



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 19, 2020 – 10:27 AM BST

PDB ID : 6V25
Title : Complex of mutant (K162M) of E. coli L-asparaginase II with L-Asp
Authors : Lubkowski, J.; Wlodawer, A.
Deposited on : 2019-11-22
Resolution : 1.78 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 : 2.14.6
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) : 2.14.6

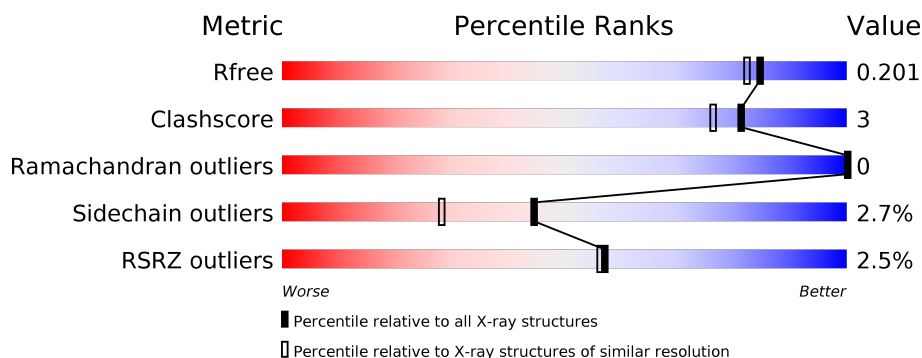
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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	333	<div> <div>4%</div> <div> <div></div> <div>89%</div> <div>7%</div> <div>••</div> </div> </div>
1	B	333	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>8%</div> </div> </div>
2	C	333	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>8%</div> <div>••</div> </div> </div>
2	D	333	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>9%</div> <div>•</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11175 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 L-asparaginase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	2	0
			2440	1522	415	494	9			
1	B	305	Total	C	N	O	S	0	1	0
			2292	1433	389	461	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	expression tag	UNP P00805
A	-5	HIS	-	expression tag	UNP P00805
A	-4	HIS	-	expression tag	UNP P00805
A	-3	HIS	-	expression tag	UNP P00805
A	-2	HIS	-	expression tag	UNP P00805
A	-1	HIS	-	expression tag	UNP P00805
A	0	HIS	-	expression tag	UNP P00805
A	162	MET	LYS	engineered mutation	UNP P00805
B	-6	MET	-	expression tag	UNP P00805
B	-5	HIS	-	expression tag	UNP P00805
B	-4	HIS	-	expression tag	UNP P00805
B	-3	HIS	-	expression tag	UNP P00805
B	-2	HIS	-	expression tag	UNP P00805
B	-1	HIS	-	expression tag	UNP P00805
B	0	HIS	-	expression tag	UNP P00805
B	162	MET	LYS	engineered mutation	UNP P00805

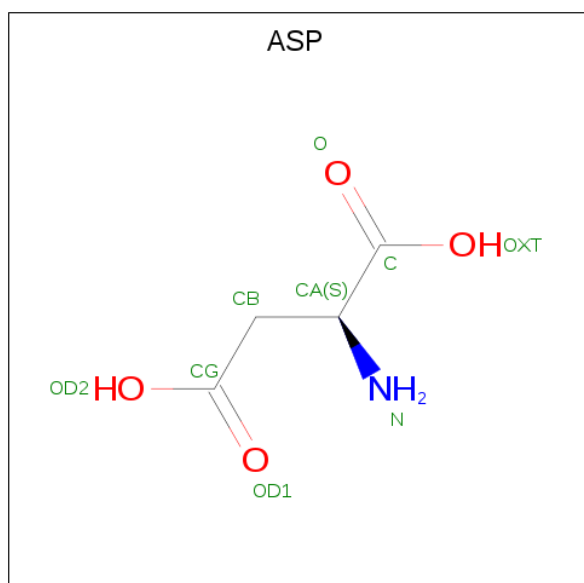
- Molecule 2 is a protein called L-asparaginase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	326	Total	C	N	O	S	0	0	0
			2438	1520	415	494	9			
2	D	332	Total	C	N	O	S	0	1	0
			2503	1561	433	500	9			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	MET	-	expression tag	UNP P00805
C	-5	HIS	-	expression tag	UNP P00805
C	-4	HIS	-	expression tag	UNP P00805
C	-3	HIS	-	expression tag	UNP P00805
C	-2	HIS	-	expression tag	UNP P00805
C	-1	HIS	-	expression tag	UNP P00805
C	0	HIS	-	expression tag	UNP P00805
C	12	AEI	THR	modified residue	UNP P00805
C	162	MET	LYS	engineered mutation	UNP P00805
D	-6	MET	-	expression tag	UNP P00805
D	-5	HIS	-	expression tag	UNP P00805
D	-4	HIS	-	expression tag	UNP P00805
D	-3	HIS	-	expression tag	UNP P00805
D	-2	HIS	-	expression tag	UNP P00805
D	-1	HIS	-	expression tag	UNP P00805
D	0	HIS	-	expression tag	UNP P00805
D	12	AEI	THR	modified residue	UNP P00805
D	162	MET	LYS	engineered mutation	UNP P00805

- Molecule 3 is ASPARTIC ACID (three-letter code: ASP) (formula: C₄H₇NO₄) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	4	1	4		

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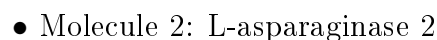
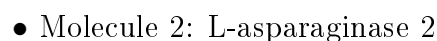
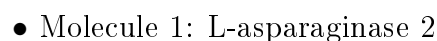
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			9	4	1	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	379	Total	O	0	4
			383	383		
4	C	378	Total	O	0	6
			384	384		
4	B	306	Total	O	0	7
			313	313		
4	D	393	Total	O	0	10
			404	404		

- Molecule 1: L-asparaginase 2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.53 Å 123.97 Å 76.30 Å 90.00° 96.80° 90.00°	Depositor
Resolution (Å)	24.61 – 1.78 24.60 – 1.78	Depositor EDS
% Data completeness (in resolution range)	93.0 (24.61-1.78) 93.1 (24.60-1.78)	Depositor EDS
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 1.78 Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.136 , 0.193 0.148 , 0.201	Depositor DCC
R_{free} test set	2442 reflections (2.42%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 55.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11175	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.57% 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: AEI

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.04	5/2483 (0.2%)	1.13	5/3382 (0.1%)
1	B	1.01	4/2330 (0.2%)	1.11	4/3174 (0.1%)
2	C	1.07	1/2459 (0.0%)	1.13	11/3347 (0.3%)
2	D	1.02	4/2533 (0.2%)	1.14	6/3448 (0.2%)
All	All	1.03	14/9805 (0.1%)	1.13	26/13351 (0.2%)

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 (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	173	SER	CA-CB	-7.50	1.41	1.52
1	A	1	LEU	N-CA	6.69	1.59	1.46
2	D	51	GLU	CD-OE2	-6.29	1.18	1.25
1	A	20	ALA	C-O	6.17	1.35	1.23
2	C	281	ASP	CG-OD2	5.99	1.39	1.25
1	B	228	ALA	C-O	5.91	1.34	1.23
1	B	106	ASP	C-O	5.89	1.34	1.23
2	D	281	ASP	CG-OD2	5.52	1.38	1.25
1	A	15	GLY	C-O	5.40	1.32	1.23
2	D	-5	HIS	N-CA	5.35	1.57	1.46
1	A	105	CYS	N-CA	5.32	1.56	1.46
1	A	246	ASN	C-O	5.23	1.33	1.23
2	D	106	ASP	C-O	5.20	1.33	1.23
1	B	6	ILE	C-O	5.08	1.33	1.23

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	105	CYS	CA-CB-SG	8.37	129.06	114.00
1	B	191	ARG	NE-CZ-NH2	-8.04	116.28	120.30
2	C	269	ARG	NE-CZ-NH2	-6.95	116.83	120.30
2	C	144	ARG	NE-CZ-NH1	6.93	123.76	120.30
2	D	281	ASP	CB-CG-OD1	-6.30	112.63	118.30
1	B	144	ARG	NE-CZ-NH1	6.29	123.45	120.30
2	C	281	ASP	CB-CG-OD1	-6.21	112.71	118.30
1	A	176	TYR	CB-CG-CD2	-6.21	117.28	121.00
2	C	139	LYS	CB-CA-C	-6.14	98.12	110.40
1	B	144	ARG	NE-CZ-NH2	-6.03	117.28	120.30
2	C	285	ASP	CB-CG-OD2	-5.85	113.03	118.30
2	C	236	TYR	CB-CG-CD2	-5.83	117.50	121.00
2	C	121	MET	CG-SD-CE	-5.82	90.89	100.20
1	B	176	TYR	CB-CG-CD2	-5.75	117.55	121.00
2	D	281	ASP	CB-CA-C	-5.67	99.06	110.40
2	D	144	ARG	NE-CZ-NH2	-5.67	117.47	120.30
2	C	269	ARG	NE-CZ-NH1	5.59	123.10	120.30
2	C	87	HIS	CA-CB-CG	5.57	123.07	113.60
2	D	285	ASP	CB-CG-OD2	-5.41	113.43	118.30
1	A	104	LYS	CA-C-O	-5.37	108.82	120.10
1	A	104	LYS	C-N-CA	5.36	135.09	121.70
1	A	61	MET	CG-SD-CE	5.27	108.64	100.20
2	D	18	ASP	CB-CA-C	-5.17	100.07	110.40
2	C	75	THR	CA-CB-OG1	-5.12	98.24	109.00
2	C	188	ASP	CB-CG-OD2	-5.08	113.72	118.30
2	D	211	LEU	CB-CG-CD1	5.01	119.52	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	277	ALA	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	2440	0	2430	15	0
1	B	2292	0	2284	14	0
2	C	2438	0	2423	11	0
2	D	2503	0	2476	12	0
3	A	9	0	3	3	0
3	B	9	0	3	1	0
4	A	383	0	0	2	0
4	B	313	0	0	0	0
4	C	384	0	0	3	0
4	D	404	0	0	7	0
All	All	11175	0	9619	51	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 3.

All (51) 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:D:183:HIS:HB2	4:D:698:HOH:O	1.58	1.03
1:A:21:THR:HG21	4:D:425:HOH:O	1.72	0.89
2:C:12:AEI:CD	4:C:428:HOH:O	2.29	0.80
1:A:12:THR:OG1	3:A:401:ASP:CG	2.25	0.73
1:A:227:PRO:HB3	2:C:227:PRO:HB3	1.70	0.73
2:D:12:AEI:CD	4:D:533:HOH:O	2.43	0.65
2:D:149:VAL:HG12	4:D:479:HOH:O	1.97	0.63
1:A:21:THR:CG2	4:D:425:HOH:O	2.40	0.59
1:B:12:THR:OG1	3:B:401:ASP:CG	2.41	0.58
1:A:19:SER:HB3	1:A:22:LYS:HG3	1.88	0.54
1:B:103:VAL:O	1:B:198:THR:HA	2.08	0.53
1:B:66:TRP:HB3	1:B:98:PHE:CE2	2.44	0.53
1:B:225:ASP:HB3	1:B:252:SER:HB3	1.90	0.53
1:B:313:THR:OG1	1:B:318:GLN:NE2	2.42	0.52
2:D:66:TRP:HB3	2:D:98:PHE:CE2	2.45	0.52
1:B:220:TYR:CZ	1:B:223:ALA:HA	2.44	0.51
2:C:73:ILE:HD11	2:C:85:ILE:HD11	1.92	0.51
2:D:220:TYR:OH	4:D:401[A]:HOH:O	2.20	0.48
1:A:64:ASN:ND2	4:A:503:HOH:O	2.40	0.48
2:D:103:VAL:O	2:D:198:THR:HA	2.14	0.47
1:A:214:VAL:HA	1:A:238:GLY:O	2.14	0.47
1:B:226:LEU:HB2	1:B:227:PRO:HD3	1.95	0.47
1:A:27:VAL:HG11	3:A:401:ASP:HA	1.95	0.47
2:C:35:LEU:HA	2:C:35:LEU:HD23	1.77	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:ASP:OD1	1:B:316:PRO:HD2	2.17	0.45
2:D:182:ILE:HG12	2:D:187:ILE:HG12	1.98	0.45
2:D:27:VAL:HG21	2:D:57:GLY:CA	2.47	0.45
2:C:182:ILE:HG12	2:C:187:ILE:HG12	1.99	0.44
1:A:20:ALA:HA	1:A:120:SER:HA	1.99	0.44
1:B:99:LEU:O	1:B:103:VAL:HG13	2.18	0.44
2:C:317:GLN:HG3	4:C:458:HOH:O	2.17	0.44
1:A:10:GLY:HA2	1:A:55:ASN:ND2	2.31	0.44
2:D:260:ALA:HB1	2:D:265:THR:HB	1.98	0.44
2:C:84:VAL:HA	2:C:110:VAL:O	2.18	0.44
1:B:3:ASN:O	1:B:81:ASP:HB2	2.19	0.43
1:A:79:LYS:HD2	4:A:658:HOH:O	2.19	0.42
2:C:51:GLU:OE1	4:C:401:HOH:O	2.22	0.42
2:C:208:LEU:HD12	2:C:208:LEU:HA	1.90	0.42
2:C:268:VAL:HG22	2:C:292:VAL:HB	2.02	0.42
2:D:139:LYS:HG3	4:D:623:HOH:O	2.19	0.42
1:B:216:ILE:HA	1:B:240:VAL:O	2.20	0.42
1:B:66:TRP:HB3	1:B:98:PHE:CD2	2.54	0.41
1:B:310:LEU:HD23	1:B:310:LEU:HA	1.95	0.41
2:C:139:LYS:HE3	2:C:139:LYS:HB2	1.95	0.41
2:D:8:ALA:HA	2:D:86:THR:OG1	2.21	0.41
1:A:28:GLY:HA2	1:A:55:ASN:ND2	2.36	0.41
1:B:182:ILE:HG12	1:B:187:ILE:HG12	2.02	0.40
2:D:261:ALA:HA	2:D:265:THR:O	2.22	0.40
1:A:11:GLY:HA2	3:A:401:ASP:OXT	2.21	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	326/333 (98%)	317 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	302/333 (91%)	297 (98%)	5 (2%)	0	100	100
2	C	323/333 (97%)	316 (98%)	7 (2%)	0	100	100
2	D	330/333 (99%)	323 (98%)	7 (2%)	0	100	100
All	All	1281/1332 (96%)	1253 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	268/273 (98%)	257 (96%)	11 (4%)	30	14
1	B	252/273 (92%)	245 (97%)	7 (3%)	43	27
2	C	265/272 (97%)	259 (98%)	6 (2%)	50	34
2	D	272/272 (100%)	267 (98%)	5 (2%)	59	45
All	All	1057/1090 (97%)	1028 (97%)	29 (3%)	44	28

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ASP
1	A	21	THR
1	A	22	LYS
1	A	43	LYS
1	A	55	ASN
1	A	79	LYS
1	A	105	CYS
1	A	208	LEU
1	A	211	LEU
1	A	222	ASN
1	A	254	PHE
2	C	33	GLU
2	C	139	LYS

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Mol	Chain	Res	Type
2	C	208	LEU
2	C	211	LEU
2	C	222	ASN
2	C	229	LYS
1	B	55	ASN
1	B	103	VAL
1	B	208	LEU
1	B	211	LEU
1	B	222	ASN
1	B	254	PHE
1	B	314	LYS
2	D	211	LEU
2	D	222	ASN
2	D	251	LYS
2	D	254	PHE
2	D	314	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	64	ASN
1	A	143	ASN
2	C	183	HIS
2	C	318	GLN
1	B	55	ASN
1	B	64	ASN
1	B	318	GLN
2	D	64	ASN
2	D	321	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	AEI	C	12	2	10,14,15	2.10	2 (20%)	11,18,20	2.00	3 (27%)
2	AEI	D	12	2	10,14,15	1.96	3 (30%)	11,18,20	1.98	2 (18%)

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	AEI	C	12	2	-	3/12/18/20	-
2	AEI	D	12	2	-	3/12/18/20	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	12	AEI	OG1-CD	5.80	1.50	1.34
2	D	12	AEI	OG1-CD	4.16	1.46	1.34
2	D	12	AEI	CZ-NH1	3.37	1.54	1.47
2	C	12	AEI	OG1-CB	-2.86	1.42	1.46
2	D	12	AEI	CE2-CD	2.12	1.54	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	12	AEI	CZ-CE2-CD	-5.42	101.39	112.85
2	C	12	AEI	CZ-CE2-CD	-4.25	103.87	112.85
2	C	12	AEI	OE1-CD-CE2	-3.21	117.63	124.73
2	C	12	AEI	OG1-CD-CE2	2.38	115.83	111.46
2	D	12	AEI	O-C-CA	-2.10	119.26	124.78

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	12	AEI	O-C-CA-CB

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Mol	Chain	Res	Type	Atoms
2	D	12	AEI	O-C-CA-CB
2	C	12	AEI	OE1-CD-CE2-CZ
2	D	12	AEI	OE1-CD-CE2-CZ
2	C	12	AEI	OG1-CD-CE2-CZ
2	D	12	AEI	OG1-CD-CE2-CZ

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	12	AEI	1	0
2	D	12	AEI	1	0

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	$\# Z > 2$
3	ASP	A	401	-	2,8,8	0.83	0	1,10,10	2.01	1 (100%)
3	ASP	B	401	-	2,8,8	1.91	1 (50%)	1,10,10	1.04	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	ASP	A	401	-	-	0/2/8/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ASP	B	401	-	-	0/2/8/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	ASP	CA-N	2.70	1.53	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	ASP	CB-CA-C	2.01	113.95	110.69

There are no chirality outliers.

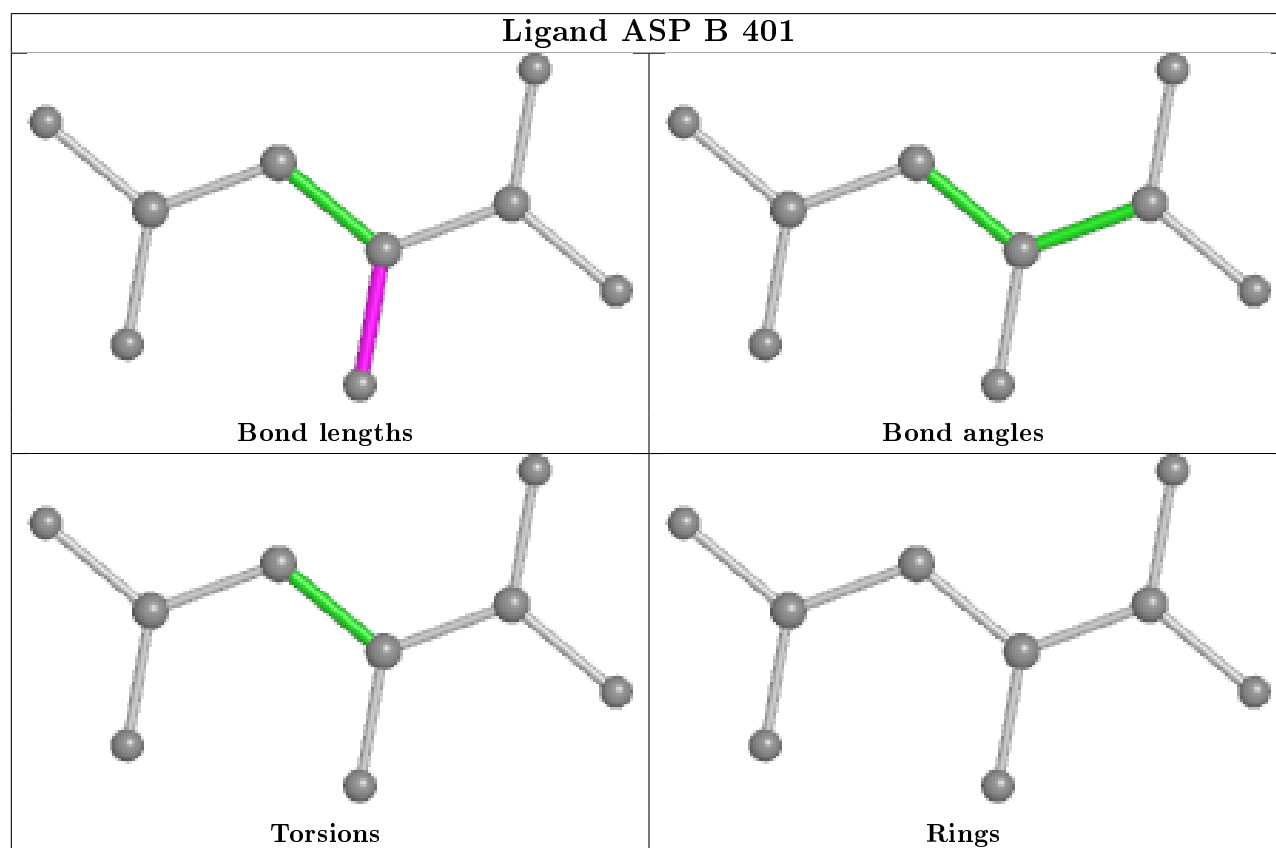
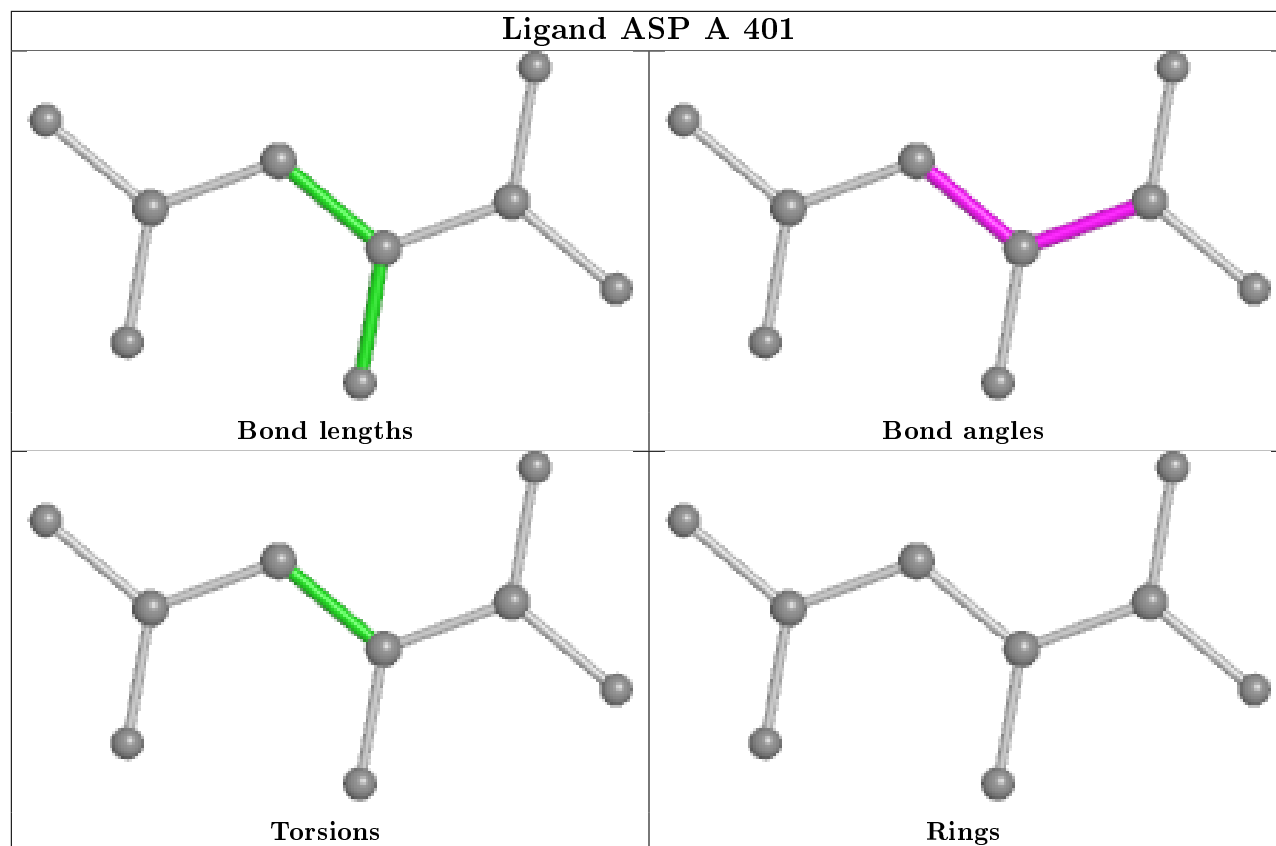
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	ASP	3	0
3	B	401	ASP	1	0

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



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	326/333 (97%)	-0.04	13 (3%) 38 36	22, 28, 51, 78	0
1	B	305/333 (91%)	0.09	6 (1%) 65 65	23, 31, 49, 70	0
2	C	325/333 (97%)	-0.03	10 (3%) 49 47	22, 28, 44, 56	0
2	D	331/333 (99%)	-0.07	3 (0%) 84 84	22, 29, 47, 69	0
All	All	1287/1332 (96%)	-0.01	32 (2%) 57 56	22, 29, 47, 78	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	19	SER	4.5
1	A	17	GLY	4.4
1	A	26	THR	4.3
1	A	16	GLY	4.1
1	A	23	SER	4.0
1	B	38	ALA	3.9
1	A	18	ASP	3.9
1	A	21	THR	3.8
1	A	25	TYR	3.2
2	C	18	ASP	3.2
2	C	19	SER	3.0
1	A	20	ALA	2.9
2	C	30	VAL	2.9
1	A	22	LYS	2.9
2	C	21	THR	2.7
2	D	-1	HIS	2.6
2	C	17	GLY	2.5
1	A	24	ASN	2.5
1	B	14	ALA	2.5
1	B	119	THR	2.4
1	A	28	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
2	C	26	THR	2.3
2	C	20	ALA	2.3
2	C	23	SER	2.3
2	D	78	ASP	2.2
1	B	78[A]	ASP	2.2
2	D	106	ASP	2.1
1	B	317	GLN	2.1
2	C	22	LYS	2.1
1	A	15	GLY	2.1
1	B	37	ASN	2.0
2	C	28	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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	AEI	D	12	15/16	0.96	0.08	23,26,29,31	0
2	AEI	C	12	15/16	0.97	0.08	23,26,36,39	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

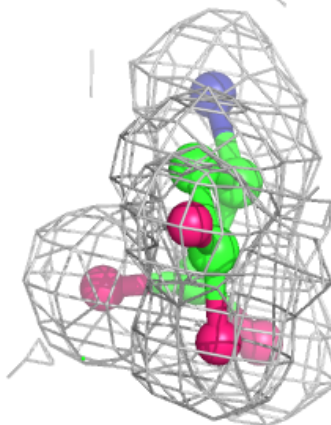
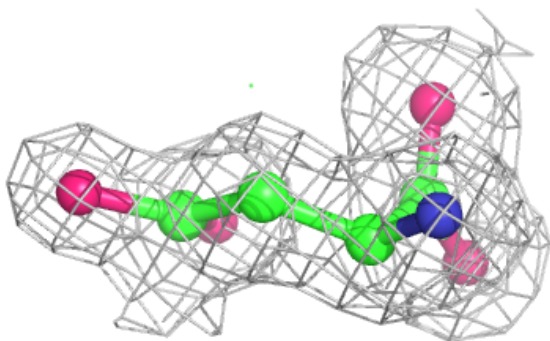
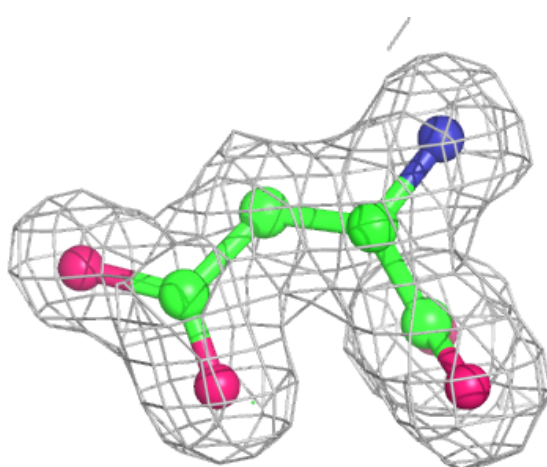
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ASP	A	401	9/9	0.95	0.09	24,25,32,32	0
3	ASP	B	401	9/9	0.95	0.08	26,29,33,35	0

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.

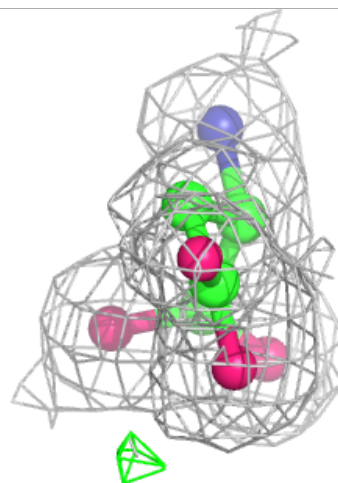
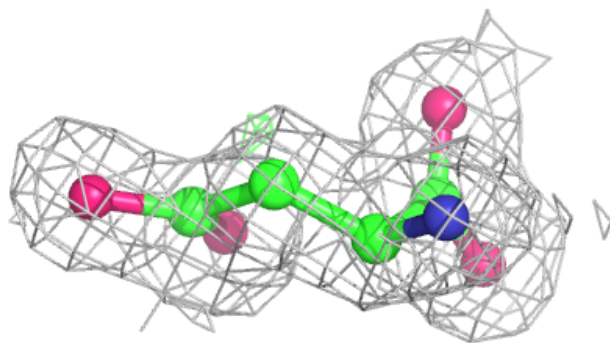
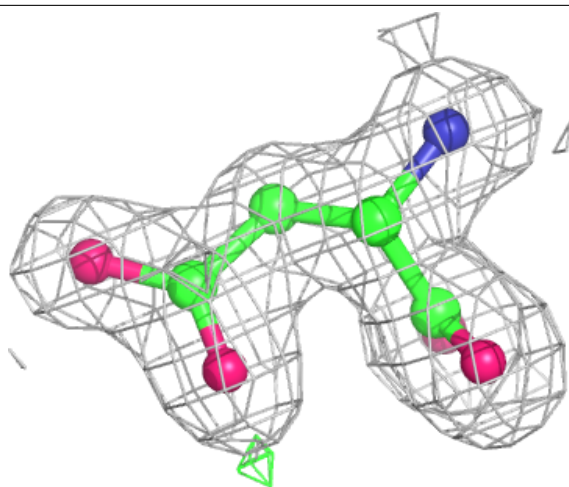
Electron density around ASP A 401:

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



Electron density around ASP B 401:

$2mF_o-DF_c$ (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.