:304:ASN:O	1:F:308:GLN:HG3	2.11	0.50
1:C:373:ARG:CD	1:C:401:ARG:HH22	2.25	0.50
1:D:304:ASN:H	1:D:307:GLN:NE2	2.09	0.50
1:B:253:LEU:HD21	1:B:257:ARG:HH11	1.77	0.50
1:A:146:LEU:C	1:A:146:LEU:HD13	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:ARG:O	1:A:86:HIS:HD2	1.95	0.49
1:C:280:ARG:NH2	1:C:347:ASP:OD1	2.45	0.49
1:D:207:ILE:O	1:D:211:VAL:HG23	2.12	0.49
1:D:144:ARG:HB3	1:D:147:ALA:HB3	1.94	0.49
1:D:202:GLN:O	1:D:206:ARG:HG3	2.12	0.49
1:F:255:ASP:HA	1:F:258:ASN:HB3	1.93	0.49
1:A:168:ILE:HG21	1:A:194:ILE:HG23	1.94	0.49
1:B:205:ASP:OD2	1:B:252:ARG:NH1	2.46	0.49
1:F:242:ILE:HG13	1:F:246:HIS:HD2	1.78	0.49
1:A:168:ILE:HG23	1:A:193:MET:HA	1.94	0.49
1:C:380:LEU:HD22	1:C:415:LEU:HD12	1.94	0.49
1:E:79:LEU:O	1:E:83:LEU:HD12	2.13	0.49
1:F:112:GLY:HA2	1:F:141:VAL:HG11	1.94	0.49
1:C:308:GLN:O	1:C:311:ALA:HB3	2.12	0.49
1:D:241:GLU:HA	1:D:244:LEU:HD13	1.93	0.49
1:D:351:ASP:OD1	3:D:502:TRS:O2	2.27	0.49
1:C:202:GLN:HE21	1:C:206:ARG:NH1	2.09	0.49
1:C:332:LEU:CD1	1:C:336:LEU:HB2	2.42	0.49
1:A:60:LEU:HD23	1:A:170:LEU:HD23	1.94	0.49
1:C:220:GLN:NE2	1:C:261:ASN:HD22	2.10	0.49
1:A:460:GLY:H	1:A:464:GLN:NE2	2.11	0.49
1:B:199:GLN:O	1:B:203:GLU:HG3	2.13	0.48
1:B:129:GLN:HG2	1:B:225:PHE:HB2	1.93	0.48
1:B:346:LEU:O	1:B:350:THR:HG23	2.13	0.48
1:E:373:ARG:NH1	1:E:379:GLN:OE1	2.45	0.48
1:D:472:ASP:OD1	1:E:442:ARG:NH2	2.46	0.48
1:C:304:ASN:HB3	1:C:307:GLN:OE1	2.13	0.48
1:F:51:GLN:HB3	1:F:480:ARG:NH2	2.24	0.48
1:B:273:ASP:OD1	1:B:344:TRP:NE1	2.46	0.48
1:C:402:TYR:OH	1:C:409:ASP:OD2	2.25	0.48
1:D:61:ARG:HA	1:D:66:LEU:HD13	1.94	0.48
1:E:203:GLU:HA	1:E:206:ARG:HB2	1.95	0.48
1:B:119:ALA:HA	1:B:290:ASN:HD21	1.76	0.48
1:C:207:ILE:O	1:C:211:VAL:HG13	2.14	0.48
1:E:105:ASN:HA	1:E:242:ILE:HB	1.95	0.48
1:B:105:ASN:HA	1:B:242:ILE:HB	1.95	0.48
1:C:452:SER:O	1:C:456:GLN:HG3	2.13	0.48
1:D:370:ARG:HG2	1:D:370:ARG:HH11	1.79	0.48
1:E:286:ASN:N	1:E:286:ASN:OD1	2.45	0.48
1:A:69:ASP:HB2	1:A:285:TYR:OH	2.13	0.48
1:A:80:GLY:O	1:A:84:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:THR:HG21	1:B:366:LEU:HD11	1.95	0.48
1:D:242:ILE:HD12	1:D:246:HIS:HD2	1.78	0.48
1:A:129:GLN:HG2	1:A:225:PHE:HB2	1.96	0.47
1:B:174:SER:HB3	1:B:176:GLN:HG2	1.95	0.47
1:E:46:ILE:HA	1:E:49:GLU:HG3	1.96	0.47
1:D:61:ARG:HG2	1:D:66:LEU:HD22	1.96	0.47
1:E:104:ILE:CG2	1:E:240:PRO:HB3	2.45	0.47
1:E:147:ALA:O	1:E:151:GLU:HG3	2.15	0.47
1:F:380:LEU:HD22	1:F:415:LEU:HD12	1.97	0.47
1:B:101:ASN:ND2	1:B:103:GLU:H	2.12	0.47
1:C:309:ARG:HB2	1:C:335:LEU:HD21	1.96	0.47
1:B:336:LEU:HD12	1:B:340:PRO:HA	1.96	0.47
1:C:373:ARG:HD3	1:C:401:ARG:HH22	1.80	0.47
1:E:384:ASN:O	1:E:388:GLN:HG2	2.15	0.47
1:E:248:LEU:HD13	1:E:252:ARG:HD3	1.96	0.47
1:D:458:LYS:O	1:D:461:SER:HB3	2.14	0.47
1:C:335:LEU:HG	1:C:345:TYR:CE2	2.50	0.46
1:C:60:LEU:HD23	1:C:170:LEU:HD23	1.98	0.46
1:E:258:ASN:O	1:E:262:GLN:HG3	2.15	0.46
1:E:209:ILE:HA	1:E:212:LEU:HB3	1.95	0.46
1:E:379:GLN:NE2	4:E:601:HOH:O	2.33	0.46
1:F:79:LEU:HD11	1:F:217:PHE:HE2	1.81	0.46
1:E:353:ASP:OD2	1:E:365:ARG:NH2	2.48	0.46
1:F:120:LEU:HD23	1:F:130:LEU:HD12	1.98	0.46
1:B:102:ASP:O	1:B:289:ARG:NH1	2.49	0.46
1:F:105:ASN:HD22	1:F:106:ALA:H	1.63	0.46
1:B:325:TYR:CB	1:B:356:GLN:HE21	2.29	0.46
1:B:301:ALA:O	1:B:308:GLN:NE2	2.49	0.45
1:C:403:THR:HB	1:C:413:TRP:CH2	2.51	0.45
1:F:128:SER:HB3	1:F:217:PHE:HB3	1.99	0.45
1:A:94:PHE:CE2	1:A:141:VAL:HG11	2.51	0.45
1:D:330:LYS:O	1:D:333:GLN:HB3	2.16	0.45
1:F:129:GLN:HG3	1:F:221:ALA:HB1	1.98	0.45
1:F:70:PRO:HB2	1:F:377:VAL:HG13	1.98	0.45
1:A:270:SER:O	1:A:306:ARG:NH1	2.46	0.45
1:B:339:GLU:HB2	1:B:342:ASN:ND2	2.32	0.45
1:D:223:PRO:HB2	1:D:257:ARG:HD2	1.98	0.45
1:E:63:SER:OG	1:E:170:LEU:HD11	2.16	0.45
1:F:200:ASN:O	1:F:203:GLU:HB2	2.17	0.45
1:F:71:LEU:HG	1:F:377:VAL:HG11	1.97	0.45
1:C:112:GLY:HA2	1:C:141:VAL:HG11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:96:PHE:HA	1:F:114:VAL:HG12	1.98	0.45
1:F:213:GLN:HG3	1:F:214:ARG:N	2.30	0.45
1:A:150:MET:HB3	1:A:161:TRP:CZ2	2.52	0.45
1:A:477:LEU:HD12	1:A:480:ARG:HH11	1.81	0.45
1:B:194:ILE:O	1:B:245:THR:HG22	2.16	0.45
1:A:284:MET:HE3	1:A:317:LEU:HD11	1.99	0.45
1:F:370:ARG:HG2	1:F:371:ASP:OD1	2.15	0.45
1:D:470:ARG:HD2	1:D:470:ARG:HA	1.81	0.45
1:E:197:THR:HG22	1:E:200:ASN:ND2	2.32	0.45
1:E:258:ASN:O	1:E:261:ASN:HB2	2.17	0.45
1:E:447:ILE:HG21	1:E:475:ARG:NH2	2.32	0.45
1:F:201:GLU:CD	1:F:246:HIS:HD1	2.14	0.45
1:C:206:ARG:HH21	1:C:259:ARG:NH1	2.15	0.44
1:C:263:MET:HG3	1:C:264:ARG:N	2.32	0.44
1:D:172:MET:HG2	1:D:193:MET:HG3	1.99	0.44
1:C:297:LEU:HD22	1:C:315:ARG:NE	2.33	0.44
1:D:457:VAL:HG23	1:D:464:GLN:HB2	1.98	0.44
1:F:280:ARG:NH2	1:F:347:ASP:OD2	2.51	0.44
1:A:458:LYS:CE	1:A:458:LYS:H	2.30	0.44
1:F:207:ILE:O	1:F:211:VAL:HG23	2.18	0.44
1:D:129:GLN:HG2	1:D:225:PHE:HB2	1.99	0.44
1:F:218:ASP:HB2	1:F:268:VAL:HG21	1.98	0.44
1:E:227:GLU:OE2	1:E:257:ARG:NH1	2.51	0.44
1:B:481:PHE:O	1:B:482:LYS:HG2	2.17	0.44
1:E:104:ILE:HD11	1:E:120:LEU:HA	2.00	0.44
1:C:199:GLN:O	1:C:203:GLU:HG3	2.18	0.43
1:D:234:ARG:HD2	1:D:235:TYR:CE1	2.53	0.43
1:D:240:PRO:HB2	1:D:242:ILE:HG22	2.00	0.43
1:D:401:ARG:NH1	4:D:603:HOH:O	2.51	0.43
1:F:255:ASP:HA	1:F:258:ASN:CB	2.48	0.43
1:F:329:ARG:HH21	1:F:356:GLN:NE2	2.16	0.43
1:D:138:ILE:O	1:D:142:THR:HG23	2.18	0.43
1:E:248:LEU:HD12	1:E:252:ARG:HB3	1.99	0.43
1:F:136:HIS:CE1	1:F:201:GLU:HG2	2.53	0.43
1:B:304:ASN:OD1	1:B:307:GLN:HG3	2.18	0.43
1:F:222:MET:O	1:F:226:LEU:HD12	2.18	0.43
1:B:354:LEU:HD13	1:B:388:GLN:HG3	2.00	0.43
1:F:228:LYS:O	1:F:232:GLN:NE2	2.50	0.43
1:C:373:ARG:HH11	1:C:401:ARG:HH22	1.62	0.43
1:F:45:SER:N	1:F:48:GLN:HE21	2.17	0.43
1:B:69:ASP:OD1	1:B:280:ARG:NH1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:206:ARG:HG2	1:C:259:ARG:NH2	2.33	0.43
1:E:366:LEU:HB2	1:E:382:LEU:HD12	2.00	0.43
1:F:222:MET:HG3	1:F:226:LEU:HD11	1.99	0.43
1:C:348:LEU:O	1:C:352:ILE:HG13	2.19	0.43
1:C:69:ASP:OD1	1:C:280:ARG:NH1	2.52	0.43
1:D:286:ASN:O	1:D:287:SER:HB3	2.19	0.43
1:E:237:SER:OG	1:E:238:ARG:N	2.51	0.43
1:E:329:ARG:NH1	1:E:353:ASP:OD1	2.47	0.43
1:B:116:LEU:HB3	1:B:120:LEU:HD12	2.00	0.43
1:F:351:ASP:OD1	3:F:502:TRS:H31	2.19	0.43
1:A:460:GLY:H	1:A:464:GLN:HE21	1.67	0.42
1:C:304:ASN:OD1	1:C:305:VAL:HG22	2.19	0.42
1:F:210:GLN:O	1:F:213:GLN:HG2	2.18	0.42
1:F:230:LEU:HD23	1:F:230:LEU:HA	1.82	0.42
1:C:122:ARG:HH11	1:C:290:ASN:ND2	2.17	0.42
1:C:335:LEU:HA	1:C:335:LEU:HD12	1.82	0.42
1:D:206:ARG:HD3	1:D:259:ARG:CZ	2.49	0.42
1:F:142:THR:HG23	1:F:143:GLN:HG2	2.01	0.42
1:F:73:THR:O	1:F:76:ILE:HG22	2.19	0.42
1:D:330:LYS:HD2	1:D:330:LYS:C	2.39	0.42
1:E:60:LEU:HD23	1:E:60:LEU:HA	1.89	0.42
1:A:462:LEU:HA	1:A:466:ARG:HH11	1.83	0.42
1:F:408:ASP:HA	1:F:439:LEU:HD21	2.02	0.42
1:D:212:LEU:CD1	1:D:217:PHE:HB2	2.50	0.42
1:A:150:MET:HB3	1:A:161:TRP:HZ2	1.85	0.42
1:B:82:ARG:NH2	1:B:215:SER:O	2.40	0.42
1:B:241:GLU:HA	1:B:244:LEU:HD13	2.02	0.42
1:D:288:GLY:O	1:D:291:GLN:HG2	2.20	0.42
1:A:126:ASN:HD21	1:A:128:SER:HB2	1.84	0.41
1:D:130:LEU:HG	1:D:134:MET:HE3	2.02	0.41
1:F:371:ASP:HB3	1:F:374:THR:HG22	2.01	0.41
1:A:110:PHE:O	1:A:113:ASN:ND2	2.51	0.41
1:A:123:TYR:O	1:A:228:LYS:NZ	2.37	0.41
1:B:286:ASN:OD1	1:B:286:ASN:N	2.52	0.41
1:B:71:LEU:HD13	1:B:344:TRP:CE3	2.55	0.41
1:E:469:ALA:O	1:E:473:GLN:HG3	2.20	0.41
1:F:290:ASN:HD22	1:F:290:ASN:HA	1.62	0.41
1:A:128:SER:HB3	1:A:217:PHE:HB3	2.02	0.41
1:B:168:ILE:O	1:B:172:MET:HG3	2.21	0.41
1:E:257:ARG:O	1:E:261:ASN:ND2	2.53	0.41
1:E:397:ASN:ND2	1:F:322:ALA:HA	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:128:SER:HB3	1:F:218:ASP:H	1.85	0.41
1:F:168:ILE:O	1:F:172:MET:HG3	2.20	0.41
1:D:272:GLU:O	1:D:276:LEU:HD12	2.19	0.41
1:D:297:LEU:HD11	1:D:318:GLN:NE2	2.33	0.41
1:F:407:LYS:CE	1:F:407:LYS:H	2.33	0.41
1:B:324:LYS:HD2	1:B:324:LYS:HA	1.73	0.41
1:D:55:TYR:HA	1:D:58:ARG:NH1	2.36	0.41
1:E:226:LEU:HD22	1:E:248:LEU:HD22	2.01	0.41
1:E:302:LYS:HE3	1:E:302:LYS:HB2	1.70	0.41
1:A:206:ARG:HD3	1:A:259:ARG:NE	2.36	0.41
1:B:207:ILE:O	1:B:211:VAL:HG23	2.21	0.41
1:A:465:ALA:HB3	1:A:466:ARG:NH1	2.35	0.41
1:B:325:TYR:HB2	1:B:356:GLN:HE21	1.85	0.41
1:C:318:GLN:HA	1:C:321:GLU:HB2	2.01	0.41
1:C:51:GLN:HG2	1:C:481:PHE:HZ	1.86	0.41
1:E:393:GLN:HE21	1:E:397:ASN:ND2	2.19	0.41
1:A:350:THR:OG1	1:A:366:LEU:HD11	2.21	0.41
1:D:335:LEU:H	1:D:335:LEU:HD12	1.86	0.41
1:B:302:LYS:HG3	1:B:302:LYS:O	2.21	0.41
1:C:143:GLN:O	1:C:148:ARG:NH2	2.54	0.41
1:D:63:SER:OG	1:D:170:LEU:HD21	2.21	0.41
1:E:125:ASP:H	1:E:129:GLN:NE2	2.19	0.41
1:D:435:GLU:OE2	1:D:470:ARG:NH2	2.53	0.40
1:B:342:ASN:HD21	1:B:345:TYR:HD2	1.63	0.40
1:C:329:ARG:HH12	1:C:356:GLN:NE2	2.18	0.40
1:C:372:LEU:HD21	1:C:382:LEU:HD22	2.03	0.40
1:D:203:GLU:O	1:D:207:ILE:HG13	2.21	0.40
1:D:461:SER:OG	1:D:463:GLN:OE1	2.40	0.40
1:E:46:ILE:HA	1:E:49:GLU:CG	2.52	0.40
1:A:298:ASP:O	1:A:302:LYS:HG3	2.21	0.40
1:B:292:LEU:HD21	1:B:297:LEU:HD21	2.03	0.40
1:C:230:LEU:HA	1:C:230:LEU:HD12	1.86	0.40
1:E:63:SER:HB2	1:E:170:LEU:HD21	2.02	0.40
1:A:168:ILE:O	1:A:172:MET:HG3	2.22	0.40
1:A:476:GLN:NE2	4:A:605:HOH:O	2.54	0.40
1:B:232:GLN:HG3	1:B:232:GLN:O	2.22	0.40
1:E:230:LEU:HD23	1:E:230:LEU:HA	1.91	0.40
1:F:220:GLN:C	1:F:223:PRO:HD2	2.41	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	412/439 (94%)	403 (98%)	9 (2%)	0	100	100
1	B	412/439 (94%)	403 (98%)	9 (2%)	0	100	100
1	C	409/439 (93%)	402 (98%)	7 (2%)	0	100	100
1	D	410/439 (93%)	402 (98%)	7 (2%)	1 (0%)	47	71
1	E	404/439 (92%)	396 (98%)	8 (2%)	0	100	100
1	F	396/439 (90%)	385 (97%)	11 (3%)	0	100	100
All	All	2443/2634 (93%)	2391 (98%)	51 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	287	SER

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	344/356 (97%)	340 (99%)	4 (1%)	71	87
1	B	342/356 (96%)	335 (98%)	7 (2%)	55	78
1	C	341/356 (96%)	336 (98%)	5 (2%)	65	83
1	D	342/356 (96%)	337 (98%)	5 (2%)	65	83
1	E	337/356 (95%)	330 (98%)	7 (2%)	53	77
1	F	332/356 (93%)	326 (98%)	6 (2%)	59	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	2038/2136 (95%)	2004 (98%)	34 (2%)	60	81

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	370	ARG
1	A	458	LYS
1	A	464	GLN
1	A	466	ARG
1	B	78	SER
1	B	101	ASN
1	B	148	ARG
1	B	238	ARG
1	B	252	ARG
1	B	333	GLN
1	B	466	ARG
1	C	195	SER
1	C	232	GLN
1	C	309	ARG
1	C	345	TYR
1	C	361	GLU
1	D	195	SER
1	D	284	MET
1	D	330	LYS
1	D	426	ARG
1	D	461	SER
1	E	78	SER
1	E	122	ARG
1	E	132	SER
1	E	228	LYS
1	E	234	ARG
1	E	252	ARG
1	E	386	TYR
1	F	105	ASN
1	F	126	ASN
1	F	161	TRP
1	F	214	ARG
1	F	259	ARG
1	F	452	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	A	86	HIS
1	A	198	GLN
1	A	262	GLN
1	A	291	GLN
1	A	464	GLN
1	A	478	GLN
1	B	74	GLN
1	B	77	ASN
1	B	101	ASN
1	B	210	GLN
1	B	220	GLN
1	B	290	ASN
1	B	307	GLN
1	B	308	GLN
1	B	342	ASN
1	B	360	ASN
1	B	400	ASN
1	B	418	GLN
1	B	478	GLN
1	C	74	GLN
1	C	113	ASN
1	C	198	GLN
1	C	202	GLN
1	C	220	GLN
1	C	261	ASN
1	C	290	ASN
1	C	342	ASN
1	C	356	GLN
1	C	357	ASN
1	C	456	GLN
1	D	74	GLN
1	D	86	HIS
1	D	232	GLN
1	D	269	GLN
1	D	307	GLN
1	D	318	GLN
1	D	357	ASN
1	D	368	ASN
1	D	476	GLN
1	E	129	GLN
1	E	145	HIS
1	E	200	ASN

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Mol	Chain	Res	Type
1	E	262	GLN
1	E	397	ASN
1	F	59	GLN
1	F	86	HIS
1	F	105	ASN
1	F	113	ASN
1	F	140	HIS
1	F	202	GLN
1	F	290	ASN
1	F	307	GLN
1	F	356	GLN
1	F	379	GLN
1	F	428	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	TRS	F	502	-	7,7,7	0.33	0	9,9,9	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	TRS	D	502	-	7,7,7	0.32	0	9,9,9	0.46	0
3	TRS	B	502	-	7,7,7	0.33	0	9,9,9	0.37	0
3	TRS	C	502	-	7,7,7	0.34	0	9,9,9	0.43	0
3	TRS	E	502	-	7,7,7	0.30	0	9,9,9	0.23	0
3	TRS	A	502	-	7,7,7	0.30	0	9,9,9	0.33	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TRS	F	502	-	-	1/9/9/9	-
3	TRS	D	502	-	-	2/9/9/9	-
3	TRS	B	502	-	-	3/9/9/9	-
3	TRS	C	502	-	-	1/9/9/9	-
3	TRS	E	502	-	-	0/9/9/9	-
3	TRS	A	502	-	-	3/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	502	TRS	N-C-C1-O1
3	B	502	TRS	C1-C-C2-O2
3	B	502	TRS	C3-C-C2-O2
3	B	502	TRS	N-C-C2-O2
3	C	502	TRS	N-C-C1-O1
3	A	502	TRS	C1-C-C2-O2
3	A	502	TRS	N-C-C2-O2
3	A	502	TRS	C3-C-C2-O2
3	D	502	TRS	C2-C-C1-O1
3	F	502	TRS	C1-C-C2-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	502	TRS	2	0
3	D	502	TRS	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	418/439 (95%)	-0.14	4 (0%) 82 80	43, 63, 110, 175	0
1	B	418/439 (95%)	-0.05	8 (1%) 66 62	41, 76, 119, 165	0
1	C	415/439 (94%)	0.08	11 (2%) 54 48	39, 75, 129, 173	0
1	D	416/439 (94%)	-0.05	9 (2%) 62 56	40, 80, 122, 154	0
1	E	410/439 (93%)	0.04	12 (2%) 51 45	43, 74, 135, 190	0
1	F	406/439 (92%)	0.16	18 (4%) 34 27	43, 84, 147, 187	0
All	All	2483/2634 (94%)	0.01	62 (2%) 57 51	39, 75, 131, 190	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	192	GLY	7.7
1	E	164	ALA	7.5
1	E	160	THR	6.5
1	B	192	GLY	6.4
1	B	177	ALA	5.2
1	C	164	ALA	5.0
1	F	243	LEU	5.0
1	B	482	LYS	4.4
1	C	161	TRP	4.4
1	E	161	TRP	4.1
1	D	292	LEU	3.9
1	F	253	LEU	3.9
1	D	192	GLY	3.8
1	F	146	LEU	3.8
1	F	153	GLN	3.8
1	B	234	ARG	3.7
1	C	44	GLY	3.6
1	F	161	TRP	3.5
1	F	233	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	235	TYR	3.4
1	E	46	ILE	3.4
1	A	161	TRP	3.3
1	C	193	MET	3.3
1	A	160	THR	3.1
1	D	161	TRP	3.1
1	E	238	ARG	3.1
1	B	176	GLN	3.1
1	A	154	GLN	3.0
1	D	176	GLN	3.0
1	D	235	TYR	3.0
1	E	162	VAL	2.9
1	B	44	GLY	2.9
1	F	227	GLU	2.7
1	F	225	PHE	2.7
1	F	257	ARG	2.7
1	F	87	ALA	2.7
1	F	296	LEU	2.7
1	D	313	TYR	2.6
1	B	164	ALA	2.6
1	F	192	GLY	2.6
1	C	302	LYS	2.5
1	F	229	LEU	2.5
1	D	481	PHE	2.5
1	F	84	VAL	2.4
1	B	160	THR	2.4
1	E	163	GLY	2.4
1	C	194	ILE	2.4
1	E	123	TYR	2.3
1	C	334	PRO	2.3
1	E	56	TYR	2.2
1	F	164	ALA	2.2
1	C	330	LYS	2.1
1	F	130	LEU	2.1
1	E	51	GLN	2.1
1	D	336	LEU	2.1
1	E	196	PHE	2.1
1	C	45	SER	2.1
1	F	228	LYS	2.0
1	F	230	LEU	2.0
1	D	266	MET	2.0
1	E	49	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	267	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

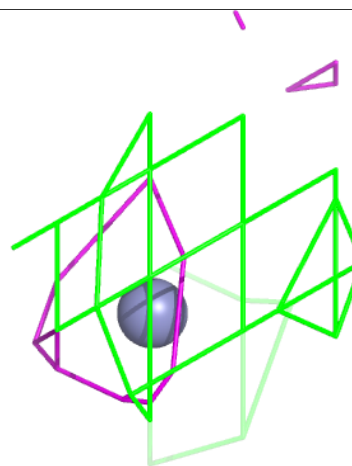
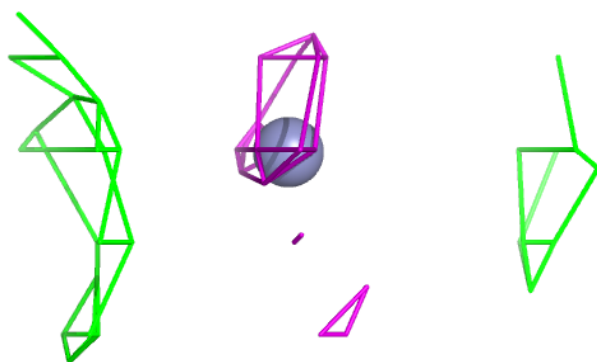
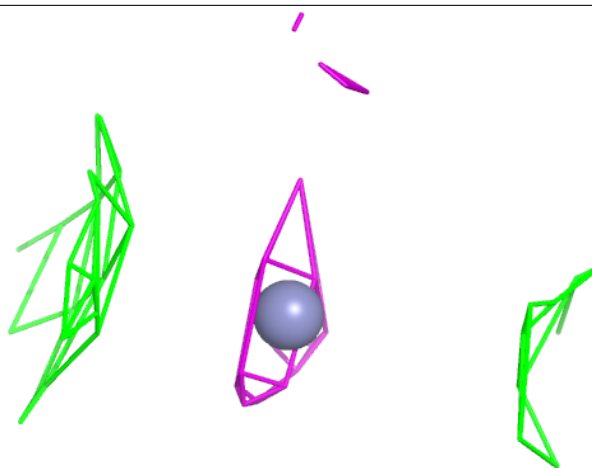
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

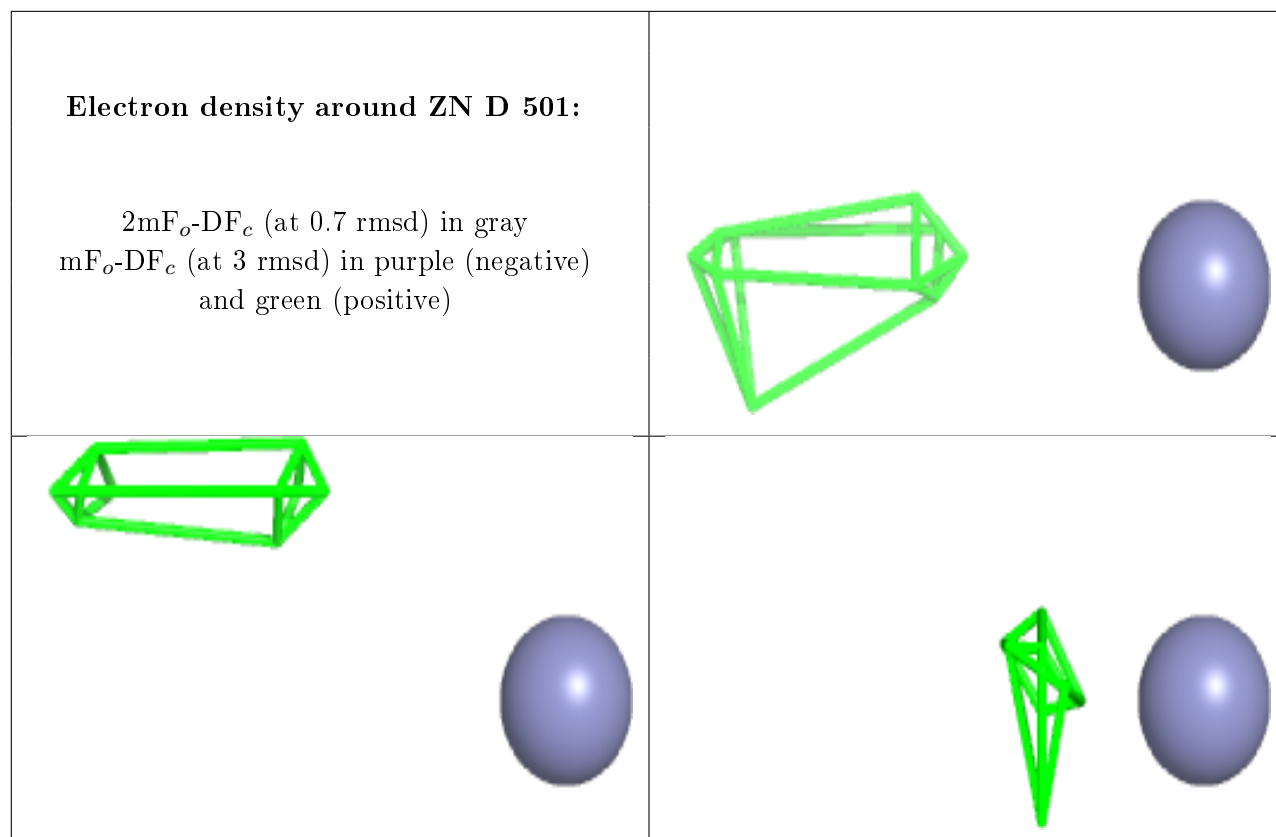
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZN	F	501	1/1	0.85	0.04	104,104,104,104	0
3	TRS	E	502	8/8	0.85	0.19	75,91,97,102	0
3	TRS	C	502	8/8	0.88	0.27	91,98,100,101	0
3	TRS	F	502	8/8	0.88	0.23	68,76,86,88	0
3	TRS	D	502	8/8	0.89	0.19	84,88,90,95	0
3	TRS	A	502	8/8	0.90	0.16	69,81,84,87	0
3	TRS	B	502	8/8	0.91	0.17	85,89,91,93	0
2	ZN	D	501	1/1	0.98	0.18	77,77,77,77	0
2	ZN	E	501	1/1	0.99	0.10	76,76,76,76	0
2	ZN	B	501	1/1	0.99	0.14	67,67,67,67	0
2	ZN	A	501	1/1	0.99	0.21	76,76,76,76	0
2	ZN	C	501	1/1	0.99	0.13	56,56,56,56	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 ZN F 501:

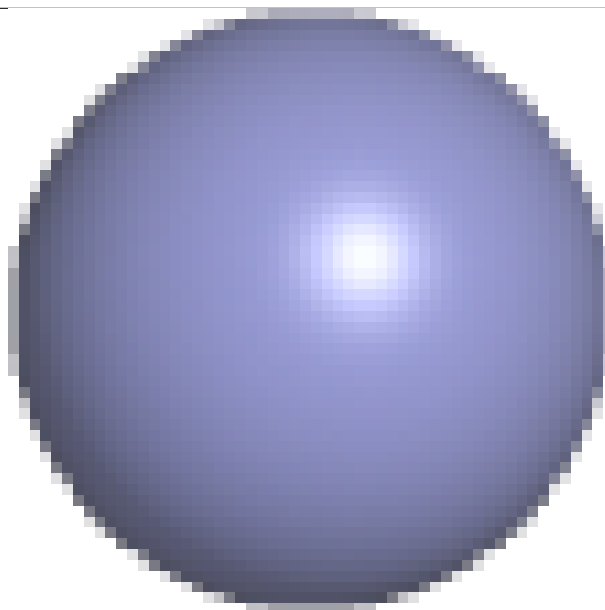
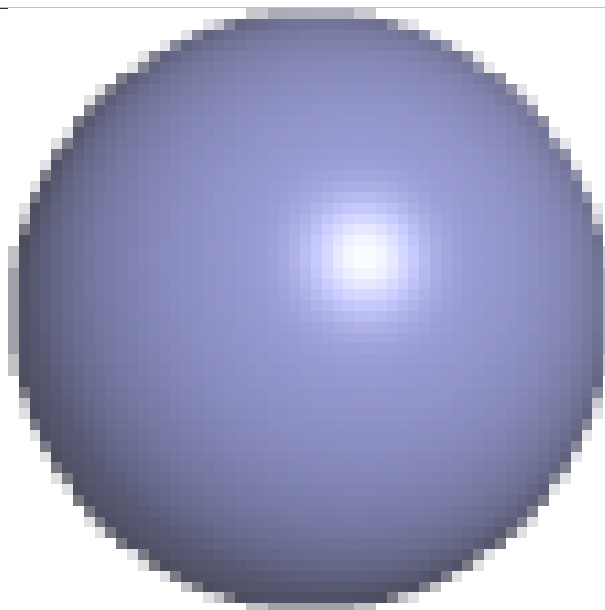
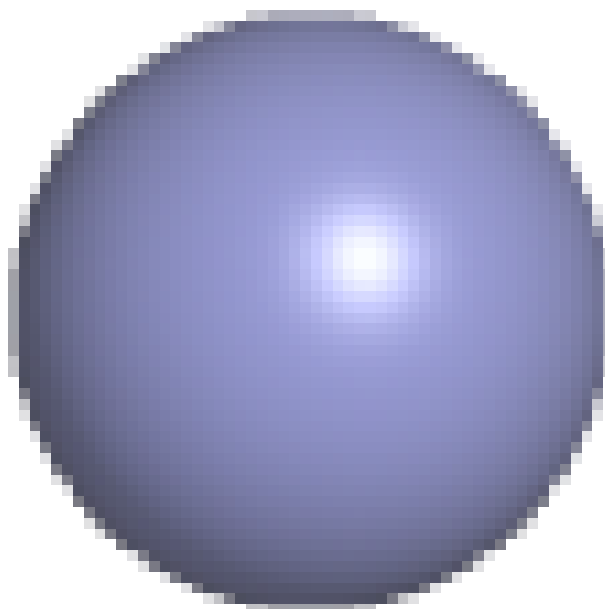
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





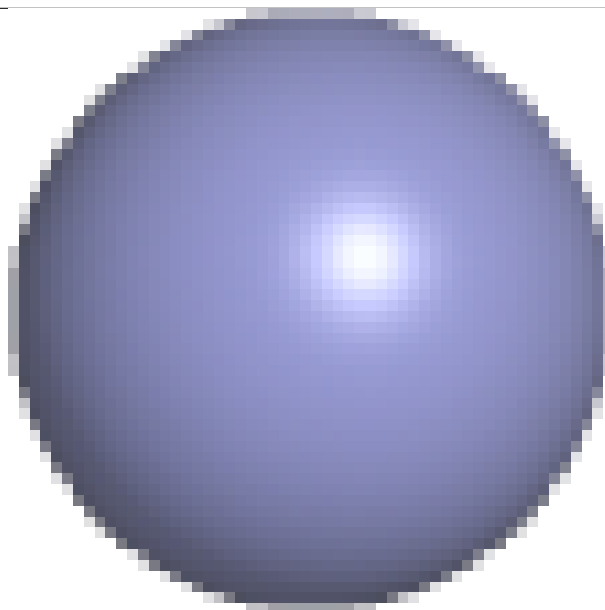
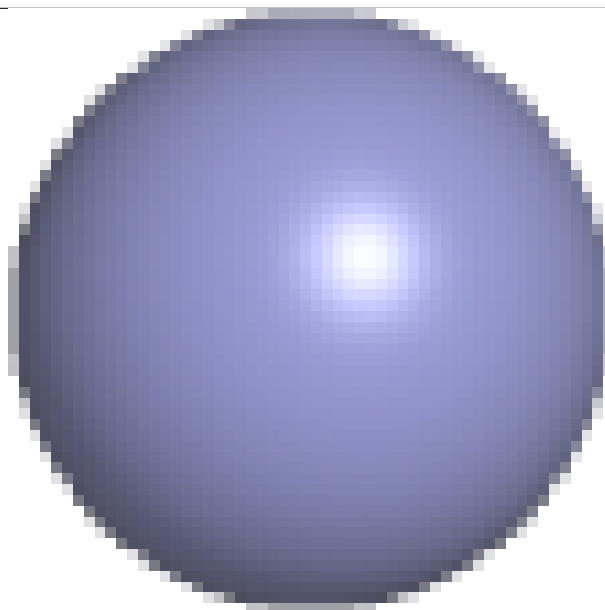
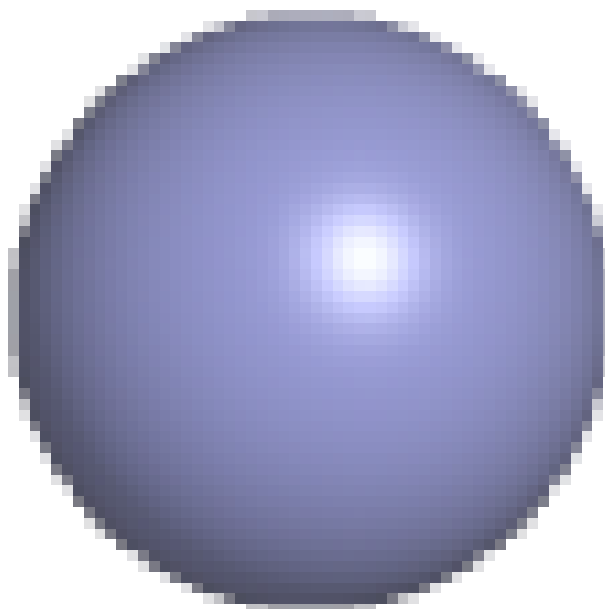
Electron density around ZN E 501:

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



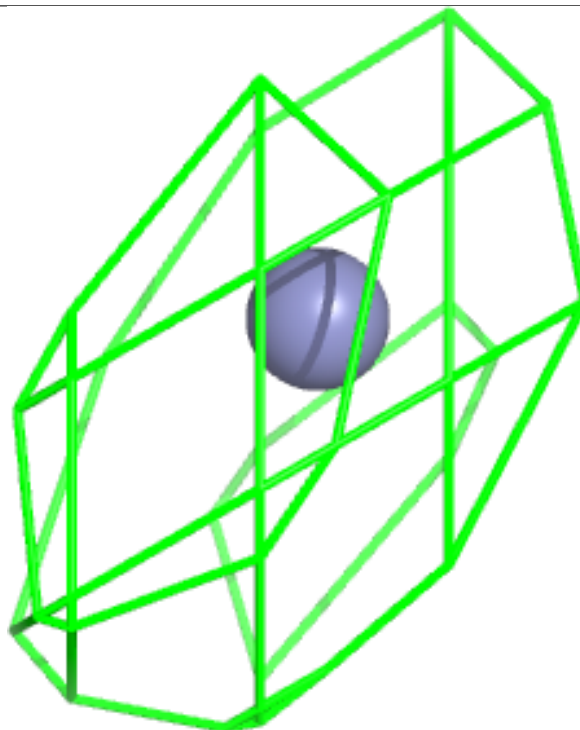
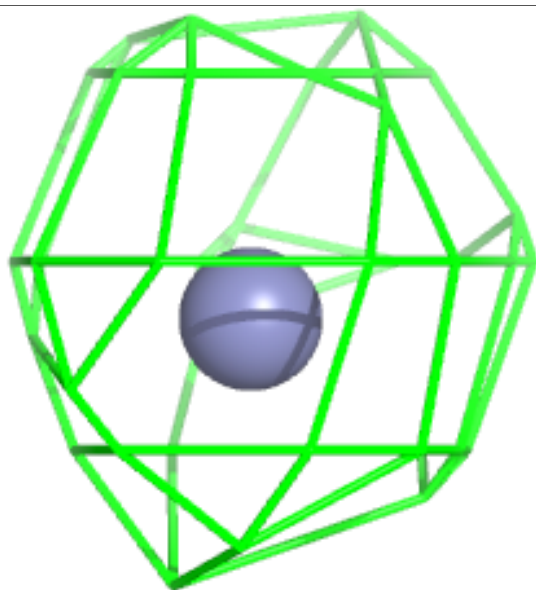
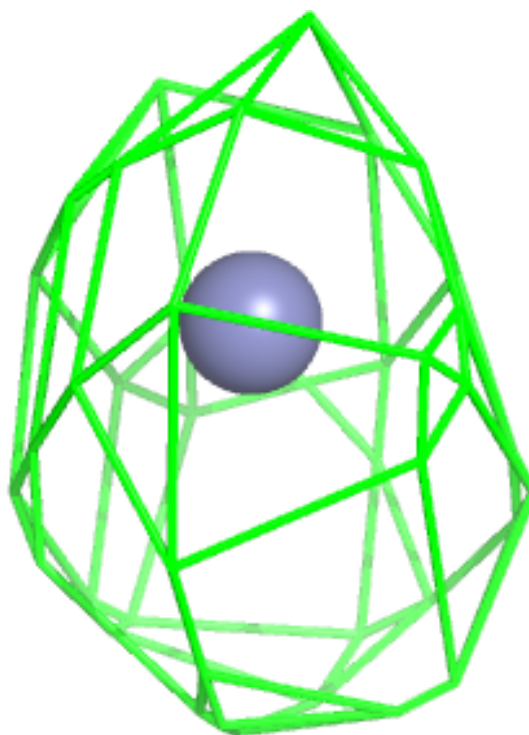
Electron density around ZN B 501:

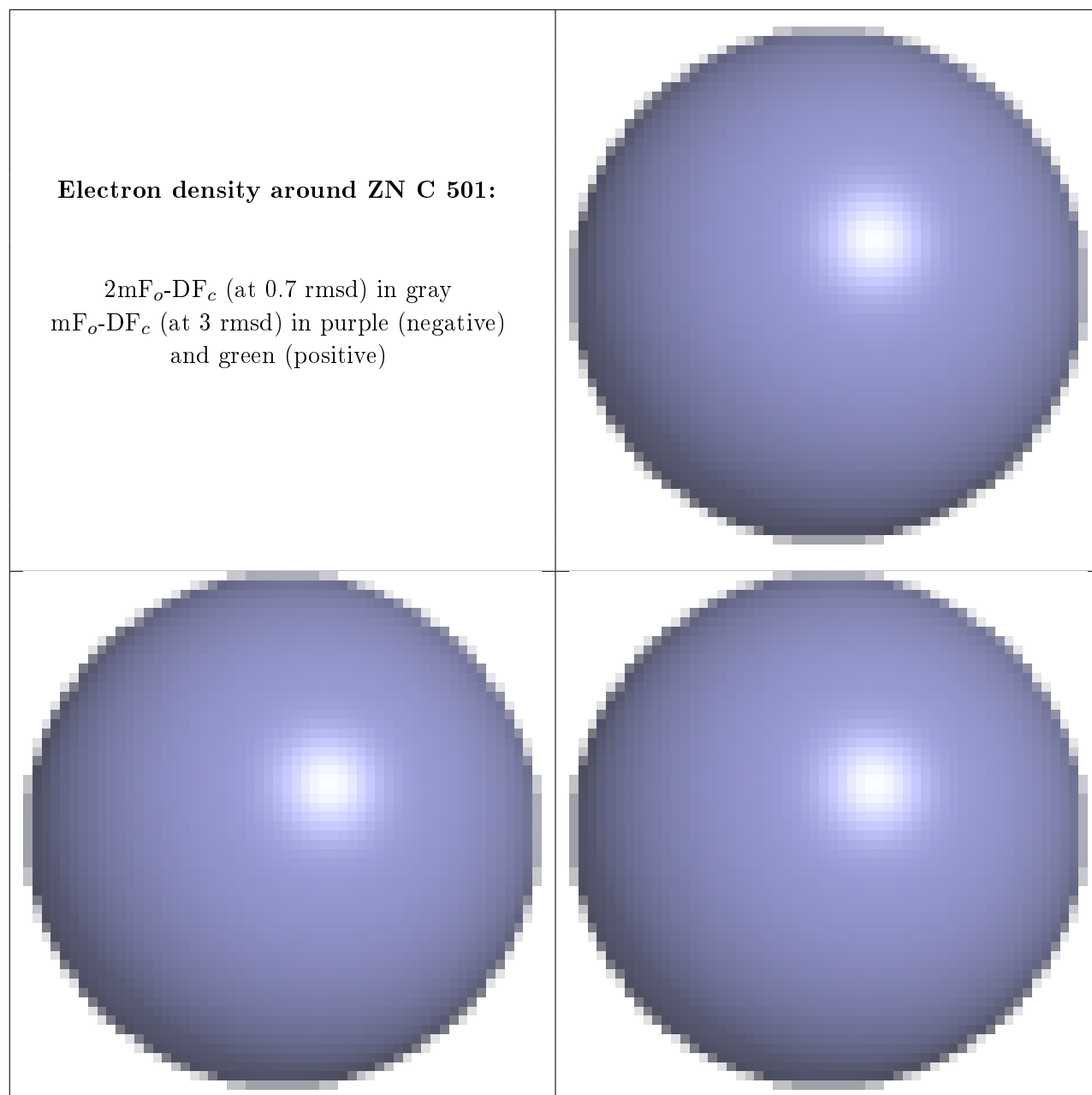
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN A 501:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.