



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 27, 2026 – 12:26 AM UTC

PDB ID : 2NZ2 / pdb_00002nz2
Title : Crystal structure of human argininosuccinate synthase in complex with aspartate and citrulline
Authors : Karlberg, T.; Uppenberg, J.; Arrowsmith, C.; Berglund, H.; Busam, R.D.; Collins, R.; Edwards, A.; Ericsson, U.B.; Flodin, S.; Flores, A.; Graslund, S.; Hallberg, B.M.; Hammarstrom, M.; Hogbom, M.; Johansson, I.; Kotenyova, T.; Magnusdottir, A.; Moche, M.; Nilsson, M.E.; Nordlund, P.; Nyman, T.; Ogg, D.; Persson, C.; Sagemark, J.; Stenmark, P.; Sundstrom, M.; Thorsell, A.G.; Van Den Berg, S.; Wallden, K.; Weigelt, J.; Holmberg-Schiavone, L.; Structural Genomics Consortium (SGC)
Deposited on : 2006-11-22
Resolution : 2.40 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
Percentile statistics	: 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	: 9.0.010 (Gargrove)

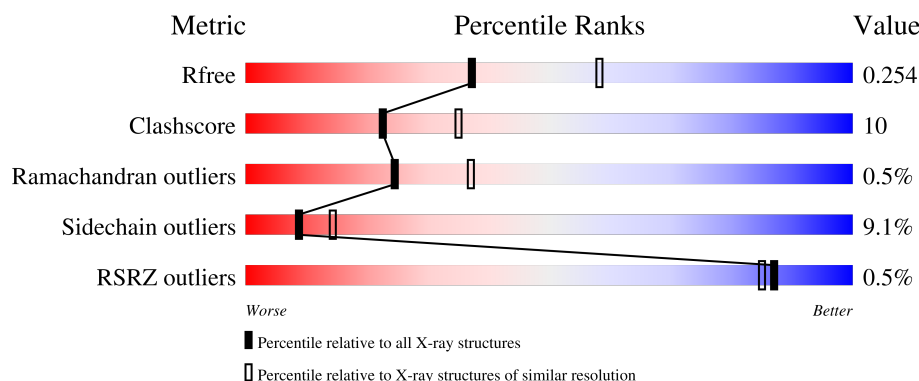
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	413	

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

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3423 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 Argininosuccinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	402	3191	2041	545	593	12	0	0	0

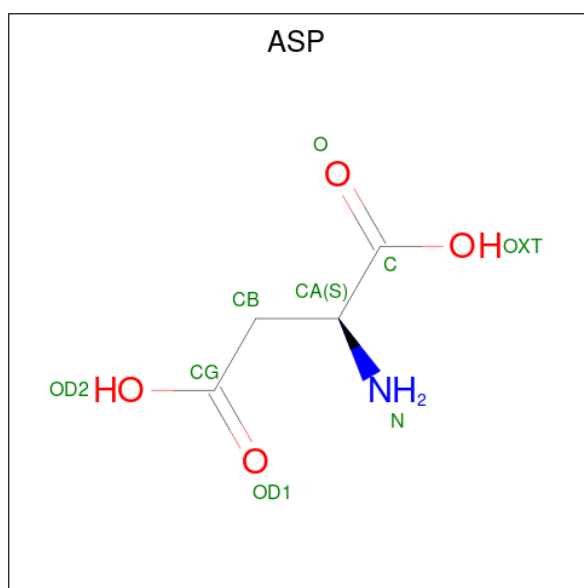
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	cloning artifact	UNP P00966

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

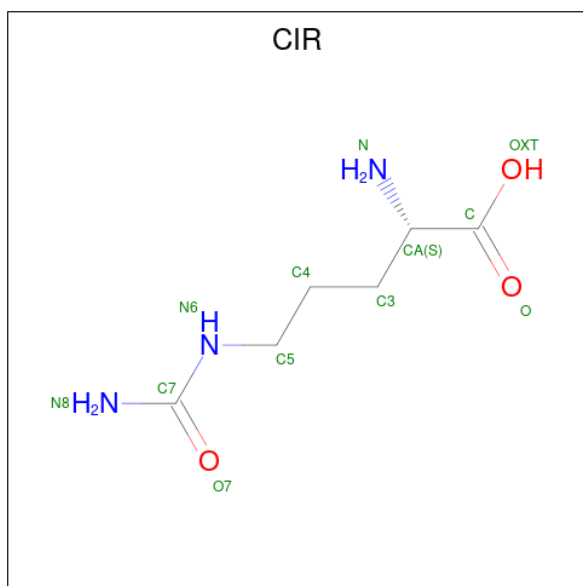
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		

- Molecule 3 is ASPARTIC ACID (CCD ID: ASP) (formula: C₄H₇NO₄).



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

- Molecule 4 is CITRULLINE (CCD ID: CIR) (formula: $C_6H_{13}N_3O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			12	6	3	3		

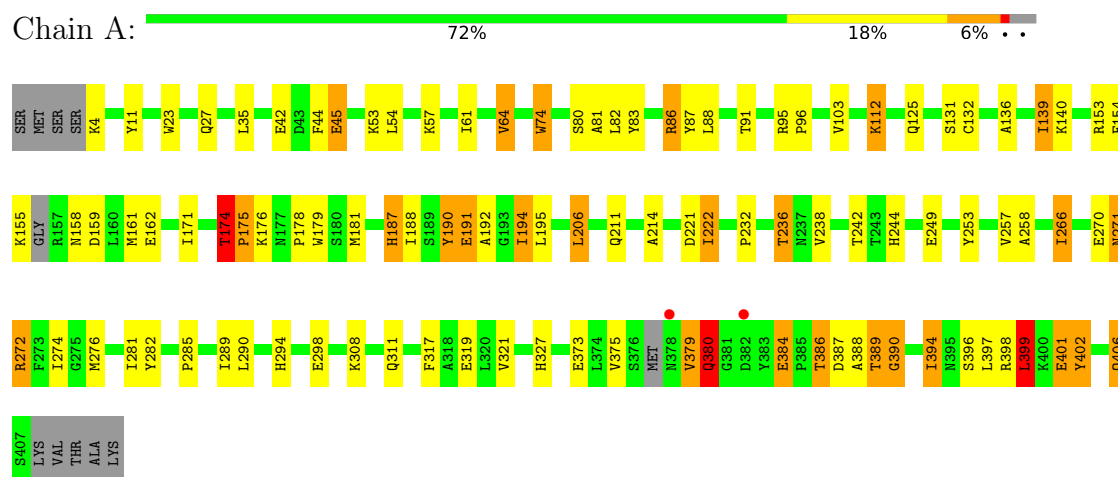
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	210	Total	O	0	0
			210	210		

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: Argininosuccinate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	95.94Å 117.47Å 155.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.41 – 2.40 19.41 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.41-2.40) 99.7 (19.41-2.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.20	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.194 , 0.265 0.192 , 0.254	Depositor DCC
R_{free} test set	864 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.512	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.8	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	0.93	EDS
Total number of atoms	3423	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.40% 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: CIR, NA

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	1.09	13/3262 (0.4%)	1.24	21/4409 (0.5%)

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	5

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	379	VAL	C-N	-21.45	1.03	1.33
1	A	380	GLN	C-N	-10.57	1.18	1.33
1	A	388	ALA	CA-CB	-8.23	1.40	1.53
1	A	192	ALA	CA-CB	-7.86	1.40	1.53
1	A	387	ASP	C-O	-7.44	1.15	1.24
1	A	384	GLU	C-O	-7.22	1.17	1.24
1	A	388	ALA	C-O	-5.91	1.17	1.24
1	A	190	TYR	C-O	-5.83	1.17	1.24
1	A	389	THR	CB-CG2	-5.68	1.33	1.52
1	A	153	ARG	C-O	-5.31	1.17	1.24
1	A	389	THR	C-O	-5.27	1.18	1.24
1	A	154	PHE	CA-C	-5.23	1.47	1.53
1	A	211	GLN	C-O	-5.06	1.17	1.23

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	402	TYR	N-CA-C	-21.48	87.46	113.88
1	A	399	LEU	N-CA-C	-18.27	89.34	112.72
1	A	272	ARG	N-CA-C	-15.52	86.09	110.14
1	A	387	ASP	CA-C-N	9.63	133.18	120.28
1	A	387	ASP	C-N-CA	9.63	133.18	120.28
1	A	387	ASP	N-CA-C	9.44	121.57	111.28
1	A	191	GLU	N-CA-C	8.72	129.38	110.80
1	A	387	ASP	O-C-N	6.95	129.48	122.12
1	A	271	ASN	CB-CA-C	-6.24	98.93	109.72
1	A	214	ALA	N-CA-C	6.07	120.30	113.01
1	A	402	TYR	N-CA-CB	5.80	118.31	110.59
1	A	401	GLU	CB-CA-C	5.78	120.39	110.79
1	A	191	GLU	CA-C-N	-5.43	111.31	122.82
1	A	191	GLU	C-N-CA	-5.43	111.31	122.82
1	A	389	THR	N-CA-CB	5.36	117.78	110.01
1	A	175	PRO	N-CA-C	5.31	123.41	112.47
1	A	64	VAL	N-CA-C	-5.27	107.99	113.10
1	A	389	THR	CB-CA-C	5.15	118.97	110.88
1	A	390	GLY	CA-C-N	5.05	127.00	120.44
1	A	390	GLY	C-N-CA	5.05	127.00	120.44
1	A	64	VAL	N-CA-CB	-5.01	105.85	112.36

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	174	THR	Peptide
1	A	271	ASN	Peptide
1	A	380	GLN	Mainchain
1	A	398	ARG	Peptide
1	A	401	GLU	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	3191	0	3168	67	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	9	0	3	0	0
4	A	12	0	7	2	0
5	A	210	0	0	14	0
All	All	3423	0	3178	67	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 10.

All (67) 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:A:175:PRO:HA	5:A:704:HOH:O	1.68	0.91
1:A:266:ILE:HD13	1:A:282:TYR:HB2	1.52	0.90
1:A:81:ALA:HB2	5:A:522:HOH:O	1.77	0.84
1:A:266:ILE:CD1	1:A:282:TYR:HB2	2.15	0.77
1:A:390:GLY:O	1:A:394:ILE:HG23	1.91	0.70
1:A:191:GLU:O	5:A:533:HOH:O	2.09	0.68
1:A:45:GLU:H	1:A:45:GLU:CD	2.01	0.68
1:A:174:THR:N	5:A:704:HOH:O	2.26	0.68
1:A:244:HIS:HD2	1:A:249:GLU:CD	2.02	0.67
1:A:161:MET:SD	1:A:171:ILE:HD13	2.35	0.66
1:A:379:VAL:O	1:A:380:GLN:C	2.34	0.66
1:A:249:GLU:OE1	5:A:626:HOH:O	2.14	0.66
1:A:174:THR:HG22	5:A:629:HOH:O	1.94	0.66
1:A:222:ILE:HG13	1:A:238:VAL:HB	1.79	0.65
1:A:131:SER:OG	1:A:327:HIS:HD2	1.80	0.64
1:A:158:ASN:O	1:A:162:GLU:HG2	1.99	0.63
1:A:244:HIS:CD2	1:A:249:GLU:CG	2.82	0.62
1:A:23:TRP:O	1:A:27:GLN:HG2	2.01	0.61
1:A:44:PHE:HB3	1:A:61:ILE:HD13	1.82	0.61
1:A:11:TYR:HD2	1:A:35:LEU:CD2	2.14	0.61
1:A:80:SER:HB2	1:A:311:GLN:HE22	1.67	0.60
1:A:384:GLU:OE1	1:A:386:THR:HB	2.04	0.58
1:A:136:ALA:O	1:A:139:ILE:HG13	2.04	0.57
1:A:11:TYR:HD2	1:A:35:LEU:HD22	1.69	0.57
1:A:244:HIS:HD2	1:A:249:GLU:CG	2.18	0.56
1:A:155:LYS:CG	1:A:159:ASP:OD2	2.53	0.55
1:A:272:ARG:HB2	1:A:276:MET:O	2.06	0.55
1:A:82:LEU:HD23	1:A:88:LEU:HD23	1.89	0.55
1:A:236:THR:CG2	5:A:507:HOH:O	2.57	0.53
1:A:402:TYR:O	1:A:406:GLN:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:ALA:HB2	1:A:289:ILE:HD11	1.90	0.52
1:A:83:TYR:HB3	1:A:87:TYR:HB3	1.92	0.52
1:A:236:THR:HG23	5:A:507:HOH:O	2.11	0.51
1:A:112:LYS:HE2	1:A:140:LYS:NZ	2.25	0.51
1:A:244:HIS:CD2	1:A:249:GLU:HG2	2.45	0.51
1:A:396:SER:O	1:A:399:LEU:HB2	2.13	0.49
1:A:266:ILE:HD11	1:A:282:TYR:CD2	2.49	0.48
1:A:80:SER:OG	1:A:294:HIS:HE1	1.97	0.47
1:A:249:GLU:HB3	5:A:509:HOH:O	2.13	0.47
1:A:187:HIS:C	1:A:187:HIS:CD2	2.93	0.47
1:A:178:PRO:O	1:A:194:ILE:HG13	2.15	0.46
1:A:181:MET:HG2	1:A:190:TYR:CD2	2.49	0.46
1:A:242:THR:HG22	1:A:244:HIS:CE1	2.50	0.46
1:A:125:GLN:HG2	5:A:511:HOH:O	2.14	0.46
1:A:327:HIS:HE1	5:A:583:HOH:O	1.98	0.46
1:A:258:ALA:HB2	1:A:289:ILE:CD1	2.47	0.45
1:A:244:HIS:CD2	1:A:249:GLU:CD	2.90	0.45
1:A:194:ILE:HD12	1:A:195:LEU:HG	1.97	0.45
1:A:95:ARG:N	1:A:96:PRO:HD2	2.32	0.45
1:A:86:ARG:HD3	5:A:515:HOH:O	2.17	0.44
1:A:103:VAL:HG21	1:A:132:CYS:HA	2.00	0.44
1:A:317:PHE:O	1:A:321:VAL:HG23	2.18	0.44
1:A:91:THR:HG21	4:A:502:CIR:H51	2.01	0.43
1:A:190:TYR:CG	1:A:206:LEU:HD11	2.53	0.43
1:A:80:SER:OG	1:A:294:HIS:CE1	2.72	0.43
1:A:194:ILE:HG13	1:A:194:ILE:H	1.57	0.43
1:A:181:MET:HE3	1:A:190:TYR:HE2	1.84	0.42
1:A:179:TRP:HE3	1:A:194:ILE:HD11	1.84	0.42
1:A:42:GLU:OE1	1:A:44:PHE:CE1	2.73	0.41
1:A:298:GLU:HG3	5:A:572:HOH:O	2.20	0.41
1:A:74:TRP:CH2	1:A:232:PRO:HG2	2.55	0.41
1:A:181:MET:HE2	1:A:188:ILE:HD11	2.02	0.41
1:A:244:HIS:HB3	1:A:249:GLU:HG2	2.02	0.41
1:A:86:ARG:CD	5:A:515:HOH:O	2.69	0.41
1:A:270:GLU:OE2	4:A:502:CIR:N	2.54	0.40
1:A:222:ILE:HD11	1:A:238:VAL:HG21	2.03	0.40
1:A:253:TYR:O	1:A:257:VAL:HG23	2.21	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	396/413 (96%)	380 (96%)	14 (4%)	2 (0%)	24	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	174	THR
1	A	285	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	340/354 (96%)	309 (91%)	31 (9%)	9	14

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	45	GLU
1	A	53	LYS
1	A	54	LEU
1	A	57	LYS
1	A	64	VAL
1	A	74	TRP
1	A	86	ARG
1	A	112	LYS

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Mol	Chain	Res	Type
1	A	139	ILE
1	A	176	LYS
1	A	187	HIS
1	A	194	ILE
1	A	206	LEU
1	A	221	ASP
1	A	222	ILE
1	A	236	THR
1	A	266	ILE
1	A	274	ILE
1	A	281	ILE
1	A	290	LEU
1	A	308	LYS
1	A	319	GLU
1	A	373	GLU
1	A	375	VAL
1	A	386	THR
1	A	389	THR
1	A	394	ILE
1	A	397	LEU
1	A	399	LEU
1	A	406	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	177	ASN
1	A	244	HIS
1	A	311	GLN
1	A	327	HIS
1	A	350	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is 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	$\# Z > 2$
3	ASP	A	501	-	7,8,8	1.13	1 (14%)	6,10,10	1.37	1 (16%)
4	CIR	A	502	-	10,11,11	0.90	0	10,13,13	0.89	1 (10%)

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	501	-	-	2/8/8/8	-
4	CIR	A	502	-	-	0/11/11/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	ASP	OXT-C	-2.13	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	ASP	OXT-C-O	-2.64	118.08	124.08
4	A	502	CIR	O7-C7-N8	-2.05	119.06	123.18

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	ASP	OXT-C-CA-CB
3	A	501	ASP	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	CIR	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	380:GLN	C	381:GLY	N	1.18
1	A	379:VAL	C	380:GLN	N	1.03

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	402/413 (97%)	-0.38	2 (0%) 87 85	7, 16, 33, 42	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	378	ASN	3.1
1	A	382	ASP	2.9

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	CIR	A	502	12/12	0.92	0.09	8,10,14,18	0
3	ASP	A	501	9/9	0.93	0.08	24,24,25,25	0
2	NA	A	503	1/1	0.96	0.10	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.