



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 19, 2021 – 06:08 PM JST

PDB ID : 7E7L
Title : The crystal structure of arylacetate decarboxylase from Olsenella scatoligenes.
Authors : Lu, Q.; Duan, Y.; Zhang, Y.; Yuchi, Z.
Deposited on : 2021-02-26
Resolution : 3.53 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 : 2.22
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) : 2.22

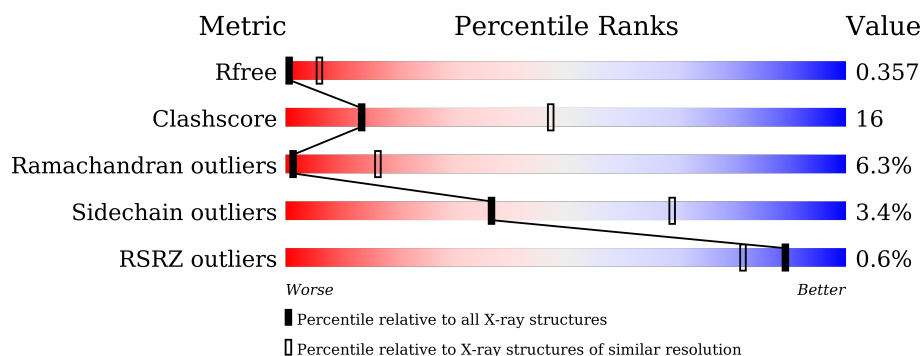
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.53 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	1028 (3.60-3.48)
Clashscore	141614	1109 (3.60-3.48)
Ramachandran outliers	138981	1073 (3.60-3.48)
Sidechain outliers	138945	1074 (3.60-3.48)
RSRZ outliers	127900	1079 (3.62-3.46)

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	808	<div> <div></div> <div>66% 26% • 5%</div> </div>
1	B	808	<div> <div>%</div> <div>56% 34% • 5%</div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 11337 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.

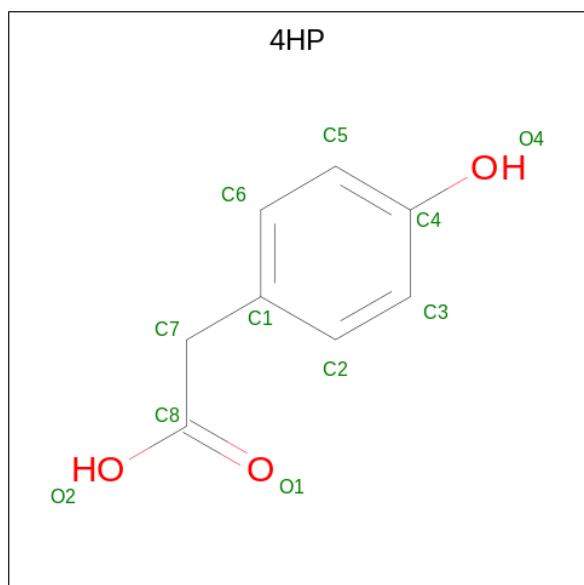
- Molecule 1 is a protein called Hydroxyphenylacetic acid decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	770	Total	C	N	O	S	0	0	0
			5563	3551	921	1054	37			
1	B	766	Total	C	N	O	S	0	0	0
			5752	3662	955	1094	41			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP A0A100YWM3
A	0	ASN	-	expression tag	UNP A0A100YWM3
B	-1	SER	-	expression tag	UNP A0A100YWM3
B	0	ASN	-	expression tag	UNP A0A100YWM3

- Molecule 2 is 4-HYDROXYPHENYLACETATE (three-letter code: 4HP) (formula: $C_8H_8O_3$) (labeled as "Ligand of Interest" by depositor).

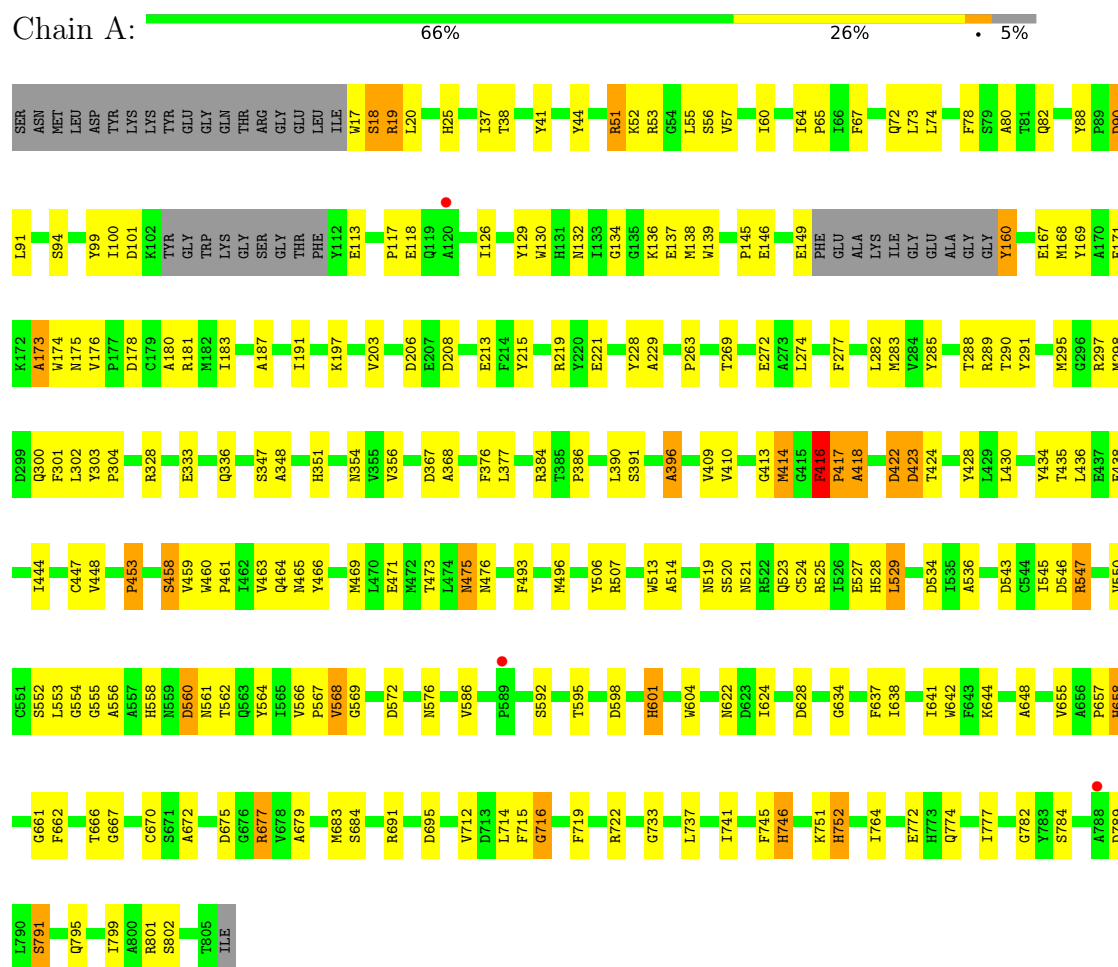


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			11	8	3		
2	B	1	Total	C	O	0	0
			11	8	3		

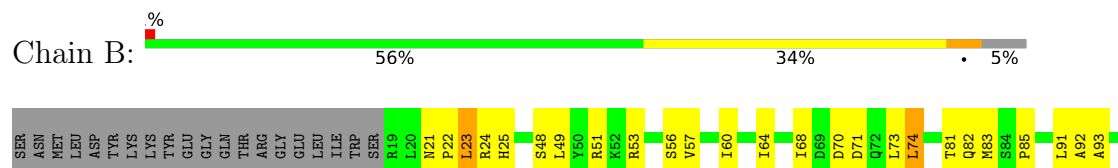
3 Residue-property plots

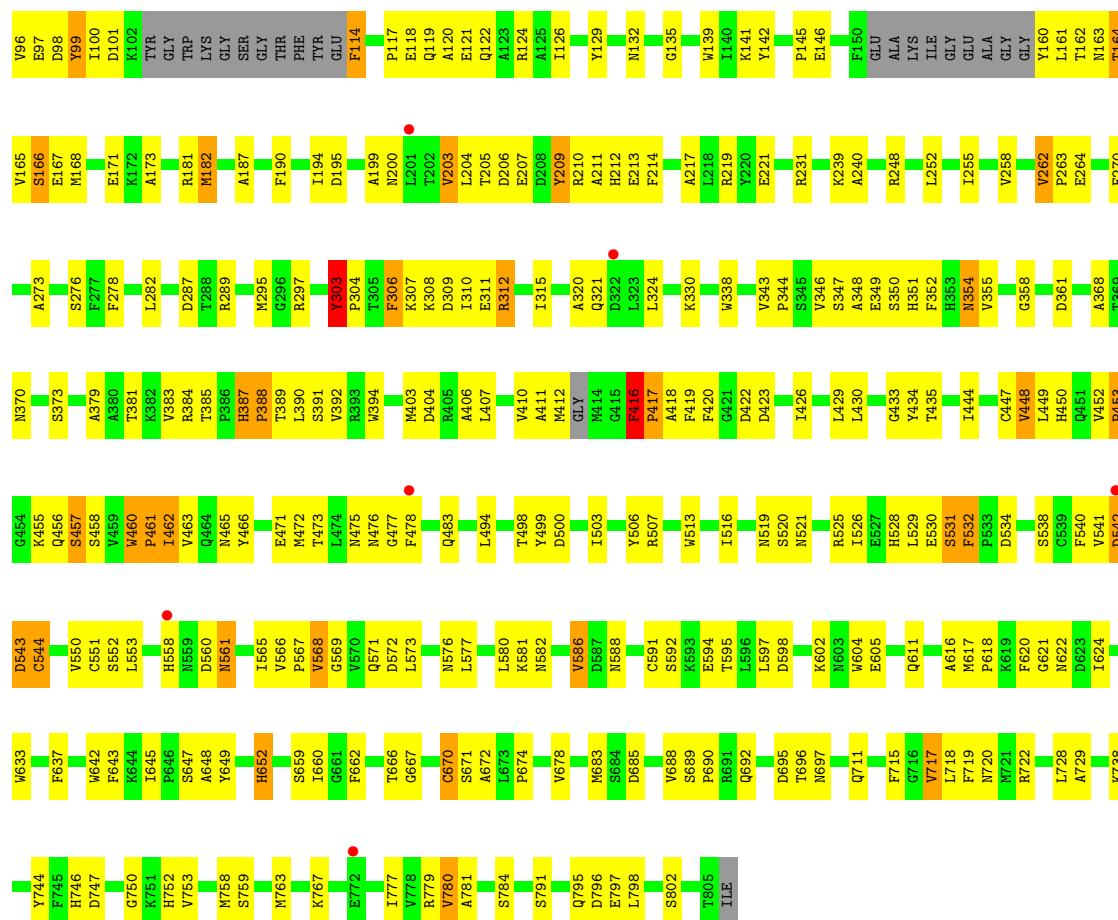
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Hydroxyphenylacetic acid decarboxylase



• Molecule 1: Hydroxyphenylacetic acid decarboxylase





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	85.95Å 225.55Å 234.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.59 – 3.53 39.38 – 3.50	Depositor EDS
% Data completeness (in resolution range)	93.4 (37.59-3.53) 92.3 (39.38-3.50)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.14_3247	Depositor
R, R_{free}	0.290 , 0.358 0.290 , 0.357	Depositor DCC
R_{free} test set	2000 reflections (6.91%)	wwPDB-VP
Wilson B-factor (Å ²)	65.2	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 32.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	11337	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.57% 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: 4HP

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	0.25	0/5713	0.44	0/7827
1	B	0.29	0/5896	0.52	1/8044 (0.0%)
All	All	0.27	0/11609	0.49	1/15871 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	4
All	All	0	5

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	99	TYR	CA-CB-CG	-6.64	100.78	113.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	416	PHE	Peptide
1	B	121	GLU	Peptide
1	B	23	LEU	Peptide
1	B	303	TYR	Peptide
1	B	416	PHE	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5563	0	4723	136	1
1	B	5752	0	5182	206	1
2	A	11	0	7	2	0
2	B	11	0	7	3	0
All	All	11337	0	9919	341	1

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 16.

All (341) 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:B:85:PRO:HG3	1:B:114:PHE:HZ	1.30	0.93
1:A:197:LYS:HZ1	1:A:546:ASP:HA	1.37	0.90
1:B:525:ARG:NH2	1:B:552:SER:O	2.10	0.84
1:B:85:PRO:HG3	1:B:114:PHE:CZ	2.11	0.84
1:B:351:HIS:HB2	1:B:387:HIS:HD2	1.43	0.82
1:A:422:ASP:O	1:A:424:THR:N	2.15	0.80
1:B:465:ASN:HB2	1:B:666:THR:HG21	1.65	0.79
1:B:270:PHE:N	1:B:309:ASP:OD2	2.17	0.78
1:B:262:VAL:HG23	1:B:263:PRO:HD3	1.66	0.77
1:B:383:VAL:HG13	1:B:385:THR:H	1.48	0.77
1:B:23:LEU:HB3	1:B:24:ARG:HD2	1.68	0.76
1:A:175:ASN:HD21	1:A:458:SER:HA	1.52	0.74
1:B:163:ASN:HB3	1:B:463:VAL:HG22	1.68	0.73
1:A:229:ALA:HB3	1:A:263:PRO:HG3	1.71	0.73
1:B:351:HIS:HB2	1:B:387:HIS:CD2	2.24	0.73
1:B:71:ASP:O	1:B:248:ARG:NH2	2.22	0.72
1:A:386:PRO:HB3	1:A:777:ILE:HG23	1.71	0.71
1:B:473:THR:HG21	1:B:506:TYR:HA	1.70	0.71
1:A:464:GLN:NE2	1:A:513:TRP:O	2.21	0.71
1:B:24:ARG:HA	1:B:24:ARG:NE	2.05	0.71
1:A:641:ILE:HA	1:A:644:LYS:HE2	1.72	0.70
1:B:416:PHE:HE2	1:B:784:SER:HG	1.38	0.70
1:B:118:GLU:O	1:B:120:ALA:N	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:572:ASP:O	1:A:576:ASN:ND2	2.25	0.69
1:B:541:VAL:HG11	1:B:551:CYS:HB3	1.74	0.68
1:B:73:LEU:HA	1:B:255:ILE:HD11	1.76	0.68
1:B:471:GLU:O	1:B:475:ASN:ND2	2.28	0.67
1:B:670:CYS:SG	1:B:671:SER:N	2.69	0.66
1:B:139:TRP:CD1	1:B:168:MET:HG2	2.31	0.66
1:A:604:TRP:NE1	1:A:677:ARG:O	2.23	0.65
1:B:411:ALA:HB2	1:B:728:LEU:HD23	1.79	0.65
1:B:572:ASP:O	1:B:576:ASN:ND2	2.26	0.65
1:B:450:HIS:O	1:B:450:HIS:ND1	2.29	0.64
1:B:391:SER:HG	1:B:420:PHE:HE1	1.46	0.63
1:B:96:VAL:O	1:B:98:ASP:N	2.29	0.63
1:A:94:SER:N	1:A:137:GLU:OE1	2.30	0.63
1:A:191:ILE:HG23	1:A:219:ARG:HG3	1.81	0.63
1:B:722:ARG:NH2	1:B:758:MET:O	2.30	0.63
1:B:719:PHE:HD2	1:B:753:VAL:HG23	1.64	0.62
1:B:448:VAL:HG21	1:B:718:LEU:HB2	1.82	0.62
1:B:767:LYS:NZ	1:B:796:ASP:OD1	2.24	0.62
1:A:410:VAL:HB	1:A:417:PRO:HD2	1.83	0.61
1:A:764:ILE:HG12	1:A:799:ILE:HD12	1.82	0.60
1:B:534:ASP:O	1:B:538:SER:OG	2.19	0.60
1:A:572:ASP:OD1	1:A:684:SER:OG	2.18	0.60
1:B:74:LEU:HD23	1:B:330:LYS:HD3	1.82	0.60
1:B:494:LEU:HD11	1:B:597:LEU:HD22	1.83	0.60
1:B:692:GLN:NE2	1:B:797:GLU:OE2	2.30	0.60
1:B:387:HIS:H	1:B:388:PRO:CD	2.14	0.60
1:B:529:LEU:HB3	1:B:553:LEU:HD21	1.83	0.60
1:B:310:ILE:HD12	1:B:311:GLU:N	2.17	0.60
1:B:262:VAL:HB	1:B:276:SER:HB2	1.84	0.59
1:B:370:ASN:O	1:B:373:SER:OG	2.19	0.59
1:B:571:GLN:NE2	1:B:689:SER:O	2.35	0.59
1:B:166:SER:O	2:B:901:4HP:H3	2.03	0.59
1:A:215:TYR:OH	1:A:545:ILE:O	2.20	0.58
1:A:471:GLU:O	1:A:475:ASN:ND2	2.28	0.58
1:B:387:HIS:ND1	1:B:388:PRO:HD3	2.18	0.58
1:B:347:SER:O	1:B:349:GLU:N	2.36	0.58
1:B:387:HIS:O	1:B:389:THR:N	2.37	0.58
1:A:416:PHE:O	1:A:418:ALA:N	2.37	0.58
1:B:161:LEU:HD22	1:B:513:TRP:CZ2	2.38	0.58
1:B:586:VAL:HG23	1:B:588:ASN:H	1.69	0.58
1:A:461:PRO:HB3	1:A:564:TYR:CZ	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:455:LYS:NZ	1:B:542:ASP:OD2	2.24	0.58
1:A:228:TYR:HE2	1:A:282:LEU:HD23	1.69	0.57
1:B:779:ARG:O	1:B:781:ALA:N	2.37	0.57
1:B:383:VAL:HG13	1:B:385:THR:N	2.18	0.57
1:B:667:GLY:HA2	1:B:683:MET:HG2	1.85	0.57
1:A:376:PHE:HB3	1:A:390:LEU:HD11	1.86	0.57
1:B:561:ASN:O	1:B:561:ASN:ND2	2.38	0.57
1:B:695:ASP:OD2	1:B:802:SER:OG	2.20	0.57
1:B:171:GLU:HB2	1:B:289:ARG:O	2.05	0.57
1:B:394:TRP:N	1:B:420:PHE:O	2.37	0.56
1:B:525:ARG:HG2	1:B:526:ILE:HD13	1.86	0.56
1:A:139:TRP:CD1	1:A:168:MET:HB3	2.40	0.56
1:A:173:ALA:O	1:A:175:ASN:ND2	2.38	0.56
1:B:538:SER:HB3	1:B:544:CYS:SG	2.44	0.56
1:B:390:LEU:O	1:B:418:ALA:N	2.36	0.56
1:B:419:PHE:HB2	1:B:753:VAL:HG12	1.88	0.56
1:A:64:ILE:HG12	1:A:65:PRO:HD2	1.87	0.56
1:A:328:ARG:HH22	1:A:416:PHE:HE2	1.52	0.56
1:B:308:LYS:O	1:B:312:ARG:HB3	2.06	0.56
1:A:466:TYR:HH	1:A:642:TRP:HE1	1.54	0.56
1:B:163:ASN:O	1:B:165:VAL:N	2.39	0.55
1:A:413:GLY:O	1:A:414:MET:HG2	2.07	0.55
1:B:711:GLN:HB3	1:B:717:VAL:HG21	1.88	0.55
1:B:210:ARG:O	1:B:212:HIS:N	2.40	0.55
1:A:534:ASP:OD1	1:A:534:ASP:N	2.40	0.54
1:A:567:PRO:O	1:A:569:GLY:N	2.41	0.54
1:A:461:PRO:HG2	2:A:901:4HP:C8	2.37	0.54
1:B:307:LYS:O	1:B:311:GLU:HB2	2.07	0.54
1:A:126:ILE:HG23	1:A:130:TRP:HD1	1.73	0.54
1:B:529:LEU:HB3	1:B:553:LEU:CD2	2.38	0.54
1:A:386:PRO:HA	1:A:416:PHE:HZ	1.73	0.54
1:B:142:TYR:HD1	1:B:145:PRO:HG2	1.71	0.54
1:B:542:ASP:OD1	1:B:543:ASP:N	2.41	0.54
1:A:180:ALA:HA	1:A:183:ILE:HG22	1.90	0.53
1:B:56:SER:O	1:B:60:ILE:HG13	2.08	0.53
1:A:430:LEU:HD21	1:A:436:LEU:HA	1.91	0.53
1:A:745:PHE:O	1:A:746:HIS:HB2	2.08	0.53
1:B:416:PHE:HE2	1:B:784:SER:OG	1.92	0.53
1:B:64:ILE:O	1:B:231:ARG:NH2	2.32	0.53
1:B:513:TRP:CE3	1:B:516:ILE:HD11	2.43	0.53
1:A:568:VAL:HG13	1:A:569:GLY:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:475:ASN:O	1:B:478:PHE:N	2.31	0.53
1:B:457:SER:OG	1:B:457:SER:O	2.27	0.52
1:A:37:ILE:HG12	1:A:60:ILE:HD11	1.90	0.52
1:A:51:ARG:HB2	1:A:213:GLU:OE1	2.10	0.52
1:A:91:LEU:HD21	1:A:169:TYR:O	2.09	0.52
1:A:466:TYR:O	1:A:506:TYR:OH	2.28	0.52
1:B:214:PHE:CD1	1:B:550:VAL:HG12	2.44	0.52
1:B:142:TYR:HB2	1:B:145:PRO:HG2	1.91	0.52
1:B:182:MET:SD	1:B:182:MET:N	2.78	0.52
1:B:306:PHE:O	1:B:310:ILE:HG13	2.10	0.52
1:A:17:TRP:O	1:A:19:ARG:N	2.41	0.52
1:B:534:ASP:OD2	1:B:552:SER:OG	2.28	0.52
1:B:404:ASP:OD1	1:B:738:LYS:NZ	2.28	0.52
1:A:269:THR:H	1:A:272:GLU:HG2	1.75	0.51
1:A:197:LYS:HG2	1:A:215:TYR:CZ	2.46	0.51
1:A:465:ASN:HB2	1:A:666:THR:HG21	1.91	0.51
1:B:262:VAL:CG2	1:B:263:PRO:HD3	2.38	0.51
1:B:142:TYR:CD1	1:B:145:PRO:HG2	2.44	0.51
1:B:381:THR:OG1	1:B:412:MET:SD	2.59	0.51
1:A:298:MET:HA	1:A:301:PHE:CE1	2.45	0.51
1:B:780:VAL:HA	1:B:798:LEU:HD21	1.93	0.51
1:A:466:TYR:HD1	1:A:567:PRO:HB3	1.76	0.51
1:B:695:ASP:C	1:B:697:ASN:H	2.15	0.51
1:B:297:ARG:NH2	1:B:358:GLY:O	2.44	0.50
1:A:288:THR:O	1:A:290:THR:N	2.43	0.50
1:A:463:VAL:HG12	1:A:566:VAL:CG1	2.41	0.50
1:A:88:TYR:OH	1:A:285:TYR:O	2.19	0.50
1:A:134:GLY:O	1:A:138:MET:N	2.25	0.50
1:A:178:ASP:C	1:A:180:ALA:H	2.15	0.50
1:A:126:ILE:HG23	1:A:130:TRP:CD1	2.47	0.50
1:B:321:GLN:HG3	1:B:379:ALA:HB2	1.93	0.50
1:A:197:LYS:NZ	1:A:215:TYR:OH	2.36	0.50
1:A:514:ALA:HA	1:A:642:TRP:CH2	2.47	0.50
1:B:338:TRP:CE3	1:B:346:VAL:HG21	2.47	0.50
1:B:81:THR:O	1:B:83:MET:N	2.45	0.49
1:B:392:VAL:N	1:B:418:ALA:O	2.42	0.49
1:B:122:GLN:O	1:B:126:ILE:N	2.45	0.49
1:B:161:LEU:HD21	1:B:472:MET:HE3	1.94	0.49
1:A:171:GLU:O	2:A:901:4HP:H3	2.12	0.49
1:A:592:SER:N	1:A:595:THR:OG1	2.46	0.49
1:B:164:THR:O	1:B:167:GLU:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:ALA:O	1:A:191:ILE:HG13	2.12	0.49
1:B:57:VAL:HG11	1:B:287:ASP:HB2	1.93	0.49
1:B:258:VAL:O	1:B:262:VAL:HG13	2.12	0.49
1:A:197:LYS:NZ	1:A:545:ILE:O	2.46	0.49
1:A:430:LEU:HD11	1:A:436:LEU:HD13	1.94	0.49
1:A:461:PRO:HB3	1:A:564:TYR:CE1	2.47	0.49
1:B:99:TYR:HE1	1:B:124:ARG:HH22	1.54	0.48
1:B:531:SER:OG	1:B:532:PHE:N	2.43	0.48
1:A:167:GLU:OE2	1:A:520:SER:OG	2.31	0.48
1:B:310:ILE:HD12	1:B:311:GLU:H	1.77	0.48
1:B:688:VAL:HG23	1:B:719:PHE:CD1	2.48	0.48
1:B:51:ARG:NH2	1:B:213:GLU:OE2	2.43	0.48
1:A:354:ASN:ND2	1:A:444:ILE:HD11	2.29	0.48
1:A:719:PHE:H	1:A:752:HIS:CE1	2.32	0.48
1:B:162:THR:HG23	1:B:164:THR:OG1	2.14	0.48
1:A:274:LEU:HD13	1:A:302:LEU:HD21	1.96	0.48
1:A:695:ASP:OD2	1:A:802:SER:OG	2.32	0.48
1:B:320:ALA:O	1:B:324:LEU:HD13	2.13	0.48
1:B:463:VAL:HG12	1:B:566:VAL:CG1	2.43	0.48
1:B:205:THR:HB	1:B:209:TYR:HB2	1.95	0.48
1:A:149:GLU:OE2	1:A:149:GLU:HA	2.13	0.48
1:A:598:ASP:HA	1:A:601:HIS:HB2	1.95	0.48
1:A:41:TYR:CD2	1:A:52:LYS:HD2	2.49	0.47
1:A:396:ALA:HB1	1:B:747:ASP:HA	1.96	0.47
1:B:452:VAL:HG21	1:B:455:LYS:HG3	1.96	0.47
1:A:554:GLY:O	1:A:556:ALA:N	2.47	0.47
1:B:187:ALA:HB3	1:B:264:GLU:HA	1.96	0.47
1:B:718:LEU:HD12	1:B:752:HIS:HE1	1.79	0.47
1:A:469:MET:O	1:A:473:THR:HG22	2.14	0.47
1:B:278:PHE:O	1:B:282:LEU:HB2	2.15	0.47
1:B:452:VAL:CG2	1:B:455:LYS:HG3	2.44	0.47
1:B:494:LEU:HD23	1:B:594:GLU:HG3	1.95	0.47
1:B:791:SER:O	1:B:795:GLN:HG2	2.14	0.47
1:A:435:THR:HG23	1:A:438:GLU:H	1.80	0.47
1:B:190:PHE:O	1:B:194:ILE:HG12	2.15	0.47
1:B:407:LEU:O	1:B:410:VAL:HG22	2.14	0.47
1:B:205:THR:C	1:B:207:GLU:H	2.18	0.47
1:B:350:SER:O	1:B:351:HIS:ND1	2.48	0.47
1:B:406:ALA:O	1:B:417:PRO:HG2	2.14	0.47
1:A:67:PHE:HE1	1:A:80:ALA:O	1.97	0.47
1:B:461:PRO:HG3	2:B:901:4HP:C2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:573:LEU:O	1:B:577:LEU:N	2.34	0.47
1:B:195:ASP:CG	1:B:219:ARG:HH12	2.18	0.46
1:B:667:GLY:CA	1:B:683:MET:HG2	2.45	0.46
1:A:367:ASP:OD1	1:A:368:ALA:N	2.48	0.46
1:A:655:VAL:O	1:A:657:PRO:HD3	2.15	0.46
1:B:182:MET:HG3	1:B:273:ALA:HA	1.98	0.46
1:B:368:ALA:O	1:B:370:ASN:ND2	2.48	0.46
1:A:714:LEU:O	1:A:716:GLY:N	2.49	0.46
1:A:560:ASP:O	1:A:562:THR:N	2.47	0.46
1:B:352:PHE:CE2	1:B:447:CYS:HB2	2.51	0.46
1:B:541:VAL:O	1:B:543:ASP:N	2.46	0.46
1:A:38:THR:HG23	1:A:129:TYR:CD1	2.51	0.46
1:A:567:PRO:HD2	1:A:657:PRO:HA	1.97	0.46
1:A:447:CYS:SG	1:A:782:GLY:HA3	2.56	0.46
1:B:466:TYR:CE2	1:B:567:PRO:HB3	2.51	0.46
1:A:221:GLU:OE2	1:A:536:ALA:HB2	2.16	0.46
1:A:72:GLN:HG2	1:A:74:LEU:H	1.80	0.46
1:B:758:MET:SD	1:B:763:MET:HG3	2.56	0.46
1:A:463:VAL:HG11	1:A:662:PHE:CD2	2.51	0.45
1:B:598:ASP:O	1:B:602:LYS:HG2	2.15	0.45
1:B:96:VAL:C	1:B:98:ASP:N	2.70	0.45
1:B:620:PHE:C	1:B:622:ASN:H	2.20	0.45
1:A:90:ASP:OD1	1:A:90:ASP:N	2.49	0.45
1:B:394:TRP:HD1	1:B:403:MET:SD	2.38	0.45
1:B:498:THR:HG22	1:B:499:TYR:H	1.80	0.45
1:B:602:LYS:O	1:B:605:GLU:HG2	2.16	0.45
1:A:303:TYR:N	1:A:304:PRO:HD2	2.31	0.45
1:B:444:ILE:HB	1:B:449:LEU:O	2.16	0.45
1:A:737:LEU:O	1:A:741:ILE:HG22	2.16	0.45
1:B:671:SER:HB3	1:B:678:VAL:O	2.15	0.45
1:B:91:LEU:HD11	1:B:168:MET:O	2.16	0.45
1:B:338:TRP:HE3	1:B:346:VAL:HG21	1.82	0.45
1:A:139:TRP:HD1	1:A:168:MET:HB3	1.81	0.45
1:B:53:ARG:O	1:B:57:VAL:HG23	2.17	0.45
1:B:205:THR:O	1:B:207:GLU:N	2.50	0.45
1:A:160:TYR:CD1	1:A:666:THR:HG23	2.51	0.45
1:A:448:VAL:HG22	1:A:658:HIS:HB3	1.99	0.45
1:A:493:PHE:HA	1:A:496:MET:HG2	1.99	0.45
1:A:386:PRO:HA	1:A:416:PHE:CZ	2.50	0.45
1:A:507:ARG:HA	1:A:637:PHE:HZ	1.81	0.45
1:B:558:HIS:C	1:B:560:ASP:H	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:592:SER:N	1:B:595:THR:OG1	2.50	0.45
1:B:195:ASP:O	1:B:199:ALA:N	2.49	0.45
1:B:642:TRP:CE3	1:B:645:ILE:HD11	2.51	0.44
1:A:336:GLN:HB3	1:A:351:HIS:CE1	2.52	0.44
1:A:657:PRO:HD2	1:A:716:GLY:O	2.17	0.44
1:B:659:SER:O	1:B:662:PHE:HB2	2.17	0.44
1:B:688:VAL:HG23	1:B:719:PHE:HD1	1.82	0.44
1:A:44:TYR:CD1	1:A:55:LEU:HD23	2.52	0.44
1:A:347:SER:OG	1:A:348:ALA:N	2.50	0.44
1:A:136:LYS:HA	1:A:139:TRP:HB3	2.00	0.44
1:A:386:PRO:HB2	1:A:784:SER:O	2.17	0.44
1:B:387:HIS:HD1	1:B:388:PRO:HD3	1.80	0.44
1:B:604:TRP:CE3	1:B:611:GLN:HB2	2.53	0.44
1:B:719:PHE:CD2	1:B:753:VAL:HG23	2.48	0.44
1:A:543:ASP:O	1:A:547:ARG:HD3	2.18	0.44
1:B:647:SER:OG	1:B:648:ALA:N	2.50	0.44
1:A:423:ASP:HB2	1:A:745:PHE:CE1	2.54	0.43
1:A:377:LEU:HB2	1:A:409:VAL:HG21	2.01	0.43
1:B:460:TRP:CZ2	1:B:525:ARG:HA	2.53	0.43
1:B:618:PRO:HB3	1:B:624:ILE:HD12	2.00	0.43
1:B:93:ALA:O	1:B:96:VAL:HG12	2.18	0.43
1:B:449:LEU:HG	1:B:715:PHE:CE2	2.54	0.43
1:B:461:PRO:HG3	2:B:901:4HP:C3	2.47	0.43
1:B:503:ILE:HD11	1:B:633:TRP:CZ2	2.53	0.43
1:B:692:GLN:NE2	1:B:797:GLU:HG2	2.34	0.43
1:A:283:MET:HG2	1:A:536:ALA:HB1	2.00	0.43
1:A:459:VAL:HA	1:A:562:THR:O	2.19	0.43
1:B:565:ILE:HD12	1:B:642:TRP:CZ2	2.53	0.43
1:B:620:PHE:O	1:B:622:ASN:N	2.51	0.43
1:B:711:GLN:CD	1:B:717:VAL:HG11	2.38	0.43
1:A:53:ARG:HH12	1:A:90:ASP:HB3	1.84	0.43
1:A:297:ARG:NH2	1:A:300:GLN:HG2	2.33	0.43
1:A:634:GLY:O	1:A:638:ILE:HG13	2.19	0.43
1:B:453:PRO:O	1:B:455:LYS:N	2.49	0.43
1:B:475:ASN:O	1:B:477:GLY:N	2.52	0.43
1:B:387:HIS:H	1:B:388:PRO:HD3	1.81	0.43
1:A:176:VAL:O	1:A:453:PRO:HA	2.18	0.42
1:A:714:LEU:O	1:A:751:LYS:NZ	2.48	0.42
1:B:22:PRO:O	1:B:23:LEU:HD23	2.19	0.42
1:B:139:TRP:HD1	1:B:168:MET:HG2	1.82	0.42
1:B:205:THR:C	1:B:207:GLU:N	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:620:PHE:HD2	1:B:690:PRO:HA	1.84	0.42
1:A:277:PHE:HZ	1:A:295:MET:HB3	1.84	0.42
1:A:301:PHE:CE1	1:A:302:LEU:HD13	2.55	0.42
1:A:175:ASN:ND2	1:A:458:SER:HA	2.29	0.42
1:A:434:TYR:HE1	1:A:558:HIS:CG	2.37	0.42
1:B:48:SER:OG	1:B:213:GLU:OE1	2.24	0.42
1:A:624:ILE:N	1:A:628:ASP:OD2	2.52	0.42
1:B:126:ILE:O	1:B:129:TYR:N	2.52	0.42
1:B:310:ILE:HG22	1:B:315:ILE:O	2.18	0.42
1:B:343:VAL:N	1:B:344:PRO:HD2	2.34	0.42
1:B:463:VAL:HG12	1:B:566:VAL:HG13	2.01	0.42
1:B:643:PHE:HA	1:B:652:HIS:HD2	1.85	0.42
1:A:56:SER:O	1:A:60:ILE:HG13	2.19	0.42
1:A:722:ARG:NH1	1:A:801:ARG:O	2.52	0.42
1:B:240:ALA:HB2	1:B:252:LEU:HB3	2.01	0.42
1:B:383:VAL:HG22	1:B:384:ARG:H	1.84	0.42
1:B:429:LEU:HD23	1:B:452:VAL:HG13	2.02	0.42
1:B:507:ARG:HA	1:B:637:PHE:HZ	1.85	0.42
1:B:728:LEU:HB3	1:B:729:ALA:H	1.63	0.42
1:A:298:MET:HA	1:A:301:PHE:CZ	2.55	0.42
1:A:356:VAL:HA	1:A:391:SER:O	2.19	0.42
1:B:462:ILE:HD11	1:B:521:ASN:HB3	2.02	0.42
1:B:744:TYR:CZ	1:B:750:GLY:HA3	2.55	0.42
1:B:777:ILE:CG2	1:B:784:SER:HB3	2.50	0.42
1:A:733:GLY:O	1:A:737:LEU:HB2	2.20	0.42
1:B:49:LEU:HD22	1:B:530:GLU:HA	2.01	0.42
1:B:577:LEU:O	1:B:581:LYS:N	2.52	0.42
1:B:604:TRP:CD2	1:B:611:GLN:HB2	2.54	0.42
1:A:78:PHE:HB2	1:A:333:GLU:HB2	2.02	0.42
1:A:348:ALA:HB3	1:A:789:ASP:HB2	2.02	0.42
1:A:550:VAL:HG23	1:A:553:LEU:H	1.85	0.42
1:B:685:ASP:OD2	1:B:720:ASN:HB2	2.20	0.42
1:B:722:ARG:NH1	1:B:763:MET:SD	2.92	0.42
1:A:53:ARG:O	1:A:57:VAL:HG23	2.20	0.41
1:A:521:ASN:HA	1:A:524:CYS:HB3	2.02	0.41
1:B:70:ASP:HA	1:B:239:LYS:NZ	2.35	0.41
1:B:303:TYR:O	1:B:303:TYR:CG	2.73	0.41
1:B:465:ASN:HA	1:B:568:VAL:HG22	2.01	0.41
1:A:174:TRP:HB2	1:A:459:VAL:HG22	2.03	0.41
1:A:428:TYR:HB2	1:A:712:VAL:O	2.20	0.41
1:A:534:ASP:OD1	1:A:552:SER:OG	2.30	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:217:ALA:O	1:B:221:GLU:HG3	2.20	0.41
1:B:465:ASN:HA	1:B:568:VAL:CG2	2.51	0.41
1:A:37:ILE:CG1	1:A:60:ILE:HD11	2.50	0.41
1:A:527:GLU:C	1:A:529:LEU:H	2.23	0.41
1:B:99:TYR:HD1	1:B:99:TYR:HA	1.39	0.41
1:B:450:HIS:O	1:B:715:PHE:HE1	2.04	0.41
1:B:580:LEU:HD11	1:B:674:PRO:HG2	2.02	0.41
1:A:390:LEU:O	1:A:417:PRO:HA	2.20	0.41
1:A:791:SER:O	1:A:795:GLN:HG3	2.21	0.41
1:B:91:LEU:HA	1:B:135:GLY:HA3	2.01	0.41
1:A:18:SER:O	1:A:20:LEU:N	2.50	0.41
1:A:460:TRP:CZ2	1:A:525:ARG:HA	2.56	0.41
1:B:423:ASP:OD1	1:B:423:ASP:N	2.53	0.41
1:B:720:ASN:ND2	1:B:781:ALA:O	2.52	0.41
1:A:667:GLY:HA2	1:A:670:CYS:HB3	2.03	0.41
1:A:772:GLU:O	1:A:774:GLN:N	2.53	0.41
1:B:203:VAL:HG23	1:B:204:LEU:H	1.86	0.41
1:B:355:VAL:HG21	1:B:444:ILE:HD11	2.02	0.41
1:B:422:ASP:O	1:B:426:ILE:HG13	2.21	0.41
1:B:25:HIS:O	1:B:25:HIS:ND1	2.53	0.40
1:B:500:ASP:HA	1:B:503:ILE:HG22	2.03	0.40
1:A:25:HIS:O	1:A:25:HIS:ND1	2.53	0.40
1:B:295:MET:HB2	1:B:354:ASN:CB	2.51	0.40
1:B:312:ARG:HG3	1:B:312:ARG:HH11	1.86	0.40
1:B:430:LEU:HA	1:B:434:TYR:HA	2.04	0.40
1:A:576:ASN:OD1	1:A:675:ASP:N	2.48	0.40
1:B:181:ARG:HH11	1:B:540:PHE:HZ	1.69	0.40
1:B:270:PHE:CD1	1:B:306:PHE:HB2	2.56	0.40
1:A:519:ASN:O	1:A:523:GLN:HG2	2.21	0.40
1:B:204:LEU:HB3	1:B:205:THR:H	1.63	0.40
1:B:444:ILE:HA	1:B:450:HIS:HA	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:ASP:OD2	1:B:649:TYR:OH[4_555]	2.02	0.18

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	764/808 (95%)	619 (81%)	99 (13%)	46 (6%)	1	17
1	B	758/808 (94%)	612 (81%)	96 (13%)	50 (7%)	1	16
All	All	1522/1616 (94%)	1231 (81%)	195 (13%)	96 (6%)	1	16

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	ILE
1	A	113	GLU
1	A	181	ARG
1	A	291	TYR
1	A	416	PHE
1	A	422	ASP
1	A	423	ASP
1	A	453	PRO
1	A	475	ASN
1	A	568	VAL
1	A	691	ARG
1	A	746	HIS
1	B	68	ILE
1	B	97	GLU
1	B	101	ASP
1	B	119	GLN
1	B	164	THR
1	B	211	ALA
1	B	387	HIS
1	B	416	PHE
1	B	417	PRO
1	B	453	PRO
1	B	483	GLN
1	B	542	ASP
1	B	591	CYS

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Mol	Chain	Res	Type
1	A	18	SER
1	A	99	TYR
1	A	132	ASN
1	A	289	ARG
1	A	414	MET
1	A	418	ALA
1	A	683	MET
1	A	715	PHE
1	B	82	GLN
1	B	100	ILE
1	B	132	ASN
1	B	206	ASP
1	B	348	ALA
1	B	354	ASN
1	B	461	PRO
1	B	476	ASN
1	B	531	SER
1	B	569	GLY
1	B	616	ALA
1	B	660	ILE
1	A	117	PRO
1	A	118	GLU
1	A	208	ASP
1	A	396	ALA
1	A	417	PRO
1	A	458	SER
1	A	560	ASP
1	A	658	HIS
1	B	74	LEU
1	B	173	ALA
1	B	304	PRO
1	B	456	GLN
1	B	458	SER
1	B	780	VAL
1	A	82	GLN
1	A	101	ASP
1	A	561	ASN
1	A	586	VAL
1	A	648	ALA
1	A	679	ALA
1	B	92	ALA
1	B	435	THR

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Mol	Chain	Res	Type
1	B	457	SER
1	B	568	VAL
1	B	672	ALA
1	B	696	THR
1	A	145	PRO
1	A	173	ALA
1	A	203	VAL
1	A	476	ASN
1	A	528	HIS
1	B	203	VAL
1	B	262	VAL
1	B	433	GLY
1	B	462	ILE
1	A	19	ARG
1	A	146	GLU
1	A	555	GLY
1	A	622	ASN
1	A	661	GLY
1	A	672	ALA
1	B	146	GLU
1	B	388	PRO
1	B	670	CYS
1	B	448	VAL
1	B	717	VAL
1	A	716	GLY
1	B	117	PRO
1	B	586	VAL
1	B	617	MET
1	B	621	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	483/681 (71%)	472 (98%)	11 (2%)	50	77
1	B	553/681 (81%)	529 (96%)	24 (4%)	29	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1036/1362 (76%)	1001 (97%)	35 (3%)	37 69

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	ARG
1	A	73	LEU
1	A	90	ASP
1	A	160	TYR
1	A	384	ARG
1	A	529	LEU
1	A	547	ARG
1	A	601	HIS
1	A	677	ARG
1	A	752	HIS
1	A	791	SER
1	B	21	ASN
1	B	114	PHE
1	B	141	LYS
1	B	160	TYR
1	B	166	SER
1	B	182	MET
1	B	200	ASN
1	B	209	TYR
1	B	303	TYR
1	B	306	PHE
1	B	312	ARG
1	B	361	ASP
1	B	460	TRP
1	B	519	ASN
1	B	520	SER
1	B	528	HIS
1	B	532	PHE
1	B	543	ASP
1	B	544	CYS
1	B	561	ASN
1	B	582	ASN
1	B	652	HIS
1	B	746	HIS
1	B	759	SER

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	175	ASN
1	B	370	ASN
1	B	601	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	4HP	B	901	-	8,11,11	0.55	0	10,14,14	0.60	0
2	4HP	A	901	-	8,11,11	0.60	0	10,14,14	0.56	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
2	4HP	B	901	-	-	0/2/4/4	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4HP	A	901	-	-	0/2/4/4	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

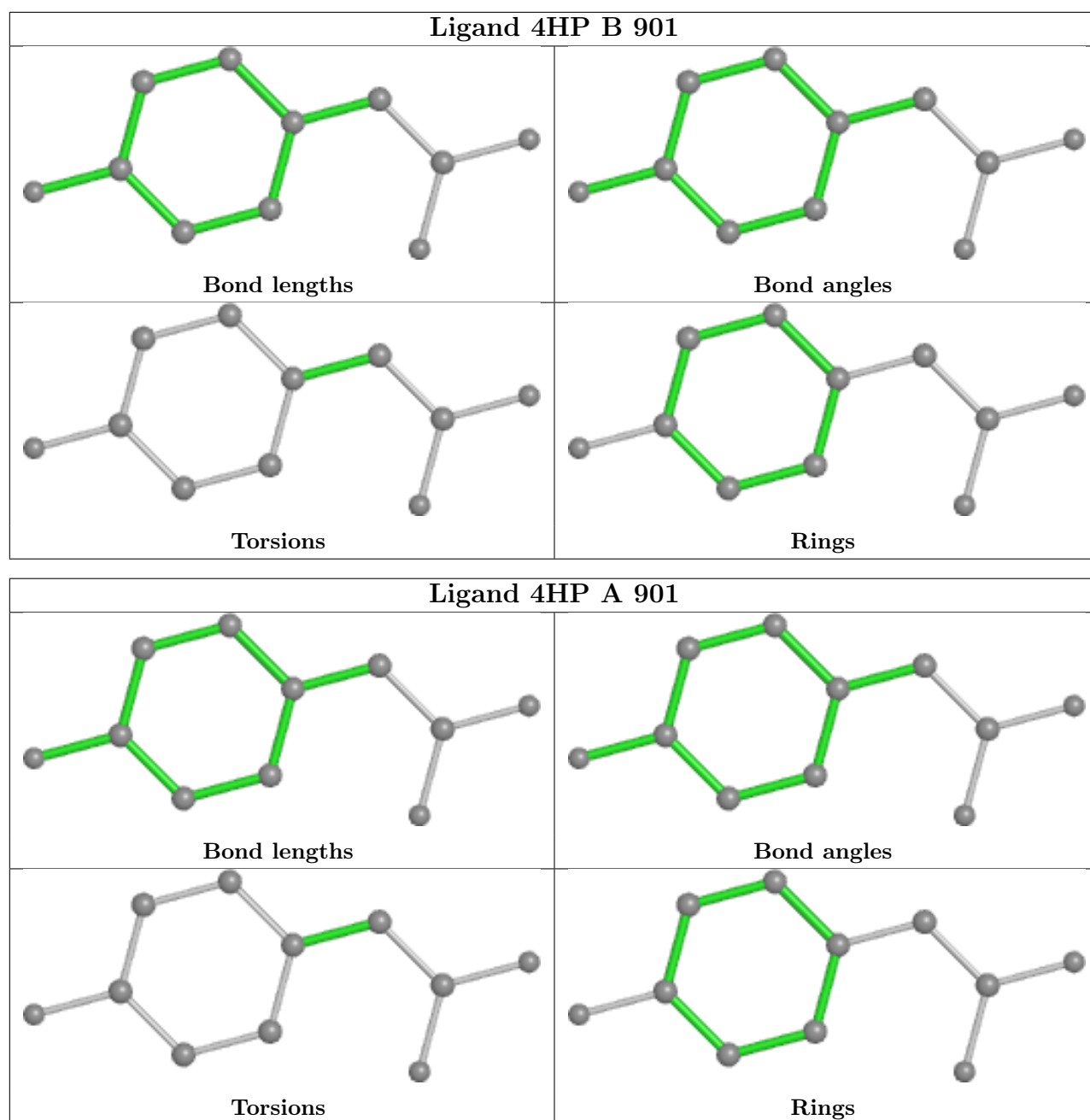
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	4HP	3	0
2	A	901	4HP	2	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	770/808 (95%)	-0.22	3 (0%)	92 87	27, 51, 69, 92	0
1	B	766/808 (94%)	-0.06	6 (0%)	86 75	26, 55, 80, 96	0
All	All	1536/1616 (95%)	-0.14	9 (0%)	89 81	26, 53, 75, 96	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	558	HIS	3.2
1	B	478	PHE	2.7
1	B	542	ASP	2.5
1	A	788	ALA	2.4
1	A	120	ALA	2.3
1	B	322	ASP	2.2
1	B	772	GLU	2.2
1	B	201	LEU	2.1
1	A	589	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

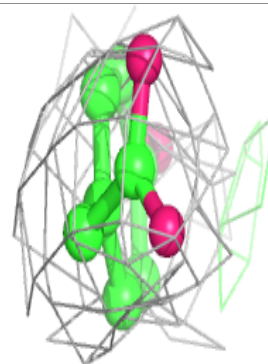
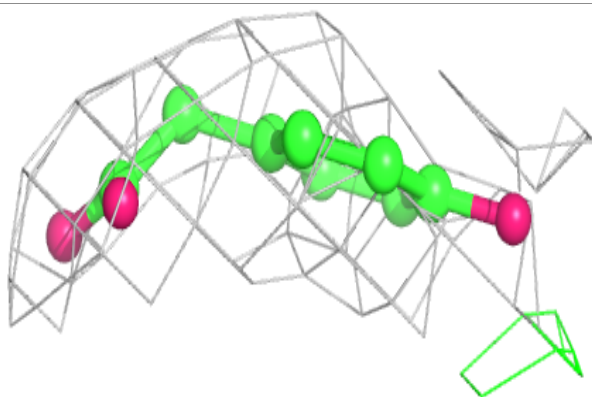
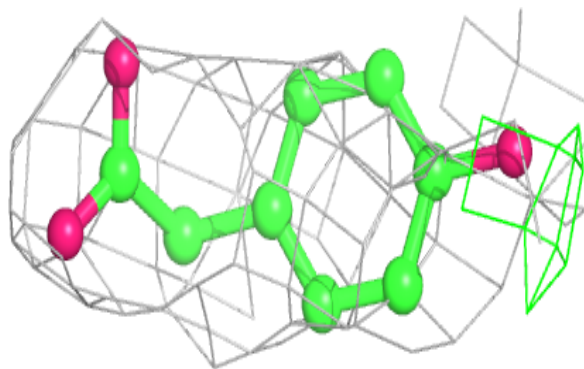
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	4HP	A	901	11/11	0.85	0.35	35,46,66,66	0
2	4HP	B	901	11/11	0.88	0.41	38,47,55,58	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.

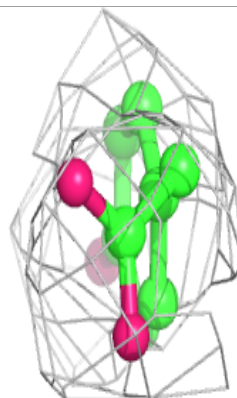
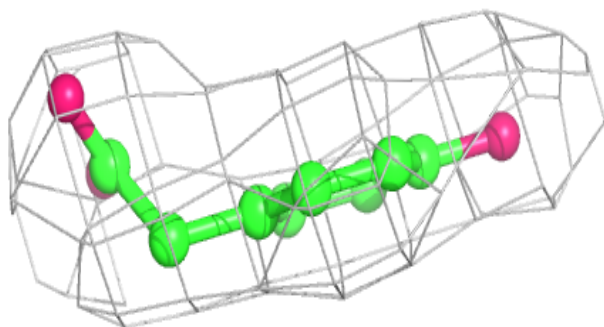
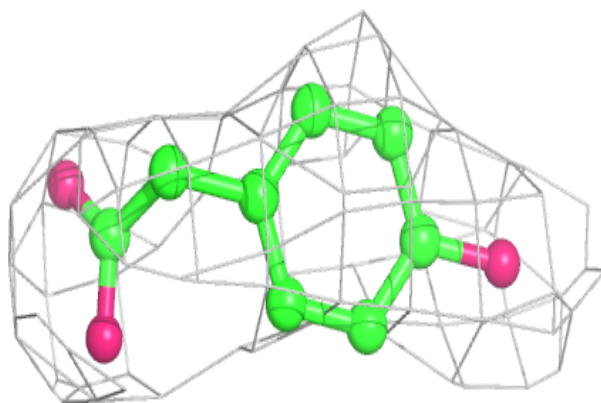
Electron density around 4HP A 901:

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 4HP 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 [i](#)

There are no such residues in this entry.