



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:44 AM UTC

PDB ID : 1ZA1 / pdb_00001za1
Title : Structure of wild-type E. coli Aspartate Transcarbamoylase in the presence of CTP at 2.20 Å resolution
Authors : Wang, J.; Stieglitz, K.A.; Cardia, J.P.; Kantrowitz, E.R.
Deposited on : 2005-04-05
Resolution : 2.20 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

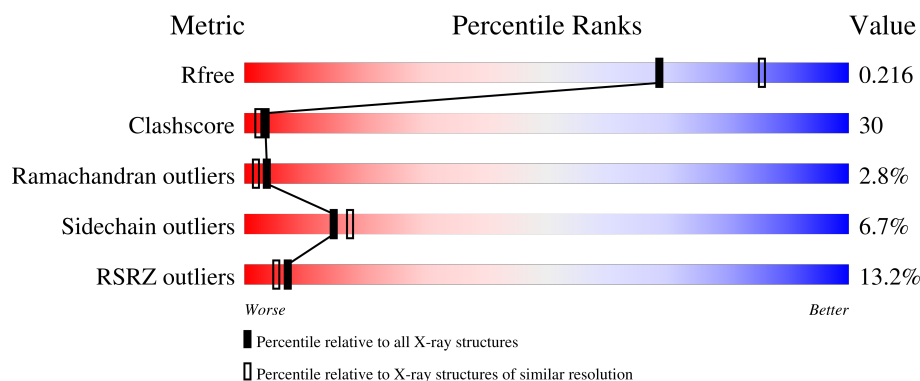
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	310	4% 66% 28% 5%
1	C	310	3% 72% 24% .
2	B	153	46% 34% 51% 13% ..
2	D	153	20% 42% 43% 14% .

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7878 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 Aspartate carbamoyltransferase catalytic chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2415	1527	423	456	9			
1	C	310	Total	C	N	O	S	0	0	0
			2415	1527	423	456	9			

- Molecule 2 is a protein called Aspartate carbamoyltransferase regulatory chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	152	Total	C	N	O	S	0	0	0
			1193	747	212	229	5			
2	D	152	Total	C	N	O	S	0	0	0
			1192	747	212	228	5			

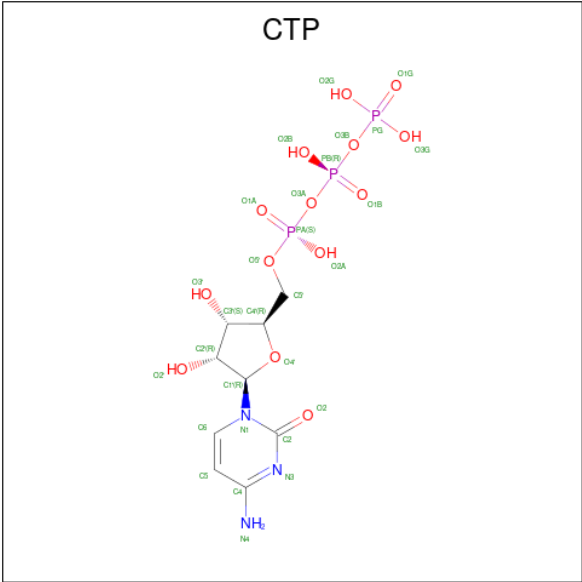
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P00478
D	1	MET	-	initiating methionine	UNP P00478

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

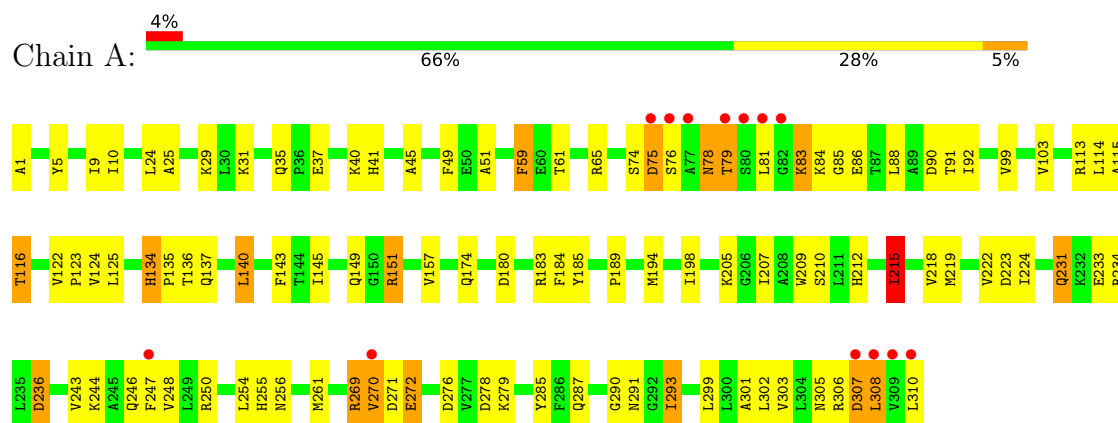
- Molecule 4 is CYTIDINE-5'-TRIPHOSPHATE (CCD ID: CTP) (formula: C₉H₁₆N₃O₁₄P₃).



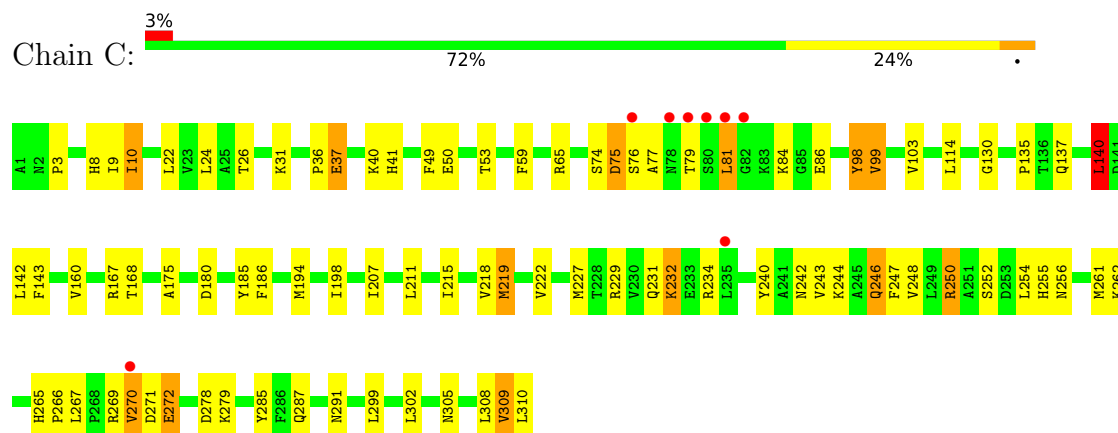
3 Residue-property plots [i](#)

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.

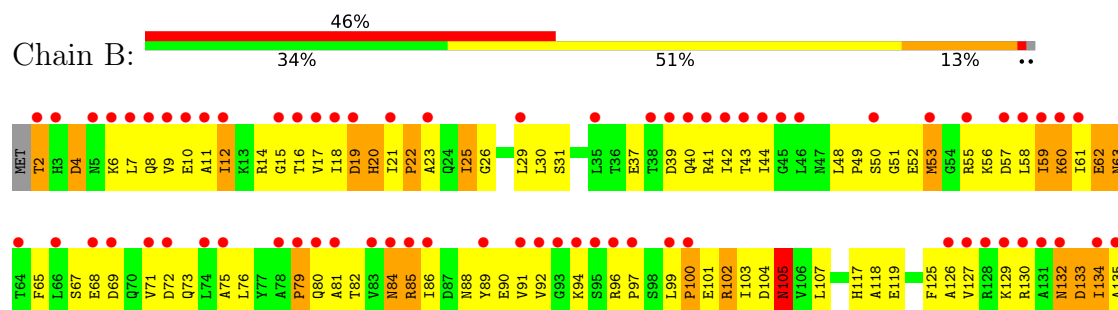
- Molecule 1: Aspartate carbamoyltransferase catalytic chain

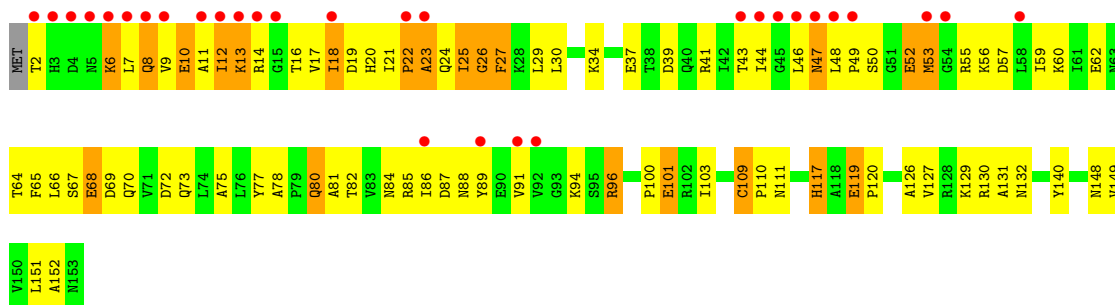


- Molecule 1: Aspartate carbamoyltransferase catalytic chain



- Molecule 2: Aspartate carbamoyltransferase regulatory chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	120.29Å 120.29Å 142.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.20 30.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.20) 99.1 (30.00-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.30 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.205 , 0.252 0.205 , 0.216	Depositor DCC
R_{free} test set	8093 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.122	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7878	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CTP, ZN

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	0.81	0/2461	1.19	20/3339 (0.6%)
1	C	0.84	1/2461 (0.0%)	1.14	18/3339 (0.5%)
2	B	0.58	0/1211	1.09	10/1637 (0.6%)
2	D	0.63	0/1210	1.14	7/1637 (0.4%)
All	All	0.76	1/7343 (0.0%)	1.15	55/9952 (0.6%)

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
2	D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	194	MET	SD-CE	5.18	1.92	1.79

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	25	ILE	N-CA-C	-12.29	101.06	113.47
1	A	269	ARG	N-CA-C	-9.96	94.31	109.94
2	D	109	CYS	CA-C-N	8.72	128.43	119.19
2	D	109	CYS	C-N-CA	8.72	128.43	119.19
2	D	117	HIS	N-CA-C	7.92	119.55	111.07
2	B	119	GLU	N-CA-C	7.72	122.78	109.82
1	C	77	ALA	N-CA-C	-7.40	103.39	113.30
2	B	117	HIS	N-CA-C	7.17	118.88	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	119	GLU	N-CA-C	7.10	120.96	110.10
1	C	222	VAL	N-CA-C	7.04	118.79	109.21
2	D	119	GLU	CA-C-N	6.96	128.54	119.84
2	D	119	GLU	C-N-CA	6.96	128.54	119.84
1	C	10	ILE	N-CA-C	6.78	117.39	111.90
1	C	99	VAL	N-CA-C	6.63	118.70	109.29
1	A	35	GLN	CA-C-N	6.58	126.26	119.82
1	A	35	GLN	C-N-CA	6.58	126.26	119.82
2	B	75	ALA	N-CA-C	6.45	119.30	111.82
1	C	49	PHE	N-CA-C	-6.30	104.46	111.71
1	C	140	LEU	CA-CB-CG	6.29	138.32	116.30
2	B	105	ASN	N-CA-C	6.28	124.18	110.80
2	B	20	HIS	N-CA-C	6.19	119.78	111.24
1	A	49	PHE	N-CA-C	-6.11	104.69	111.71
1	C	180	ASP	N-CA-C	6.10	119.64	109.95
1	C	219	MET	N-CA-C	5.95	118.25	111.11
1	C	53	THR	N-CA-C	5.92	118.21	111.11
2	B	102	ARG	N-CA-C	5.90	118.03	108.41
1	A	103	VAL	N-CA-C	-5.85	99.98	108.17
1	C	160	VAL	N-CA-C	5.85	117.17	108.46
1	A	194	MET	CA-C-N	5.83	125.84	119.89
1	A	194	MET	C-N-CA	5.83	125.84	119.89
1	C	278	ASP	N-CA-C	5.82	118.40	111.71
1	A	88	LEU	N-CA-C	-5.79	104.96	111.28
1	A	134	HIS	CA-C-N	5.76	127.04	119.84
1	A	134	HIS	C-N-CA	5.76	127.04	119.84
1	C	103	VAL	N-CA-C	-5.76	100.11	108.17
1	A	254	LEU	N-CA-C	5.75	120.28	113.16
1	A	276	ASP	N-CA-C	-5.72	105.80	112.89
1	A	236	ASP	N-CA-C	-5.65	102.93	109.93
1	A	287	GLN	N-CA-C	-5.62	105.30	111.82
1	C	98	TYR	CB-CA-C	-5.54	100.42	109.56
1	A	140	LEU	CA-CB-CG	5.51	135.59	116.30
1	A	10	ILE	N-CA-C	5.48	116.88	111.67
2	B	84	ASN	N-CA-C	5.47	117.30	108.34
1	A	180	ASP	N-CA-C	5.44	118.60	109.95
1	C	287	GLN	N-CA-C	-5.25	105.64	111.36
1	A	61	THR	N-CA-C	-5.12	105.70	111.28
2	D	126	ALA	N-CA-C	-5.11	102.13	110.20
1	A	157	VAL	N-CA-C	5.10	115.20	107.75
1	C	194	MET	CA-C-N	5.10	125.01	119.76
1	C	194	MET	C-N-CA	5.10	125.01	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	146	SER	N-CA-C	-5.10	102.73	110.28
1	A	215	ILE	N-CA-C	5.09	115.70	110.36
1	C	135	PRO	N-CA-C	5.08	121.33	113.75
2	B	4	ASP	N-CA-C	5.04	117.96	110.14
1	C	242	ASN	N-CA-C	5.02	118.17	111.75

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	140	TYR	Sidechain

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	2415	0	2422	105	0
1	C	2415	0	2422	72	0
2	B	1193	0	1207	144	0
2	D	1192	0	1207	119	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	B	29	0	12	7	0
4	D	29	0	12	8	0
5	A	189	0	0	7	0
5	B	92	0	0	10	0
5	C	237	0	0	6	0
5	D	85	0	0	8	0
All	All	7878	0	7282	433	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 30.

All (433) 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)
2:B:4:ASP:HB3	2:B:9:VAL:HG11	1.20	1.20
2:B:10:GLU:HA	2:D:7:LEU:HB3	1.33	1.10
2:D:27:PHE:HA	2:D:30:LEU:HD13	1.42	0.99
2:D:23:ALA:HA	2:D:57:ASP:OD2	1.64	0.96
1:A:78:ASN:ND2	1:A:84:LYS:HG3	1.81	0.95
2:D:12:ILE:HD13	2:D:13:LYS:N	1.81	0.94
2:D:67:SER:H	2:D:70:GLN:HE21	1.10	0.94
2:B:99:LEU:HD21	2:B:127:VAL:HG11	1.46	0.94
2:D:11:ALA:HB1	4:D:902:CTP:N4	1.86	0.91
2:D:14:ARG:HG2	2:D:65:PHE:HZ	1.38	0.88
2:B:26:GLY:O	2:B:30:LEU:HD12	1.74	0.87
2:B:84:ASN:HD22	2:B:91:VAL:HG11	1.37	0.86
5:B:932:HOH:O	2:D:39:ASP:HB3	1.74	0.86
1:C:308:LEU:HB3	1:C:310:LEU:HG	1.56	0.86
2:B:22:PRO:HG2	2:B:25:ILE:HG13	1.55	0.86
2:D:101:GLU:HG3	5:D:941:HOH:O	1.74	0.85
2:D:46:LEU:HA	2:D:57:ASP:OD1	1.76	0.85
2:B:12:ILE:HG22	2:B:41:ARG:NH1	1.91	0.85
2:B:12:ILE:HD13	2:B:12:ILE:H	1.42	0.85
2:B:12:ILE:HG22	2:B:41:ARG:HH12	1.40	0.84
1:A:308:LEU:HD23	1:A:310:LEU:HD21	1.60	0.82
1:C:8:HIS:HB3	1:C:10:ILE:CD1	2.09	0.81
2:D:12:ILE:HD13	2:D:13:LYS:H	1.43	0.80
1:A:290:GLY:O	1:A:293:ILE:HG12	1.82	0.80
2:B:104:ASP:HB2	5:B:977:HOH:O	1.81	0.79
1:A:302:LEU:HD23	1:A:308:LEU:HD22	1.63	0.79
2:D:18:ILE:HG22	2:D:21:ILE:HD11	1.63	0.79
2:D:12:ILE:HG13	2:D:62:GLU:CD	2.08	0.78
2:B:4:ASP:CB	2:B:9:VAL:HG11	2.08	0.78
1:C:8:HIS:HB3	1:C:10:ILE:HD11	1.64	0.78
1:A:302:LEU:CD2	1:A:308:LEU:HD22	2.13	0.78
2:B:86:ILE:HG12	2:B:91:VAL:HG22	1.66	0.78
1:C:270:VAL:HG13	1:C:271:ASP:H	1.48	0.77
2:B:130:ARG:NH2	2:B:135:ALA:HB2	2.00	0.77
2:B:82:THR:HG22	2:B:84:ASN:OD1	1.84	0.76
2:D:48:LEU:CD1	2:D:49:PRO:HD2	2.14	0.76
2:B:42:ILE:HB	2:D:46:LEU:HB2	1.65	0.76
2:D:21:ILE:HB	2:D:57:ASP:O	1.86	0.76
2:B:79:PRO:HG2	2:B:80:GLN:NE2	2.00	0.75
1:C:255:HIS:HB3	5:C:325:HOH:O	1.85	0.75
1:A:29:LYS:CD	1:A:310:LEU:HB3	2.16	0.75
1:C:270:VAL:HG13	1:C:271:ASP:N	2.02	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:ARG:O	1:A:270:VAL:HB	1.86	0.74
2:B:18:ILE:HG22	2:B:21:ILE:HD11	1.68	0.73
2:D:11:ALA:HB1	4:D:902:CTP:HN41	1.51	0.73
1:A:31:LYS:NZ	1:A:291:ASN:HD21	1.87	0.73
2:B:39:ASP:HA	2:D:47:ASN:ND2	2.04	0.73
2:D:86:ILE:HD13	2:D:91:VAL:HA	1.71	0.73
2:B:129:LYS:HA	2:B:134:ILE:HA	1.70	0.72
2:D:65:PHE:HB3	2:D:85:ARG:NH1	2.04	0.72
2:B:137:LYS:HB2	2:B:144:GLU:CG	2.19	0.72
2:B:137:LYS:HB2	2:B:144:GLU:HG2	1.69	0.72
1:A:215:ILE:HD12	1:A:215:ILE:H	1.55	0.72
1:A:29:LYS:HD2	1:A:310:LEU:HB3	1.73	0.71
2:D:27:PHE:CA	2:D:30:LEU:HD13	2.21	0.71
2:D:48:LEU:O	2:D:55:ARG:HA	1.90	0.71
2:D:129:LYS:HD2	2:D:130:ARG:H	1.55	0.71
4:D:902:CTP:H5'2	5:D:906:HOH:O	1.91	0.70
2:D:6:LYS:C	2:D:7:LEU:HD22	2.17	0.70
2:B:42:ILE:HG23	2:B:61:ILE:HD13	1.74	0.70
1:A:183:ARG:NH2	1:A:210:SER:OG	2.24	0.70
2:B:84:ASN:ND2	2:B:91:VAL:HG11	2.08	0.69
1:A:306:ARG:HH21	1:A:307:ASP:HB2	1.57	0.69
1:A:270:VAL:HG13	1:A:271:ASP:N	2.06	0.69
2:B:14:ARG:HA	2:B:86:ILE:O	1.92	0.69
2:B:20:HIS:HB3	5:B:944:HOH:O	1.92	0.69
2:B:84:ASN:HD22	2:B:91:VAL:CG1	2.05	0.69
1:A:24:LEU:HD13	1:A:143:PHE:HA	1.74	0.68
1:A:9:ILE:HD13	1:A:299:LEU:HG	1.74	0.68
2:B:69:ASP:HA	2:B:72:ASP:OD2	1.93	0.68
2:D:101:GLU:CD	2:D:101:GLU:H	2.02	0.68
1:A:215:ILE:CG2	1:A:219:MET:HE2	2.23	0.68
2:D:18:ILE:CG2	2:D:21:ILE:HD11	2.24	0.68
2:D:19:ASP:OD2	2:D:20:HIS:N	2.28	0.67
2:D:25:ILE:HD13	2:D:77:TYR:O	1.94	0.67
2:D:22:PRO:HD3	2:D:80:GLN:HE22	1.59	0.67
2:B:84:ASN:HD21	2:B:94:LYS:HB2	1.60	0.67
1:C:305:ASN:HB2	1:C:308:LEU:HD21	1.76	0.66
2:B:82:THR:HG21	2:B:94:LYS:NZ	2.11	0.66
1:C:265:HIS:HE2	1:C:272:GLU:HG3	1.59	0.66
2:D:48:LEU:HD12	2:D:49:PRO:HD2	1.76	0.66
1:A:51:ALA:HB2	1:A:75:ASP:HB2	1.76	0.66
2:B:48:LEU:O	2:B:55:ARG:HA	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:10:GLU:CA	2:D:7:LEU:HB3	2.20	0.66
2:D:11:ALA:HB1	4:D:902:CTP:C4	2.31	0.66
1:A:269:ARG:O	1:A:270:VAL:CB	2.44	0.65
2:D:117:HIS:HD2	5:D:942:HOH:O	1.80	0.65
2:D:69:ASP:HB3	5:D:945:HOH:O	1.97	0.65
2:B:99:LEU:HD23	2:B:100:PRO:HD2	1.78	0.65
1:A:231:GLN:HG3	1:A:234:ARG:HG3	1.79	0.64
2:B:82:THR:CG2	2:B:94:LYS:HG3	2.27	0.64
1:C:26:THR:HG23	1:C:310:LEU:CD1	2.28	0.64
2:B:20:HIS:HA	2:B:56:LYS:HE2	1.78	0.64
2:B:81:ALA:O	2:B:96:ARG:HD2	1.98	0.63
1:C:308:LEU:HD13	1:C:310:LEU:HD11	1.80	0.63
2:B:101:GLU:O	2:B:127:VAL:HG23	1.98	0.63
2:D:65:PHE:HB3	2:D:85:ARG:HH12	1.63	0.63
1:A:31:LYS:HZ1	1:A:291:ASN:HD21	1.47	0.62
1:C:248:VAL:HG22	1:C:271:ASP:O	1.99	0.62
1:A:279:LYS:N	1:A:279:LYS:HE2	2.14	0.62
2:B:133:ASP:HB2	5:B:918:HOH:O	2.00	0.62
2:B:96:ARG:CZ	2:B:96:ARG:HB3	2.30	0.61
2:B:18:ILE:CG2	2:B:21:ILE:HD11	2.30	0.61
2:D:6:LYS:O	2:D:7:LEU:HD13	2.00	0.61
1:C:37:GLU:HG3	1:C:40:LYS:HD3	1.82	0.61
1:A:248:VAL:HG12	1:A:272:GLU:HA	1.83	0.61
2:B:130:ARG:HB3	2:B:130:ARG:NH1	2.16	0.60
2:D:23:ALA:O	2:D:24:GLN:HB2	2.00	0.60
2:B:14:ARG:HD2	5:B:958:HOH:O	2.01	0.60
2:B:49:PRO:HD3	2:D:41:ARG:NE	2.14	0.60
2:D:21:ILE:O	2:D:57:ASP:N	2.32	0.60
2:D:100:PRO:HG2	2:D:103:ILE:HD11	1.84	0.60
1:A:215:ILE:HD12	1:A:215:ILE:N	2.16	0.60
2:D:12:ILE:HG13	2:D:62:GLU:OE2	2.02	0.60
2:D:17:VAL:HB	2:D:84:ASN:HB2	1.84	0.60
2:D:73:GLN:HE22	2:D:103:ILE:HG23	1.67	0.60
1:C:250:ARG:HD2	5:C:354:HOH:O	2.02	0.60
2:D:131:ALA:O	2:D:132:ASN:HB2	2.00	0.60
1:A:151:ARG:HG3	1:A:151:ARG:HH11	1.66	0.60
2:D:21:ILE:CG2	2:D:57:ASP:HB2	2.32	0.59
2:D:75:ALA:HB3	5:D:973:HOH:O	2.02	0.59
1:A:79:THR:HG22	1:A:81:LEU:H	1.65	0.59
1:C:31:LYS:NZ	1:C:291:ASN:HD21	2.00	0.59
2:D:129:LYS:HD2	2:D:130:ARG:N	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:79:PRO:HG2	2:B:80:GLN:HE22	1.68	0.59
1:C:308:LEU:HB3	1:C:310:LEU:CG	2.29	0.59
1:A:215:ILE:HG22	1:A:219:MET:HE2	1.84	0.59
2:B:23:ALA:O	2:B:25:ILE:HG12	2.03	0.59
2:B:50:SER:HB2	2:B:56:LYS:HG2	1.84	0.59
2:D:67:SER:OG	2:D:70:GLN:HG3	2.03	0.59
1:A:255:HIS:HD2	5:A:428:HOH:O	1.85	0.58
1:C:215:ILE:HD12	1:C:215:ILE:N	2.17	0.58
1:A:37:GLU:OE1	1:A:40:LYS:HD2	2.03	0.58
2:B:82:THR:CG2	2:B:84:ASN:OD1	2.52	0.58
2:B:25:ILE:O	2:B:29:LEU:HG	2.04	0.58
1:A:278:ASP:C	1:A:279:LYS:HE2	2.29	0.58
1:C:40:LYS:O	1:C:41:HIS:HB2	2.03	0.57
2:B:130:ARG:HH22	2:B:135:ALA:HB2	1.68	0.57
2:D:20:HIS:HA	2:D:56:LYS:HD2	1.84	0.57
2:B:43:THR:HB	2:B:60:LYS:HD2	1.87	0.57
1:C:215:ILE:HG22	1:C:219:MET:HE2	1.86	0.57
2:B:58:LEU:C	2:B:59:ILE:HD13	2.29	0.57
2:B:82:THR:HG21	2:B:94:LYS:HZ3	1.68	0.57
1:C:309:VAL:HG12	1:C:309:VAL:O	2.03	0.57
2:B:99:LEU:HD23	2:B:100:PRO:CD	2.33	0.57
2:D:26:GLY:O	2:D:29:LEU:N	2.37	0.57
2:B:137:LYS:CB	2:B:144:GLU:HG2	2.35	0.57
1:C:250:ARG:HB3	1:C:250:ARG:CZ	2.31	0.57
1:A:149:GLN:O	1:A:151:ARG:HD3	2.04	0.57
2:D:101:GLU:OE1	2:D:101:GLU:N	2.22	0.57
2:D:148:ASN:O	2:D:152:ALA:HB2	2.04	0.57
1:A:9:ILE:HD11	1:A:303:VAL:CG2	2.35	0.57
1:A:92:ILE:HG12	1:A:115:ALA:HB1	1.86	0.57
1:A:246:GLN:HB2	1:A:247:PHE:CZ	2.40	0.57
2:B:92:VAL:HG12	2:B:92:VAL:O	2.05	0.57
1:A:308:LEU:CD2	1:A:310:LEU:HD21	2.33	0.56
2:B:82:THR:HG21	2:B:94:LYS:HG3	1.85	0.56
1:C:229:ARG:NH2	1:C:231:GLN:HG2	2.20	0.56
4:D:902:CTP:PA	5:D:906:HOH:O	2.63	0.56
2:D:6:LYS:HB2	2:D:6:LYS:HZ2	1.70	0.56
2:D:21:ILE:HB	2:D:57:ASP:C	2.30	0.56
2:D:6:LYS:HG3	2:D:7:LEU:H	1.71	0.56
2:D:14:ARG:HG2	2:D:65:PHE:CZ	2.29	0.56
2:D:26:GLY:O	2:D:30:LEU:HD12	2.06	0.56
2:B:21:ILE:HB	2:B:57:ASP:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:126:ALA:HB3	2:B:137:LYS:HB3	1.88	0.56
1:A:270:VAL:CG1	1:A:271:ASP:N	2.68	0.55
1:A:305:ASN:HB3	1:A:308:LEU:HD12	1.88	0.55
1:A:215:ILE:H	1:A:215:ILE:CD1	2.19	0.55
1:A:218:VAL:HG22	1:A:222:VAL:HG13	1.88	0.55
1:C:75:ASP:CG	1:C:76:SER:H	2.14	0.55
1:A:81:LEU:HA	1:A:86:GLU:HB3	1.89	0.55
2:B:96:ARG:HE	2:B:97:PRO:HD2	1.72	0.55
1:A:40:LYS:O	1:A:41:HIS:HB2	2.07	0.55
1:C:246:GLN:HG3	1:C:247:PHE:CE2	2.41	0.55
2:D:22:PRO:O	2:D:23:ALA:O	2.25	0.55
1:A:9:ILE:HD13	1:A:299:LEU:CG	2.37	0.55
2:B:17:VAL:HG12	2:B:19:ASP:OD1	2.07	0.55
1:A:125:LEU:HD12	1:A:125:LEU:N	2.22	0.54
1:C:229:ARG:HH22	1:C:231:GLN:HG2	1.70	0.54
2:D:66:LEU:HA	2:D:70:GLN:NE2	2.22	0.54
2:B:56:LYS:HZ1	2:B:58:LEU:HD12	1.71	0.54
2:B:99:LEU:HD23	2:B:100:PRO:N	2.23	0.54
1:A:231:GLN:HG3	1:A:234:ARG:CG	2.38	0.54
1:C:215:ILE:HD12	1:C:215:ILE:H	1.72	0.54
1:A:222:VAL:HG23	1:A:261:MET:HG3	1.90	0.54
2:D:103:ILE:HG12	2:D:127:VAL:CG2	2.37	0.54
2:B:39:ASP:OD1	2:B:39:ASP:O	2.26	0.54
1:A:134:HIS:N	1:A:135:PRO:HD3	2.23	0.54
2:B:99:LEU:HD21	2:B:127:VAL:CG1	2.31	0.54
1:C:270:VAL:CG1	1:C:271:ASP:H	2.19	0.53
2:D:149:VAL:O	2:D:152:ALA:HB3	2.09	0.53
2:D:47:ASN:O	2:D:48:LEU:HD22	2.08	0.53
2:D:44:ILE:CD1	2:D:59:ILE:HG23	2.37	0.53
1:A:261:MET:SD	1:A:261:MET:C	2.92	0.53
1:A:76:SER:C	1:A:78:ASN:H	2.17	0.53
2:B:85:ARG:HH11	2:B:85:ARG:HB3	1.72	0.53
2:D:27:PHE:HA	2:D:30:LEU:CD1	2.29	0.53
2:D:87:ASP:O	2:D:88:ASN:C	2.51	0.53
2:B:118:ALA:HB1	5:B:933:HOH:O	2.09	0.53
1:C:250:ARG:NH1	1:C:252:SER:OG	2.42	0.53
2:D:34:LYS:HD3	2:D:37:GLU:OE2	2.08	0.52
2:B:147:HIS:CD2	2:B:148:ASN:ND2	2.77	0.52
1:A:9:ILE:HD11	1:A:303:VAL:HG21	1.90	0.52
2:B:43:THR:HB	2:B:60:LYS:CG	2.40	0.52
1:C:244:LYS:O	1:C:248:VAL:HG23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:48:LEU:HD13	2:D:49:PRO:HD2	1.90	0.52
4:D:902:CTP:O1A	5:D:906:HOH:O	2.19	0.52
2:B:82:THR:HG23	2:B:94:LYS:HG3	1.92	0.52
1:C:240:TYR:CD1	1:C:240:TYR:C	2.87	0.52
1:A:81:LEU:C	1:A:91:THR:OG1	2.53	0.51
2:B:12:ILE:CG2	2:B:41:ARG:HH12	2.18	0.51
2:B:12:ILE:HB	2:B:62:GLU:HG2	1.92	0.51
2:B:20:HIS:HA	2:B:56:LYS:CE	2.40	0.51
1:C:31:LYS:HZ2	1:C:291:ASN:HD21	1.57	0.51
2:B:76:LEU:HD22	2:B:151:LEU:HD11	1.91	0.51
2:B:147:HIS:NE2	2:B:148:ASN:ND2	2.58	0.51
2:B:41:ARG:HB3	2:B:62:GLU:HG3	1.91	0.51
1:A:255:HIS:CD2	1:A:256:ASN:ND2	2.79	0.51
2:B:15:GLY:HA3	2:B:61:ILE:O	2.10	0.51
1:C:308:LEU:CB	1:C:310:LEU:HG	2.35	0.51
2:D:14:ARG:HG3	2:D:87:ASP:OD1	2.10	0.51
2:B:26:GLY:O	2:B:30:LEU:CD1	2.53	0.50
2:D:85:ARG:HG3	2:D:85:ARG:HH11	1.75	0.50
1:C:240:TYR:O	1:C:244:LYS:HB3	2.11	0.50
2:B:67:SER:O	2:B:71:VAL:HG23	2.11	0.50
5:B:970:HOH:O	2:D:48:LEU:HD21	2.10	0.50
2:D:67:SER:N	2:D:70:GLN:HE21	1.94	0.50
2:B:43:THR:HB	2:B:60:LYS:CD	2.41	0.50
2:B:73:GLN:OE1	2:B:103:ILE:HD13	2.11	0.50
2:B:43:THR:O	2:B:60:LYS:HG2	2.12	0.50
2:B:102:ARG:HG2	2:B:104:ASP:OD1	2.12	0.50
2:D:9:VAL:HG11	2:D:43:THR:HG21	1.92	0.50
2:D:22:PRO:HG2	2:D:25:ILE:HD12	1.93	0.50
2:B:107:LEU:HD22	2:B:150:VAL:HG12	1.94	0.50
2:D:131:ALA:O	2:D:132:ASN:CB	2.59	0.50
2:B:99:LEU:CD2	2:B:127:VAL:HG11	2.31	0.50
4:B:901:CTP:O1B	4:B:901:CTP:O2G	2.30	0.50
1:A:113:ARG:O	1:A:116:THR:HG22	2.12	0.49
2:B:71:VAL:HG12	2:B:71:VAL:O	2.11	0.49
2:B:26:GLY:C	2:B:30:LEU:HD12	2.37	0.49
2:B:51:GLY:C	2:B:53:MET:H	2.19	0.49
1:C:75:ASP:CG	1:C:76:SER:N	2.70	0.49
2:D:30:LEU:HD21	2:D:44:ILE:CD1	2.42	0.49
1:A:74:SER:O	1:A:75:ASP:C	2.54	0.49
1:C:207:ILE:HD13	5:C:358:HOH:O	2.12	0.49
1:C:308:LEU:C	1:C:310:LEU:H	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:ILE:HD13	4:B:901:CTP:N3	2.28	0.49
2:B:63:ASN:N	2:B:63:ASN:ND2	2.60	0.49
2:D:85:ARG:NH1	2:D:85:ARG:HG3	2.27	0.49
2:B:10:GLU:HG2	2:D:9:VAL:HG22	1.93	0.49
2:D:100:PRO:HG2	2:D:103:ILE:CD1	2.41	0.49
1:A:5:TYR:CD1	1:A:306:ARG:HA	2.48	0.49
2:B:11:ALA:H	2:D:7:LEU:HG	1.78	0.49
1:A:9:ILE:CD1	1:A:299:LEU:HG	2.40	0.49
1:A:218:VAL:HG22	1:A:218:VAL:O	2.13	0.49
2:B:17:VAL:HG21	2:B:86:ILE:HD12	1.95	0.49
2:B:85:ARG:HH11	2:B:85:ARG:CB	2.26	0.49
1:C:266:PRO:O	1:C:267:LEU:HB2	2.13	0.49
2:B:147:HIS:CD2	2:B:148:ASN:N	2.81	0.49
1:C:137:GLN:HA	1:C:140:LEU:HD13	1.95	0.49
1:C:185:TYR:CG	1:C:218:VAL:HG11	2.47	0.49
1:A:74:SER:O	1:A:75:ASP:O	2.31	0.48
2:B:146:SER:OG	2:B:148:ASN:HB2	2.13	0.48
4:B:901:CTP:O1B	4:B:901:CTP:H5'1	2.13	0.48
1:C:79:THR:HG22	1:C:81:LEU:H	1.78	0.48
2:D:30:LEU:HD12	2:D:30:LEU:H	1.76	0.48
1:A:83:LYS:NZ	1:A:84:LYS:HE2	2.27	0.48
1:A:210:SER:OG	1:A:212:HIS:HE1	1.96	0.48
1:A:136:THR:HG22	1:A:299:LEU:CD2	2.43	0.48
1:C:3:PRO:HD2	1:C:22:LEU:CD2	2.44	0.48
1:C:186:PHE:HB2	1:C:211:LEU:HD23	1.95	0.48
1:A:84:LYS:HA	5:A:465:HOH:O	2.14	0.48
1:A:306:ARG:HD3	5:A:482:HOH:O	2.12	0.48
1:A:223:ASP:C	1:A:224:ILE:HD12	2.38	0.48
2:D:8:GLN:HE21	2:D:8:GLN:HB2	1.50	0.48
1:C:9:ILE:HG21	1:C:299:LEU:HD21	1.94	0.48
1:C:246:GLN:O	1:C:247:PHE:CD1	2.67	0.48
2:D:20:HIS:HB2	2:D:81:ALA:HA	1.96	0.48
2:B:41:ARG:NH1	2:B:41:ARG:HG2	2.28	0.48
2:D:100:PRO:CG	2:D:103:ILE:HD11	2.44	0.48
2:D:6:LYS:HB2	2:D:6:LYS:NZ	2.28	0.47
2:B:12:ILE:HD13	2:B:12:ILE:N	2.20	0.47
2:B:22:PRO:HG2	2:B:25:ILE:CG1	2.36	0.47
1:A:255:HIS:O	5:A:411:HOH:O	2.20	0.47
1:A:270:VAL:HG13	1:A:271:ASP:CG	2.39	0.47
1:C:215:ILE:H	1:C:215:ILE:CD1	2.27	0.47
1:C:232:LYS:CB	1:C:232:LYS:NZ	2.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:68:GLU:CD	2:D:68:GLU:H	2.22	0.47
2:B:12:ILE:H	2:B:12:ILE:CD1	2.22	0.47
2:B:2:THR:OG1	2:B:11:ALA:HB2	2.14	0.47
2:B:90:GLU:O	2:B:92:VAL:HG23	2.14	0.47
1:A:81:LEU:N	1:A:81:LEU:HD23	2.29	0.47
1:A:184:PHE:O	1:A:209:TRP:HA	2.14	0.47
2:B:63:ASN:N	2:B:63:ASN:HD22	2.12	0.47
2:B:130:ARG:HB3	2:B:130:ARG:HH11	1.78	0.47
2:B:130:ARG:HG3	5:B:951:HOH:O	2.14	0.47
2:D:68:GLU:O	2:D:72:ASP:OD1	2.33	0.47
2:D:81:ALA:O	2:D:96:ARG:HG3	2.15	0.47
2:D:52:GLU:O	2:D:53:MET:HB3	2.14	0.46
1:A:24:LEU:HD22	1:A:143:PHE:HB2	1.97	0.46
1:A:25:ALA:O	1:A:29:LYS:HG3	2.15	0.46
2:B:88:ASN:O	2:B:90:GLU:N	2.49	0.46
2:B:19:ASP:HB3	2:B:20:HIS:ND1	2.30	0.46
1:C:269:ARG:O	1:C:270:VAL:HB	2.15	0.46
1:A:76:SER:C	1:A:78:ASN:N	2.73	0.46
2:B:147:HIS:CD2	2:B:148:ASN:HD22	2.33	0.46
2:D:86:ILE:CD1	2:D:91:VAL:HG22	2.45	0.46
2:B:41:ARG:HG2	2:B:41:ARG:HH11	1.81	0.46
2:B:11:ALA:N	2:D:7:LEU:HG	2.31	0.45
2:B:136:LEU:O	2:B:144:GLU:HA	2.16	0.45
2:D:100:PRO:O	2:D:127:VAL:HB	2.16	0.45
1:C:256:ASN:OD1	1:C:256:ASN:N	2.48	0.45
2:B:14:ARG:NH1	2:B:65:PHE:CE2	2.84	0.45
2:B:2:THR:HG1	2:B:11:ALA:HB2	1.80	0.45
2:D:16:THR:OG1	2:D:64:THR:O	2.31	0.45
2:B:60:LYS:O	2:B:60:LYS:HG3	2.16	0.45
2:B:99:LEU:HD23	2:B:99:LEU:C	2.41	0.45
2:B:88:ASN:C	2:B:90:GLU:H	2.23	0.45
2:B:137:LYS:CA	2:B:144:GLU:HG2	2.47	0.45
2:D:22:PRO:CD	2:D:80:GLN:HE22	2.29	0.45
1:A:145:ILE:HG12	1:A:224:ILE:HG12	1.99	0.45
1:A:223:ASP:O	1:A:224:ILE:HD12	2.17	0.45
1:A:305:ASN:HB3	1:A:308:LEU:CD1	2.47	0.44
1:C:243:VAL:O	1:C:244:LYS:C	2.60	0.44
2:B:40:GLN:HB3	2:B:62:GLU:O	2.16	0.44
1:C:142:LEU:HD11	1:C:175:ALA:HB1	2.00	0.44
1:A:114:LEU:C	1:A:114:LEU:HD23	2.42	0.44
2:D:65:PHE:HB3	2:D:85:ARG:CZ	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:ALA:C	5:A:425:HOH:O	2.61	0.44
1:A:59:PHE:CZ	1:A:136:THR:HG21	2.52	0.44
2:B:25:ILE:HG22	2:B:29:LEU:HG	1.98	0.44
1:A:231:GLN:H	1:A:231:GLN:HG2	1.43	0.44
2:B:130:ARG:HD3	5:B:951:HOH:O	2.17	0.44
2:D:13:LYS:HA	2:D:89:TYR:H	1.83	0.44
2:B:60:LYS:NZ	2:B:60:LYS:HB3	2.32	0.44
2:B:86:ILE:CG1	2:B:91:VAL:HG22	2.44	0.44
2:D:50:SER:HB2	2:D:56:LYS:HE2	1.99	0.44
2:D:41:ARG:HB3	2:D:62:GLU:CD	2.43	0.44
2:D:50:SER:HB2	2:D:56:LYS:HG2	2.00	0.44
1:C:8:HIS:CB	1:C:10:ILE:CD1	2.89	0.44
1:A:210:SER:OG	1:A:212:HIS:CE1	2.71	0.44
1:A:306:ARG:HE	1:A:307:ASP:HB2	1.83	0.43
2:B:40:GLN:O	2:D:47:ASN:HB2	2.18	0.43
2:B:86:ILE:HD13	4:B:901:CTP:C4	2.53	0.43
1:A:9:ILE:HD13	1:A:299:LEU:CD1	2.48	0.43
1:C:232:LYS:HB2	1:C:232:LYS:HZ2	1.83	0.43
2:D:17:VAL:HG22	2:D:60:LYS:HG2	1.99	0.43
1:A:215:ILE:HG21	1:A:219:MET:HE2	1.99	0.43
2:B:68:GLU:CD	2:B:68:GLU:H	2.26	0.43
2:B:136:LEU:HD12	2:B:147:HIS:HA	2.00	0.43
2:D:30:LEU:HD21	2:D:44:ILE:HD12	2.00	0.43
1:A:83:LYS:HZ3	1:A:84:LYS:HE2	1.84	0.43
1:A:250:ARG:NH1	1:A:250:ARG:HG3	2.33	0.43
2:B:129:LYS:HB2	2:B:134:ILE:HG12	1.99	0.43
1:A:81:LEU:HG	1:A:81:LEU:O	2.19	0.43
1:A:205:LYS:HB2	1:A:207:ILE:HG12	2.01	0.43
2:B:67:SER:C	2:B:69:ASP:N	2.75	0.43
1:C:130:GLY:O	1:C:167:ARG:NH1	2.51	0.43
1:C:265:HIS:HE2	1:C:272:GLU:CG	2.26	0.43
2:D:82:THR:HG21	2:D:94:LYS:HE3	2.00	0.43
1:A:9:ILE:CD1	1:A:303:VAL:HG21	2.48	0.43
2:B:43:THR:HB	2:B:60:LYS:HG2	2.01	0.43
2:B:138:CYS:O	2:B:142:GLU:HA	2.17	0.43
1:C:40:LYS:O	1:C:41:HIS:CB	2.66	0.43
1:C:262:LYS:NZ	5:C:424:HOH:O	2.48	0.43
2:D:2:THR:HG21	2:D:50:SER:HA	2.00	0.43
2:B:8:GLN:HB2	2:D:10:GLU:HA	2.00	0.43
1:A:184:PHE:HE2	1:A:207:ILE:HG21	1.83	0.43
1:C:50:GLU:HG3	5:C:430:HOH:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:168:THR:HB	5:C:420:HOH:O	2.19	0.43
2:D:101:GLU:CD	2:D:101:GLU:N	2.74	0.43
1:A:86:GLU:HG3	1:A:90:ASP:HB2	2.01	0.42
1:A:218:VAL:HG22	1:A:222:VAL:CG1	2.48	0.42
1:A:137:GLN:NE2	5:A:366:HOH:O	2.52	0.42
1:A:246:GLN:O	1:A:247:PHE:CD1	2.72	0.42
2:B:86:ILE:HD13	4:B:901:CTP:C5	2.54	0.42
1:C:254:LEU:HD22	1:C:261:MET:HE1	2.00	0.42
2:D:67:SER:H	2:D:70:GLN:NE2	1.95	0.42
1:A:174:GLN:HE21	1:A:198:ILE:CD1	2.32	0.42
1:C:279:LYS:HD2	1:C:279:LYS:N	2.35	0.42
2:B:84:ASN:HB3	2:B:91:VAL:HG13	2.00	0.42
2:D:82:THR:OG1	2:D:96:ARG:NH1	2.40	0.42
2:D:100:PRO:CG	2:D:103:ILE:CD1	2.97	0.42
2:D:111:ASN:O	2:D:117:HIS:HE1	2.01	0.42
1:C:98:TYR:HB2	1:C:99:VAL:HG13	2.01	0.42
1:C:232:LYS:C	1:C:234:ARG:N	2.78	0.42
1:A:84:LYS:HD3	5:A:465:HOH:O	2.19	0.42
1:A:250:ARG:HG3	1:A:250:ARG:HH11	1.84	0.42
2:B:132:ASN:O	2:B:133:ASP:HB2	2.19	0.42
2:B:133:ASP:O	2:B:134:ILE:C	2.62	0.42
2:D:26:GLY:C	2:D:30:LEU:HD12	2.45	0.42
2:D:103:ILE:HD12	5:D:921:HOH:O	2.19	0.42
1:A:270:VAL:CG1	1:A:271:ASP:H	2.33	0.42
2:D:109:CYS:HA	2:D:110:PRO:HD3	1.76	0.42
2:D:119:GLU:HA	2:D:120:PRO:HD3	1.80	0.42
1:A:189:PRO:HB3	1:A:247:PHE:CE2	2.55	0.42
2:B:2:THR:HG21	4:B:901:CTP:C6	2.55	0.42
1:C:36:PRO:HA	1:C:65:ARG:O	2.20	0.42
1:A:149:GLN:CG	1:A:224:ILE:HD11	2.50	0.42
2:B:44:ILE:HD11	2:D:46:LEU:CD1	2.50	0.42
2:B:142:GLU:HG2	5:B:956:HOH:O	2.20	0.42
1:C:305:ASN:HB2	1:C:308:LEU:CD2	2.46	0.42
1:A:24:LEU:N	1:A:24:LEU:HD23	2.34	0.41
2:D:60:LYS:HE2	4:D:902:CTP:O2	2.20	0.41
1:A:45:ALA:HB2	1:A:99:VAL:HG11	2.02	0.41
1:A:122:VAL:HA	1:A:123:PRO:HD3	1.90	0.41
2:B:7:LEU:HB3	2:B:8:GLN:H	1.54	0.41
1:C:215:ILE:N	1:C:215:ILE:CD1	2.82	0.41
1:A:270:VAL:HG13	1:A:271:ASP:H	1.84	0.41
1:C:270:VAL:CG1	1:C:271:ASP:N	2.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:TYR:CG	1:A:218:VAL:HG21	2.55	0.41
2:B:125:PHE:HA	2:B:137:LYS:O	2.21	0.41
1:C:24:LEU:HD13	1:C:143:PHE:HA	2.02	0.41
1:C:291:ASN:HD22	1:C:291:ASN:HA	1.71	0.41
2:D:78:ALA:HB1	2:D:81:ALA:HB2	2.02	0.41
1:C:114:LEU:C	1:C:114:LEU:HD23	2.46	0.41
1:C:227:MET:HE3	1:C:227:MET:HB3	1.84	0.41
1:A:306:ARG:NH2	1:A:307:ASP:HB2	2.31	0.41
2:B:41:ARG:HH11	2:B:41:ARG:CG	2.34	0.41
1:A:174:GLN:HE21	1:A:198:ILE:HD13	1.85	0.41
2:B:17:VAL:HG22	2:B:60:LYS:HB2	2.04	0.41
2:B:2:THR:HB	4:B:901:CTP:O2'	2.21	0.40
2:B:39:ASP:HA	2:D:47:ASN:HD21	1.85	0.40
2:D:17:VAL:HG11	4:D:902:CTP:H1'	2.04	0.40
1:A:246:GLN:C	1:A:247:PHE:CD1	2.99	0.40
1:C:232:LYS:NZ	1:C:232:LYS:HB2	2.36	0.40
1:A:301:ALA:HB1	1:A:308:LEU:HD11	2.02	0.40
2:B:129:LYS:HB3	2:B:129:LYS:HE2	1.85	0.40
1:C:81:LEU:HD23	1:C:86:GLU:OE1	2.21	0.40
2:D:151:LEU:O	2:D:152:ALA:C	2.64	0.40
2:B:50:SER:C	2:B:52:GLU:H	2.30	0.40
1:C:302:LEU:HA	1:C:302:LEU:HD23	1.91	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	308/310 (99%)	287 (93%)	15 (5%)	6 (2%)	6	4
1	C	308/310 (99%)	287 (93%)	17 (6%)	4 (1%)	9	8
2	B	150/153 (98%)	113 (75%)	28 (19%)	9 (6%)	1	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	150/153 (98%)	124 (83%)	19 (13%)	7 (5%)	2	0
All	All	916/926 (99%)	811 (88%)	79 (9%)	26 (3%)	4	2

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	ASP
1	A	270	VAL
2	B	89	TYR
2	B	105	ASN
2	B	133	ASP
1	C	75	ASP
1	C	270	VAL
2	D	23	ALA
2	D	53	MET
1	A	79	THR
2	B	6	LYS
2	B	53	MET
1	C	84	LYS
2	D	26	GLY
1	A	83	LYS
2	D	27	PHE
1	A	78	ASN
2	B	132	ASN
1	C	309	VAL
2	D	13	LYS
2	D	47	ASN
1	A	85	GLY
2	B	79	PRO
2	B	134	ILE
2	B	22	PRO
2	D	22	PRO

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	261/261 (100%)	244 (94%)	17 (6%)	15	18
1	C	261/261 (100%)	250 (96%)	11 (4%)	26	36
2	B	136/137 (99%)	122 (90%)	14 (10%)	7	7
2	D	136/137 (99%)	125 (92%)	11 (8%)	11	12
All	All	794/796 (100%)	741 (93%)	53 (7%)	15	17

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	PHE
1	A	65	ARG
1	A	116	THR
1	A	124	VAL
1	A	140	LEU
1	A	151	ARG
1	A	215	ILE
1	A	231	GLN
1	A	233	GLU
1	A	236	ASP
1	A	243	VAL
1	A	244	LYS
1	A	272	GLU
1	A	285	TYR
1	A	293	ILE
1	A	307	ASP
1	A	308	LEU
2	B	2	THR
2	B	12	ILE
2	B	16	THR
2	B	19	ASP
2	B	31	SER
2	B	37	GLU
2	B	59	ILE
2	B	60	LYS
2	B	62	GLU
2	B	63	ASN
2	B	85	ARG
2	B	100	PRO
2	B	105	ASN
2	B	146	SER
1	C	37	GLU
1	C	59	PHE

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Mol	Chain	Res	Type
1	C	74	SER
1	C	81	LEU
1	C	140	LEU
1	C	198	ILE
1	C	232	LYS
1	C	246	GLN
1	C	250	ARG
1	C	272	GLU
1	C	285	TYR
2	D	6	LYS
2	D	8	GLN
2	D	10	GLU
2	D	12	ILE
2	D	18	ILE
2	D	25	ILE
2	D	52	GLU
2	D	68	GLU
2	D	80	GLN
2	D	96	ARG
2	D	101	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	21	ASN
1	A	78	ASN
1	A	137	GLN
1	A	156	HIS
1	A	174	GLN
1	A	212	HIS
1	A	231	GLN
1	A	246	GLN
1	A	255	HIS
1	A	256	ASN
1	A	291	ASN
1	A	305	ASN
2	B	3	HIS
2	B	24	GLN
2	B	40	GLN
2	B	63	ASN
2	B	80	GLN

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Mol	Chain	Res	Type
2	B	84	ASN
2	B	147	HIS
2	B	148	ASN
2	B	153	ASN
1	C	13	ASN
1	C	21	ASN
1	C	33	ASN
1	C	156	HIS
1	C	246	GLN
1	C	291	ASN
1	C	297	GLN
2	D	8	GLN
2	D	20	HIS
2	D	63	ASN
2	D	70	GLN
2	D	73	GLN
2	D	80	GLN
2	D	105	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
4	CTP	D	902	-	29,30,30	1.58	5 (17%)	43,47,47	1.18	5 (11%)
4	CTP	B	901	-	29,30,30	1.58	5 (17%)	43,47,47	1.30	6 (13%)

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
4	CTP	D	902	-	-	4/22/38/38	0/2/2/2
4	CTP	B	901	-	-	3/22/38/38	0/2/2/2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	901	CTP	PG-O1G	3.57	1.61	1.50
4	D	902	CTP	PG-O1G	3.56	1.61	1.50
4	D	902	CTP	PA-O1A	3.10	1.61	1.50
4	B	901	CTP	PA-O1A	3.08	1.61	1.50
4	B	901	CTP	C4-N3	3.07	1.40	1.34
4	B	901	CTP	PB-O1B	3.07	1.61	1.50
4	D	902	CTP	PB-O1B	3.00	1.61	1.50
4	D	902	CTP	C4-N3	2.99	1.40	1.34
4	D	902	CTP	C2-N3	2.14	1.40	1.36
4	B	901	CTP	C2-N3	2.04	1.40	1.36

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	901	CTP	O2B-PB-O3A	3.51	116.77	107.27
4	B	901	CTP	O4'-C1'-C2'	-3.27	99.63	106.62
4	D	902	CTP	O2B-PB-O3A	2.48	113.99	107.27
4	D	902	CTP	O4'-C1'-N1	2.48	113.98	108.36
4	B	901	CTP	C4'-O4'-C1'	-2.44	104.08	109.47
4	B	901	CTP	O4'-C1'-N1	2.31	113.60	108.36
4	B	901	CTP	O3G-PG-O3B	2.15	111.84	104.64
4	B	901	CTP	O3B-PB-O1B	-2.14	104.28	110.70
4	D	902	CTP	O3G-PG-O3B	2.09	111.63	104.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	902	CTP	O3B-PB-O1B	-2.07	104.46	110.70
4	D	902	CTP	O3A-PB-O1B	-2.01	104.66	110.70

There are no chirality outliers.

All (7) torsion outliers are listed below:

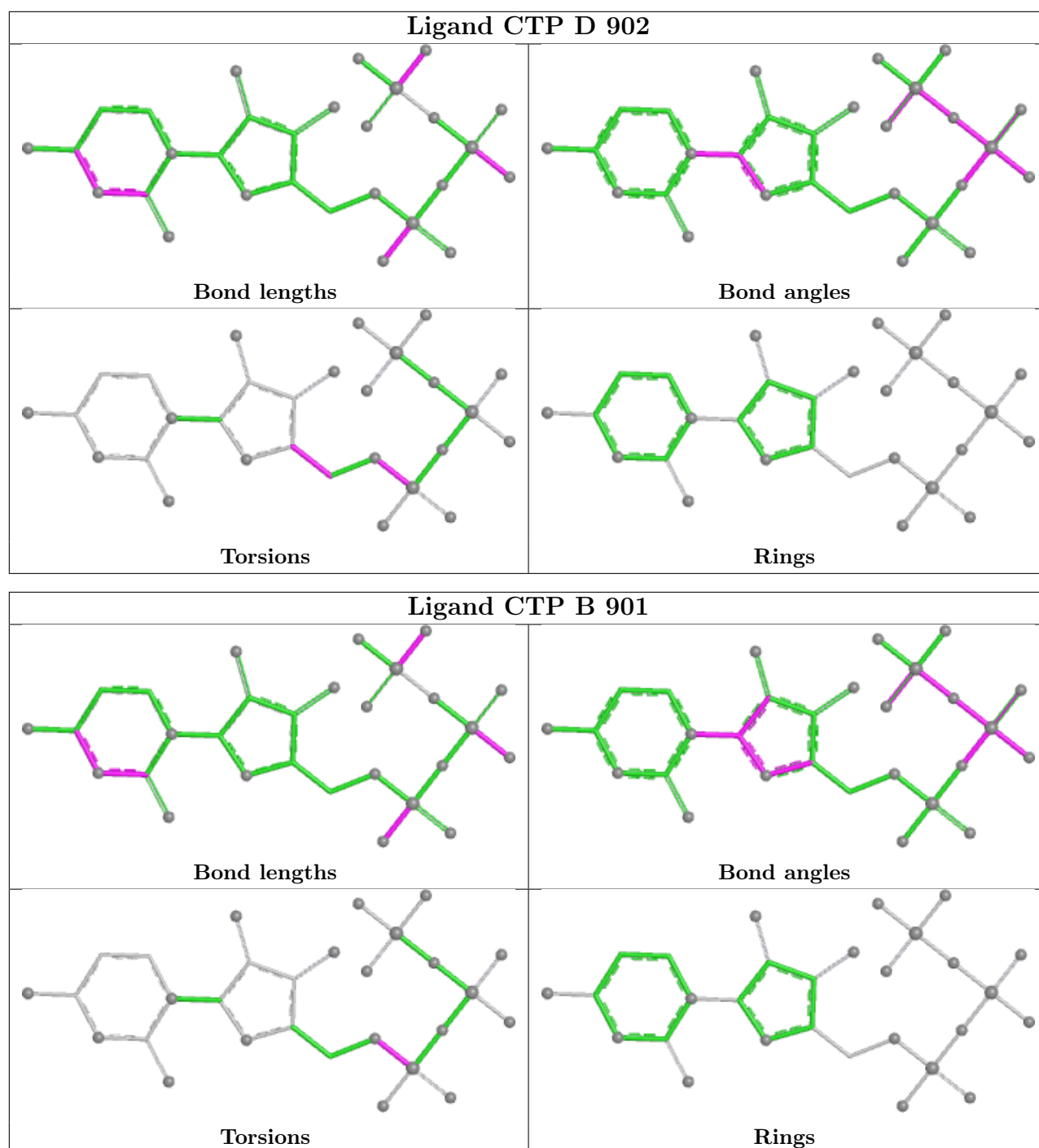
Mol	Chain	Res	Type	Atoms
4	B	901	CTP	C5'-O5'-PA-O1A
4	B	901	CTP	C5'-O5'-PA-O2A
4	B	901	CTP	C5'-O5'-PA-O3A
4	D	902	CTP	C5'-O5'-PA-O1A
4	D	902	CTP	C5'-O5'-PA-O2A
4	D	902	CTP	C5'-O5'-PA-O3A
4	D	902	CTP	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	902	CTP	8	0
4	B	901	CTP	7	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	310/310 (100%)	-0.19	13 (4%) 40 37	20, 34, 70, 132	0
1	C	310/310 (100%)	-0.38	8 (2%) 57 54	15, 29, 75, 122	0
2	B	152/153 (99%)	1.78	71 (46%) 0 0	23, 78, 147, 159	0
2	D	152/153 (99%)	0.93	30 (19%) 3 2	22, 60, 126, 152	0
All	All	924/926 (99%)	0.25	122 (13%) 7 5	15, 38, 111, 159	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	7	LEU	6.4
2	B	11	ALA	6.3
2	D	12	ILE	5.9
2	D	9	VAL	5.9
2	B	12	ILE	5.8
1	C	81	LEU	5.4
2	B	131	ALA	5.3
1	A	81	LEU	4.9
2	B	2	THR	4.7
2	B	58	LEU	4.5
2	B	9	VAL	4.5
2	D	6	LYS	4.5
1	C	79	THR	4.4
2	B	89	TYR	4.4
1	A	309	VAL	4.4
2	B	17	VAL	4.4
2	B	61	ILE	4.4
2	D	7	LEU	4.2
2	B	18	ILE	4.1
2	B	99	LEU	3.9
2	B	97	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	82	GLY	3.8
1	A	80	SER	3.7
2	B	43	THR	3.7
2	D	44	ILE	3.6
2	B	85	ARG	3.5
2	D	53	MET	3.5
2	B	44	ILE	3.5
2	D	46	LEU	3.5
2	B	86	ILE	3.5
1	A	310	LEU	3.5
2	D	11	ALA	3.4
1	A	77	ALA	3.4
2	B	21	ILE	3.4
1	C	80	SER	3.3
2	B	74	LEU	3.3
2	B	100	PRO	3.3
1	A	76	SER	3.3
2	D	13	LYS	3.3
2	D	47	ASN	3.2
2	B	78	ALA	3.2
2	D	3	HIS	3.2
2	B	71	VAL	3.2
2	D	4	ASP	3.2
1	A	308	LEU	3.2
2	B	132	ASN	3.1
2	D	2	THR	3.1
2	D	45	GLY	3.1
2	D	48	LEU	3.1
1	C	82	GLY	3.1
2	B	83	VAL	3.1
2	D	15	GLY	3.0
2	B	64	THR	3.0
2	B	93	GLY	3.0
1	A	247	PHE	3.0
2	D	89	TYR	3.0
2	B	8	GLN	3.0
2	B	60	LYS	3.0
2	B	92	VAL	2.9
2	B	19	ASP	2.9
2	D	54	GLY	2.9
2	B	75	ALA	2.9
2	B	3	HIS	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	38	THR	2.9
2	B	79	PRO	2.9
1	A	270	VAL	2.9
1	C	76	SER	2.9
2	D	91	VAL	2.9
2	B	134	ILE	2.9
2	B	81	ALA	2.8
2	B	39	ASP	2.8
2	D	49	PRO	2.8
2	B	95	SER	2.8
2	B	41	ARG	2.8
2	B	96	ARG	2.7
2	D	58	LEU	2.7
2	B	53	MET	2.7
1	A	79	THR	2.6
2	B	94	LYS	2.6
2	B	10	GLU	2.5
2	B	91	VAL	2.5
2	B	66	LEU	2.5
1	A	307	ASP	2.5
1	C	78	ASN	2.5
2	B	5	ASN	2.5
2	B	6	LYS	2.5
2	B	68	GLU	2.5
2	D	23	ALA	2.5
2	B	129	LYS	2.4
2	B	29	LEU	2.4
2	B	35	LEU	2.4
2	B	130	ARG	2.4
2	B	16	THR	2.4
2	B	127	VAL	2.4
2	B	135	ALA	2.3
2	D	43	THR	2.3
1	C	235	LEU	2.3
2	B	59	ILE	2.3
2	B	69	ASP	2.3
2	B	128	ARG	2.3
2	B	23	ALA	2.3
2	B	50	SER	2.3
2	B	42	ILE	2.3
1	A	75	ASP	2.2
2	B	57	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
2	D	22	PRO	2.2
1	C	270	VAL	2.2
2	D	5	ASN	2.2
2	B	80	GLN	2.2
2	B	126	ALA	2.2
2	B	55	ARG	2.1
2	D	18	ILE	2.1
2	B	15	GLY	2.1
2	B	40	GLN	2.1
2	B	84	ASN	2.1
2	B	45	GLY	2.1
2	D	92	VAL	2.1
2	D	14	ARG	2.1
2	D	8	GLN	2.0
2	B	46	LEU	2.0
2	D	86	ILE	2.0
2	B	72	ASP	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 oligosaccharides 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.

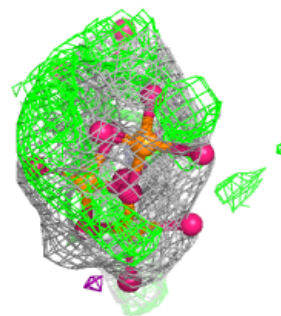
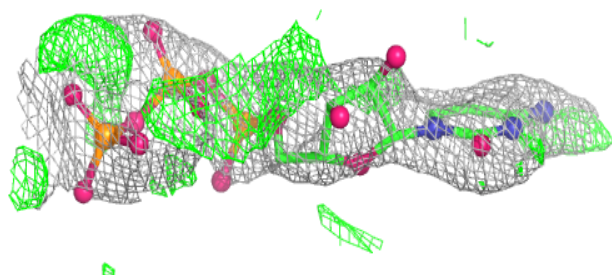
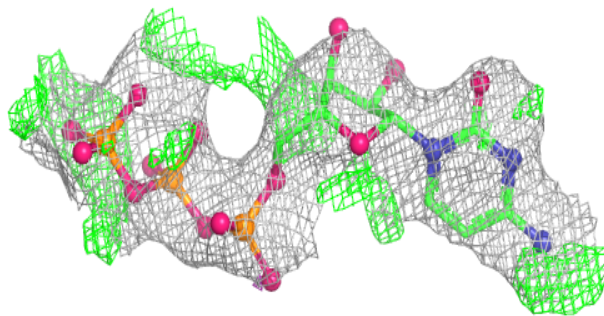
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CTP	B	901	29/29	0.68	0.15	30,41,59,66	29
4	CTP	D	902	29/29	0.81	0.12	35,47,66,71	29
3	ZN	B	154	1/1	0.99	0.02	32,32,32,32	0
3	ZN	D	154	1/1	1.00	0.04	29,29,29,29	0

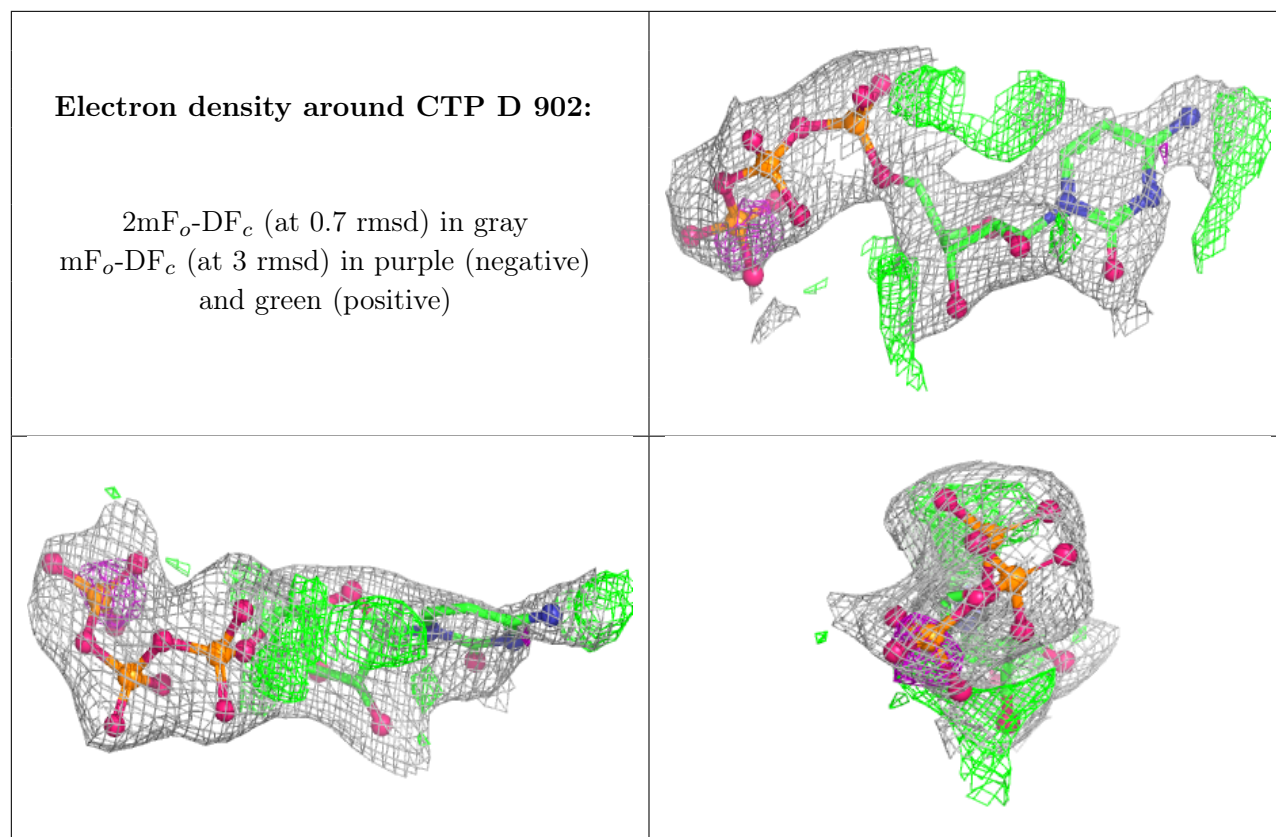
The following is a graphical depiction of the model fit to experimental electron density of all

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 CTP B 901:

$2mF_o-DF_c$ (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.