



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:24 PM UTC

PDB ID : 5FDN / pdb_00005fdn
Title : Crystal structure of phosphoenolpyruvate carboxylase from *Arabidopsis thaliana* in complex with aspartate and citrate
Authors : Connell, M.B.; Lee, M.J.Y.; Plaxton, W.C.; Jia, Z.
Deposited on : 2015-12-16
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
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

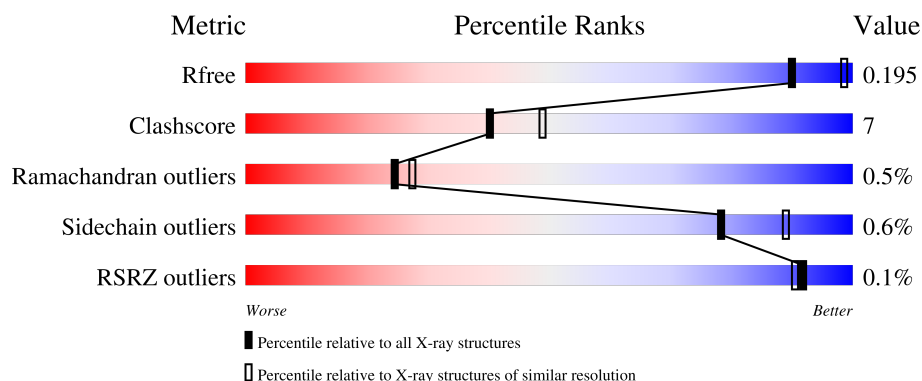
1 Overall quality at a glance

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	987	 81% 11% • 7%
1	B	987	 80% 11% • 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16218 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 Phosphoenolpyruvate carboxylase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	914	Total	C	N	O	S	0	0	0
			7346	4659	1279	1380	28			
1	B	900	Total	C	N	O	S	0	0	0
			7227	4587	1251	1361	28			

There are 38 discrepancies between the modelled and reference sequences:

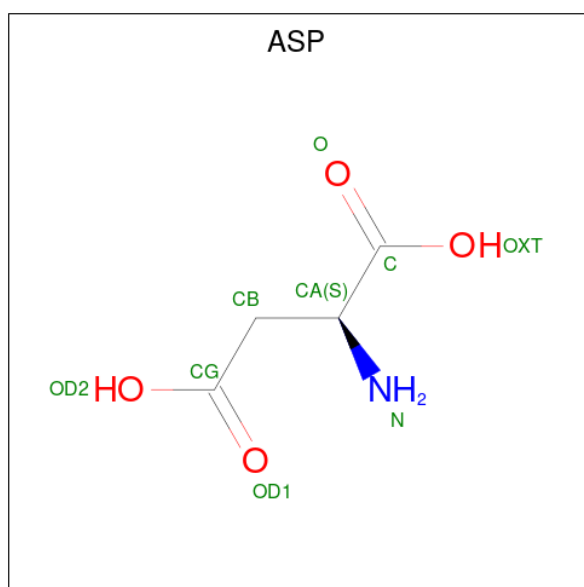
Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP Q84VW9
A	-17	GLY	-	expression tag	UNP Q84VW9
A	-16	SER	-	expression tag	UNP Q84VW9
A	-15	SER	-	expression tag	UNP Q84VW9
A	-14	HIS	-	expression tag	UNP Q84VW9
A	-13	HIS	-	expression tag	UNP Q84VW9
A	-12	HIS	-	expression tag	UNP Q84VW9
A	-11	HIS	-	expression tag	UNP Q84VW9
A	-10	HIS	-	expression tag	UNP Q84VW9
A	-9	HIS	-	expression tag	UNP Q84VW9
A	-8	SER	-	expression tag	UNP Q84VW9
A	-7	SER	-	expression tag	UNP Q84VW9
A	-6	GLY	-	expression tag	UNP Q84VW9
A	-5	LEU	-	expression tag	UNP Q84VW9
A	-4	VAL	-	expression tag	UNP Q84VW9
A	-3	PRO	-	expression tag	UNP Q84VW9
A	-2	ARG	-	expression tag	UNP Q84VW9
A	-1	GLY	-	expression tag	UNP Q84VW9
A	0	SER	-	expression tag	UNP Q84VW9
B	-18	MET	-	initiating methionine	UNP Q84VW9
B	-17	GLY	-	expression tag	UNP Q84VW9
B	-16	SER	-	expression tag	UNP Q84VW9
B	-15	SER	-	expression tag	UNP Q84VW9
B	-14	HIS	-	expression tag	UNP Q84VW9
B	-13	HIS	-	expression tag	UNP Q84VW9

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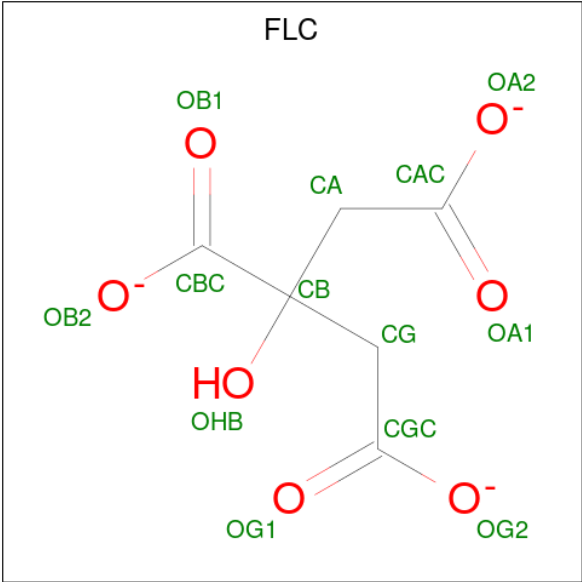
Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP Q84VW9
B	-11	HIS	-	expression tag	UNP Q84VW9
B	-10	HIS	-	expression tag	UNP Q84VW9
B	-9	HIS	-	expression tag	UNP Q84VW9
B	-8	SER	-	expression tag	UNP Q84VW9
B	-7	SER	-	expression tag	UNP Q84VW9
B	-6	GLY	-	expression tag	UNP Q84VW9
B	-5	LEU	-	expression tag	UNP Q84VW9
B	-4	VAL	-	expression tag	UNP Q84VW9
B	-3	PRO	-	expression tag	UNP Q84VW9
B	-2	ARG	-	expression tag	UNP Q84VW9
B	-1	GLY	-	expression tag	UNP Q84VW9
B	0	SER	-	expression tag	UNP Q84VW9

- Molecule 2 is ASPARTIC ACID (CCD ID: ASP) (formula: $C_4H_7NO_4$).



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

- Molecule 3 is CITRATE ANION (CCD ID: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		

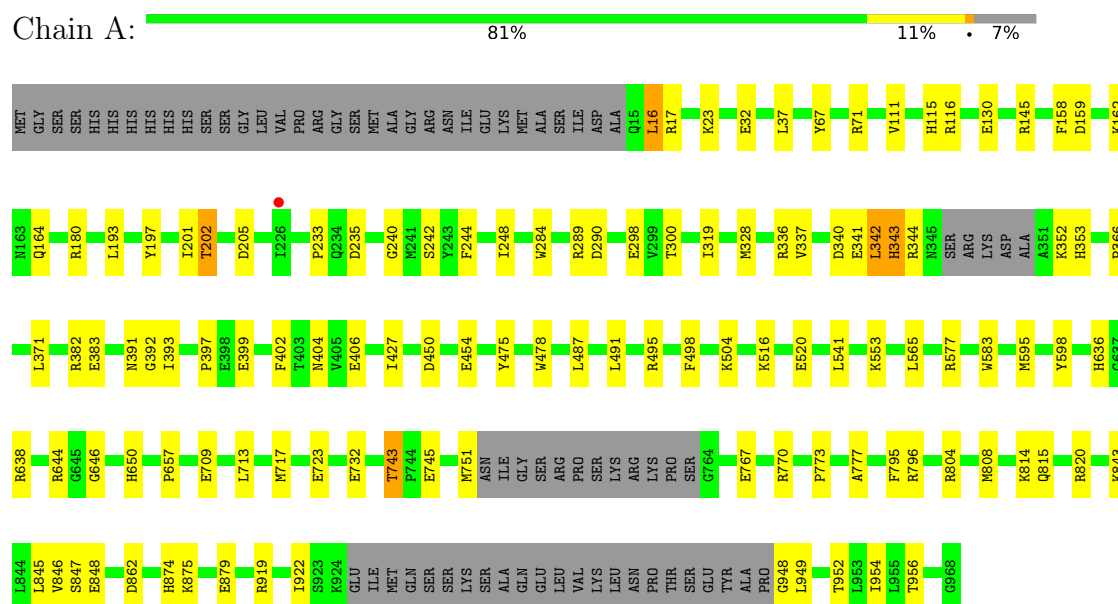
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	807	Total	O	0	0
			807	807		
4	B	794	Total	O	0	0
			794	794		

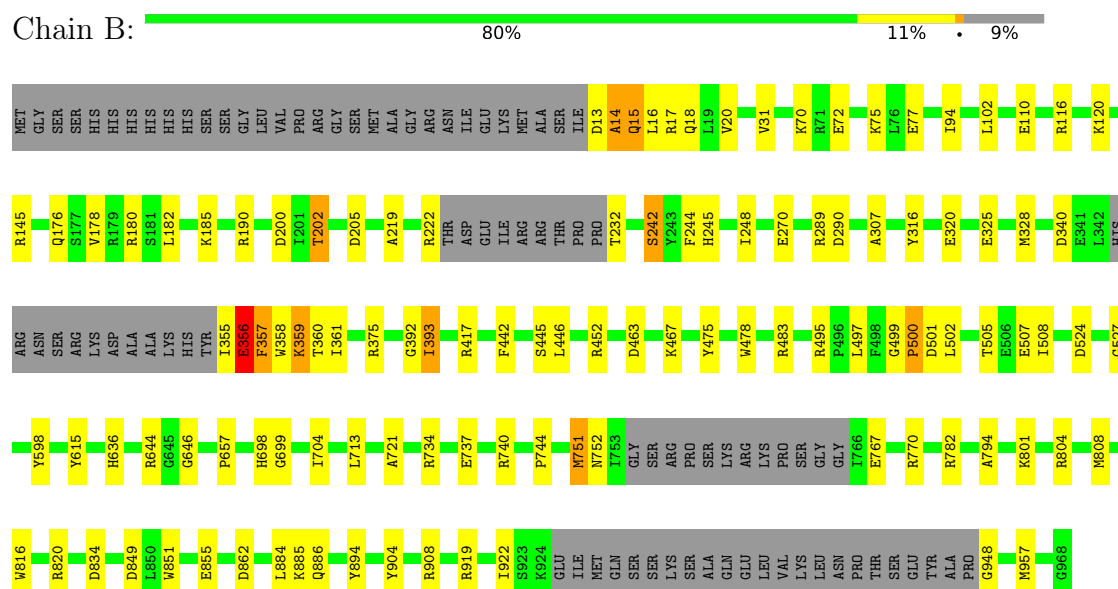
3 Residue-property plots

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: Phosphoenolpyruvate carboxylase 3



• Molecule 1: Phosphoenolpyruvate carboxylase 3



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	264.26Å 268.13Å 77.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.87 – 2.20 48.87 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.87-2.20) 99.9 (48.87-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.41 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.173 , 0.193 0.175 , 0.195	Depositor DCC
R_{free} test set	2013 reflections (1.43%)	wwPDB-VP
Wilson B-factor (Å ²)	22.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 26.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.249 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16218	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% 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: FLC

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	0.36	1/7498 (0.0%)	0.53	1/10146 (0.0%)
1	B	0.36	0/7373	0.59	10/9976 (0.1%)
All	All	0.36	1/14871 (0.0%)	0.56	11/20122 (0.1%)

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	2
1	B	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	657	PRO	CA-C	6.82	1.55	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	356	GLU	N-CA-C	11.27	123.62	108.07
1	B	751	MET	CA-C-N	8.05	136.20	121.70
1	B	751	MET	C-N-CA	8.05	136.20	121.70
1	B	242	SER	CA-C-N	-6.24	109.41	121.58
1	B	242	SER	C-N-CA	-6.24	109.41	121.58
1	B	359	LYS	CA-C-N	5.79	132.60	121.54
1	B	359	LYS	C-N-CA	5.79	132.60	121.54
1	A	657	PRO	O-C-N	5.43	123.81	121.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	698	HIS	CA-C-N	-5.22	113.28	122.09
1	B	698	HIS	C-N-CA	-5.22	113.28	122.09
1	B	751	MET	CA-CB-CG	5.08	124.26	114.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	16	LEU	Peptide
1	A	343	HIS	Peptide
1	B	356	GLU	Peptide
1	B	699	GLY	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	7346	0	7319	88	0
1	B	7227	0	7201	102	0
2	A	9	0	3	0	0
2	B	9	0	3	0	0
3	A	13	0	5	1	0
3	B	13	0	5	2	0
4	A	807	0	0	39	0
4	B	794	0	0	34	3
All	All	16218	0	14536	192	3

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 7.

All (192) 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:316:TYR:HH	1:B:355:ILE:N	1.41	1.19
1:B:232:THR:N	4:B:1101:HOH:O	1.84	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:ARG:NH2	4:B:1104:HOH:O	1.97	0.96
1:B:316:TYR:OH	1:B:355:ILE:N	1.99	0.96
1:A:71:ARG:N	4:A:1102:HOH:O	1.97	0.96
1:B:919:ARG:HD2	1:B:922:ILE:HD11	1.46	0.96
1:B:497:LEU:O	4:B:1102:HOH:O	1.89	0.91
1:B:14:ALA:O	1:B:16:LEU:N	2.06	0.87
1:B:245:HIS:NE2	4:B:1108:HOH:O	2.07	0.86
1:B:644:ARG:O	4:B:1103:HOH:O	1.94	0.84
1:B:202:THR:HG22	1:B:205:ASP:H	1.42	0.83
1:A:948:GLY:O	4:A:1103:HOH:O	1.98	0.81
1:A:116:ARG:NH2	4:A:1108:HOH:O	2.03	0.80
1:A:919:ARG:HD2	1:A:922:ILE:HD11	1.61	0.80
1:B:804:ARG:NH1	4:B:1106:HOH:O	2.05	0.80
1:A:553:LYS:HD3	4:A:1568:HOH:O	1.83	0.79
1:A:732:GLU:OE1	4:A:1105:HOH:O	2.00	0.79
1:A:845:LEU:O	4:A:1104:HOH:O	1.98	0.78
1:A:723:GLU:OE2	4:A:1107:HOH:O	2.00	0.78
1:A:328:MET:HE2	1:A:427:ILE:HD13	1.66	0.78
1:A:815:GLN:OE1	4:A:1106:HOH:O	2.00	0.78
1:A:804:ARG:NH1	4:A:1101:HOH:O	1.97	0.77
1:A:498:PHE:HA	4:A:1294:HOH:O	1.85	0.76
1:B:13:ASP:N	4:B:1113:HOH:O	2.17	0.76
1:A:723:GLU:HG2	4:A:1781:HOH:O	1.86	0.75
1:B:180:ARG:NH1	1:B:242:SER:HA	2.02	0.75
1:B:834:ASP:OD1	4:B:1105:HOH:O	2.04	0.75
1:B:500:PRO:HG2	1:B:502:LEU:HB2	1.67	0.75
1:B:499:GLY:H	1:B:500:PRO:HD3	1.50	0.75
1:B:15:GLN:HA	1:B:18:GLN:HG3	1.70	0.74
1:A:23:LYS:NZ	4:A:1119:HOH:O	2.22	0.72
1:B:14:ALA:HA	1:B:17:ARG:HH11	1.54	0.72
1:B:222:ARG:O	4:B:1107:HOH:O	2.07	0.72
1:A:404:ASN:OD1	1:A:406:GLU:HB2	1.90	0.72
1:B:499:GLY:N	1:B:500:PRO:HD3	2.06	0.71
1:B:744:PRO:HB2	1:B:957:MET:HE2	1.72	0.70
1:A:202:THR:HG22	1:A:205:ASP:H	1.56	0.69
1:A:919:ARG:NH1	4:A:1109:HOH:O	2.10	0.69
1:B:885:LYS:NZ	4:B:1120:HOH:O	2.25	0.69
3:B:1002:FLC:OHB	3:B:1002:FLC:OA1	2.10	0.69
1:A:745:GLU:OE2	4:A:1110:HOH:O	2.12	0.67
1:B:908:ARG:O	4:B:1109:HOH:O	2.12	0.67
1:A:16:LEU:HD23	1:A:17:ARG:H	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:ASP:O	4:B:1111:HOH:O	2.12	0.67
1:B:417:ARG:NH2	4:B:1116:HOH:O	2.21	0.66
1:A:879:GLU:OE1	4:A:1112:HOH:O	2.14	0.66
1:A:862:ASP:HB2	4:A:1675:HOH:O	1.95	0.66
1:A:848:GLU:OE1	4:A:1111:HOH:O	2.13	0.66
1:B:751:MET:HB2	1:B:752:ASN:CA	2.25	0.66
1:B:524:ASP:OD2	4:B:1110:HOH:O	2.12	0.65
1:A:644:ARG:O	4:A:1113:HOH:O	2.15	0.64
1:B:948:GLY:O	4:B:1112:HOH:O	2.13	0.64
1:A:202:THR:HB	4:A:1188:HOH:O	1.96	0.64
1:A:341:GLU:O	1:A:342:LEU:HB2	1.97	0.64
1:B:245:HIS:CE1	4:B:1108:HOH:O	2.47	0.62
1:B:358:TRP:HE1	1:B:361:ILE:HG12	1.63	0.62
1:B:505:THR:HG21	4:B:1807:HOH:O	1.98	0.62
1:A:337:VAL:O	1:A:341:GLU:HG2	2.00	0.61
1:B:392:GLY:O	1:B:393:ILE:HG13	2.00	0.61
1:B:751:MET:HB2	1:B:752:ASN:HA	1.84	0.60
1:A:235:ASP:OD1	4:A:1114:HOH:O	2.17	0.59
1:A:495:ARG:NH2	4:A:1130:HOH:O	2.34	0.59
1:A:289:ARG:NH2	1:A:300:THR:OG1	2.32	0.58
1:B:355:ILE:HG23	1:B:356:GLU:HG3	1.86	0.58
1:A:116:ARG:HG2	4:A:1493:HOH:O	2.02	0.58
1:B:20:VAL:HG11	1:B:886:GLN:HG3	1.84	0.58
1:B:77:GLU:OE2	1:B:904:TYR:OH	2.22	0.57
1:B:340:ASP:OD2	4:B:1114:HOH:O	2.18	0.57
1:A:402:PHE:O	4:A:1115:HOH:O	2.17	0.57
1:A:796:ARG:NH2	4:A:1136:HOH:O	2.38	0.56
1:B:505:THR:CG2	1:B:508:ILE:H	2.18	0.56
1:B:851:TRP:O	1:B:855:GLU:HG3	2.05	0.56
1:A:180:ARG:HG3	1:A:242:SER:HB3	1.88	0.56
1:A:743:THR:HG22	1:A:745:GLU:H	1.70	0.55
1:B:70:LYS:HD3	1:B:72:GLU:CG	2.37	0.55
1:B:14:ALA:HA	1:B:17:ARG:NH1	2.21	0.55
1:A:577:ARG:NE	4:A:1143:HOH:O	2.40	0.54
1:A:159:ASP:OD2	4:A:1116:HOH:O	2.18	0.54
1:A:32:GLU:HG3	4:A:1710:HOH:O	2.07	0.54
1:B:290:ASP:O	1:B:770:ARG:NH2	2.35	0.53
1:B:180:ARG:CZ	1:B:242:SER:HA	2.37	0.53
1:A:353:HIS:NE2	4:A:1129:HOH:O	2.33	0.53
1:B:442:PHE:HB3	1:B:446:LEU:HD23	1.91	0.52
1:B:713:LEU:HD22	1:B:808:MET:CE	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:LYS:NZ	1:A:520:GLU:OE2	2.37	0.52
1:B:289:ARG:HG3	1:B:452:ARG:O	2.11	0.51
1:B:358:TRP:O	1:B:359:LYS:HE2	2.11	0.51
1:B:704:ILE:HD11	1:B:816:TRP:HA	1.93	0.51
1:A:743:THR:CG2	1:A:777:ALA:HB1	2.41	0.51
1:B:713:LEU:HD22	1:B:808:MET:HE3	1.92	0.51
1:A:770:ARG:HB2	1:A:773:PRO:HD2	1.93	0.51
1:B:646:GLY:N	4:B:1142:HOH:O	2.42	0.51
1:A:820:ARG:HD3	4:A:1204:HOH:O	2.10	0.51
1:B:358:TRP:CB	1:B:375:ARG:HH12	2.24	0.51
1:B:358:TRP:HB2	1:B:375:ARG:HH12	1.76	0.50
1:B:178:VAL:HG13	1:B:182:LEU:HD23	1.93	0.50
1:B:804:ARG:HG2	4:B:1816:HOH:O	2.10	0.50
1:A:638:ARG:NH1	4:A:1131:HOH:O	2.35	0.50
1:A:874:HIS:CE1	4:A:1137:HOH:O	2.64	0.50
1:B:767:GLU:H	1:B:767:GLU:CD	2.20	0.49
1:B:176:GLN:HG3	1:B:176:GLN:O	2.12	0.49
1:B:820:ARG:HD3	4:B:1298:HOH:O	2.12	0.49
1:A:767:GLU:H	1:A:767:GLU:CD	2.21	0.49
1:A:843:LYS:NZ	4:A:1133:HOH:O	2.38	0.49
3:A:1002:FLC:OA1	3:A:1002:FLC:OHB	2.27	0.49
1:A:751:MET:HG2	1:A:954:ILE:HD11	1.93	0.48
1:B:782:ARG:NH2	4:B:1148:HOH:O	2.45	0.48
1:A:240:GLY:O	4:A:1117:HOH:O	2.20	0.48
1:B:15:GLN:NE2	4:B:1113:HOH:O	2.29	0.48
1:A:743:THR:CG2	1:A:745:GLU:H	2.26	0.48
1:B:505:THR:HG22	1:B:508:ILE:HB	1.96	0.47
1:B:180:ARG:NH1	4:B:1129:HOH:O	2.36	0.47
1:A:111:VAL:O	1:A:115:HIS:HD2	1.97	0.47
1:B:500:PRO:C	1:B:502:LEU:H	2.22	0.47
1:B:598:TYR:OH	1:B:636:HIS:ND1	2.44	0.46
1:A:340:ASP:O	1:A:343:HIS:HB2	2.16	0.46
1:B:751:MET:HB2	1:B:752:ASN:HB2	1.97	0.46
1:A:399:GLU:H	1:A:399:GLU:CD	2.24	0.46
1:A:382:ARG:NH1	1:A:383:GLU:OE2	2.49	0.45
1:B:445:SER:O	1:B:446:LEU:HB2	2.16	0.45
1:A:952:THR:O	1:A:956:THR:HG23	2.16	0.45
1:B:180:ARG:CZ	1:B:242:SER:CA	2.93	0.45
1:B:505:THR:HG23	1:B:508:ILE:H	1.80	0.45
1:B:615:TYR:CD2	1:B:657:PRO:HG3	2.52	0.45
1:A:284:TRP:CD1	1:A:450:ASP:HB2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:504:LYS:NZ	4:A:1159:HOH:O	2.49	0.45
1:B:320:GLU:OE1	1:B:357:PHE:HB3	2.17	0.45
1:A:319:ILE:HD11	1:A:371:LEU:HD22	1.99	0.45
1:B:734:ARG:HD2	1:B:737:GLU:OE1	2.16	0.45
1:B:202:THR:HG23	4:B:1523:HOH:O	2.16	0.44
1:B:501:ASP:O	1:B:502:LEU:C	2.60	0.44
1:B:734:ARG:HH22	1:B:849:ASP:CG	2.25	0.44
1:A:391:ASN:O	1:A:393:ILE:N	2.50	0.44
1:B:325:GLU:OE1	4:B:1115:HOH:O	2.20	0.44
1:B:475:TYR:HA	1:B:478:TRP:CE3	2.52	0.44
1:B:307:ALA:HB1	1:B:445:SER:O	2.18	0.44
1:A:244:PHE:HA	1:A:248:ILE:HB	2.00	0.43
1:A:298:GLU:CD	1:A:298:GLU:H	2.26	0.43
1:B:499:GLY:N	1:B:500:PRO:CD	2.80	0.43
1:A:197:TYR:HB2	4:A:1513:HOH:O	2.18	0.43
1:A:814:LYS:HA	1:A:820:ARG:HH21	1.84	0.43
1:A:158:PHE:CE2	1:A:162:LYS:HD2	2.53	0.43
1:A:598:TYR:OH	1:A:636:HIS:ND1	2.47	0.43
1:A:130:GLU:O	1:A:650:HIS:HB3	2.18	0.43
1:A:67:TYR:O	1:A:71:ARG:N	2.50	0.43
1:A:487:LEU:HD13	1:A:541:LEU:HB2	2.01	0.43
1:A:336:ARG:NH1	1:A:366:PRO:HG3	2.34	0.43
1:B:102:LEU:HG	1:B:894:TYR:HB2	2.01	0.43
1:A:397:PRO:HB2	1:A:399:GLU:OE1	2.18	0.43
1:A:743:THR:HG21	1:A:777:ALA:HB1	2.00	0.43
1:A:713:LEU:O	1:A:717:MET:HG3	2.18	0.43
1:B:740:ARG:NH2	4:B:1160:HOH:O	2.51	0.43
1:B:721:ALA:HB2	1:B:794:ALA:HB2	2.01	0.42
1:B:862:ASP:HB2	4:B:1646:HOH:O	2.19	0.42
1:A:145:ARG:HD2	4:A:1439:HOH:O	2.18	0.42
1:B:704:ILE:H	1:B:704:ILE:HG13	1.72	0.42
1:A:201:ILE:HG22	1:A:201:ILE:O	2.19	0.42
1:A:475:TYR:HA	1:A:478:TRP:CE3	2.55	0.42
1:A:709:GLU:HG3	1:A:808:MET:HE2	2.01	0.42
1:B:751:MET:HB2	1:B:752:ASN:CB	2.50	0.42
1:B:884:LEU:HB2	3:B:1002:FLC:OA2	2.20	0.42
1:B:527:GLY:HA3	4:B:1191:HOH:O	2.18	0.42
1:A:717:MET:HE1	1:A:795:PHE:CD1	2.55	0.42
1:A:491:LEU:HD22	1:A:583:TRP:CZ2	2.54	0.42
1:B:145:ARG:HD2	4:B:1645:HOH:O	2.20	0.42
1:B:185:LYS:HE3	1:B:219:ALA:HB1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:475:TYR:CZ	1:B:483:ARG:HD3	2.55	0.42
1:B:495:ARG:HD2	4:B:1613:HOH:O	2.19	0.42
1:B:704:ILE:HD12	1:B:704:ILE:O	2.19	0.42
1:B:801:LYS:NZ	4:B:1161:HOH:O	2.51	0.42
1:A:949:LEU:HA	4:A:1103:HOH:O	2.19	0.42
1:B:14:ALA:C	1:B:16:LEU:N	2.75	0.42
1:B:244:PHE:HA	1:B:248:ILE:HB	2.01	0.42
1:B:110:GLU:OE1	1:B:190:ARG:HD3	2.20	0.41
1:A:646:GLY:N	4:A:1165:HOH:O	2.52	0.41
1:A:393:ILE:O	1:A:393:ILE:HG13	2.19	0.41
1:A:846:VAL:HG12	1:A:847:SER:O	2.20	0.41
1:A:875:LYS:N	1:A:875:LYS:HD3	2.34	0.41
1:B:15:GLN:HG2	4:B:1113:HOH:O	2.19	0.41
1:B:120:LYS:HA	1:B:120:LYS:HD3	1.78	0.41
1:B:270:GLU:OE2	4:B:1117:HOH:O	2.21	0.41
1:A:233:PRO:HB3	4:A:1770:HOH:O	2.20	0.41
1:B:17:ARG:HG2	1:B:31:VAL:HG11	2.03	0.41
1:A:37:LEU:HD11	1:A:193:LEU:HD11	2.03	0.41
1:A:743:THR:HG23	1:A:777:ALA:HB1	2.02	0.41
1:B:355:ILE:C	1:B:356:GLU:HG3	2.45	0.41
1:A:290:ASP:OD1	1:A:454:GLU:HG3	2.20	0.41
1:B:70:LYS:HE2	1:B:72:GLU:HG2	2.03	0.40
1:B:463:ASP:O	1:B:467:LYS:HB2	2.21	0.40
1:A:284:TRP:CH2	1:A:595:MET:HE1	2.57	0.40
1:A:391:ASN:C	1:A:393:ILE:H	2.28	0.40
1:B:505:THR:HG23	1:B:507:GLU:N	2.36	0.40

All (3) 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)
4:B:1731:HOH:O	4:B:1735:HOH:O[4_566]	1.83	0.37
4:B:1253:HOH:O	4:B:1592:HOH:O[1_554]	2.08	0.12
4:B:1759:HOH:O	4:B:1799:HOH:O[4_566]	2.18	0.02

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	906/987 (92%)	879 (97%)	24 (3%)	3 (0%)	36	42
1	B	890/987 (90%)	858 (96%)	26 (3%)	6 (1%)	18	19
All	All	1796/1974 (91%)	1737 (97%)	50 (3%)	9 (0%)	24	27

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	344	ARG
1	B	14	ALA
1	B	15	GLN
1	B	360	THR
1	B	393	ILE
1	B	357	PHE
1	B	500	PRO
1	A	352	LYS
1	A	392	GLY

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	798/860 (93%)	793 (99%)	5 (1%)	78	89
1	B	786/860 (91%)	782 (100%)	4 (0%)	81	90
All	All	1584/1720 (92%)	1575 (99%)	9 (1%)	78	89

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	164	GLN
1	A	202	THR
1	A	342	LEU
1	A	565	LEU
1	A	743	THR
1	B	75	LYS
1	B	94	ILE
1	B	202	THR
1	B	328	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	176	GLN
1	A	186	HIS
1	A	195	GLN
1	A	245	HIS
1	A	387	GLN
1	A	551	HIS
1	A	592	GLN
1	A	866	ASN
1	A	886	GLN
1	A	915	ASN
1	B	245	HIS
1	B	321	ASN
1	B	586	ASN
1	B	592	GLN
1	B	807	HIS
1	B	886	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](#)

4 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	ASP	B	1001	-	7,8,8	1.18	1 (14%)	6,10,10	0.96	0
2	ASP	A	1001	-	7,8,8	1.05	0	6,10,10	0.92	0
3	FLC	A	1002	-	12,12,12	1.33	1 (8%)	17,17,17	2.31	6 (35%)
3	FLC	B	1002	-	12,12,12	1.38	1 (8%)	17,17,17	2.17	5 (29%)

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	ASP	B	1001	-	-	0/8/8/8	-
2	ASP	A	1001	-	-	0/8/8/8	-
3	FLC	A	1002	-	-	0/16/16/16	-
3	FLC	B	1002	-	-	0/16/16/16	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1002	FLC	CB-CBC	2.52	1.56	1.53
3	A	1002	FLC	CB-CBC	2.47	1.56	1.53
2	B	1001	ASP	OXT-C	-2.22	1.23	1.30

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1002	FLC	OB2-CBC-CB	6.00	124.65	113.14
3	A	1002	FLC	CB-CA-CAC	-5.13	99.89	113.92
3	A	1002	FLC	OB2-CBC-CB	5.10	122.93	113.14
3	B	1002	FLC	CB-CA-CAC	-4.03	102.91	113.92
3	B	1002	FLC	OB2-CBC-OB1	-2.53	115.78	123.86
3	A	1002	FLC	OB2-CBC-OB1	-2.39	116.21	123.86
3	A	1002	FLC	OHB-CB-CBC	2.32	112.25	108.96
3	A	1002	FLC	CG-CB-CA	2.17	114.89	109.31
3	B	1002	FLC	CG-CB-CBC	2.16	114.82	110.03
3	A	1002	FLC	OHB-CB-CA	-2.07	104.65	109.38
3	B	1002	FLC	OG2-CGC-OG1	-2.04	118.08	123.33

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1002	FLC	1	0
3	B	1002	FLC	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	914/987 (92%)	-1.63	1 (0%) 92 90	11, 24, 50, 100	0
1	B	900/987 (91%)	-1.67	0 100 100	10, 24, 48, 72	0
All	All	1814/1974 (91%)	-1.65	1 (0%) 92 90	10, 24, 49, 100	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	226	ILE	2.1

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
2	ASP	A	1001	9/9	0.99	0.03	16,21,22,23	0
2	ASP	B	1001	9/9	0.99	0.03	18,21,24,24	0
3	FLC	A	1002	13/13	0.99	0.03	16,26,34,46	0
3	FLC	B	1002	13/13	0.99	0.03	18,23,35,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.