



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 10:17 PM BST

PDB ID : 6O7L
Title : Nitrogenase MoFeP mutant S188A from *Azotobacter vinelandii* in the dithionite reduced state after redox cycling
Authors : Rutledge, H.L.; Tezcan, F.A.
Deposited on : 2019-03-08
Resolution : 2.26 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 : 2.13.1
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) : 2.13.1

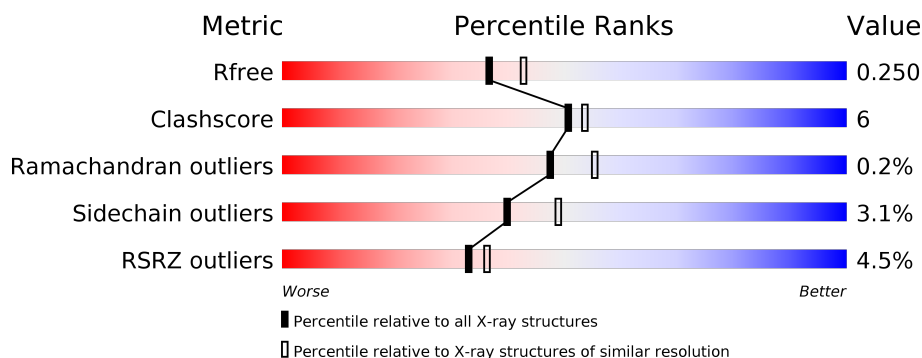
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	492	<div> <div>6%</div> <div> <div></div> <div>79%</div> <div>15%</div> <div></div> </div> <div></div> </div>
1	C	492	<div> <div>7%</div> <div> <div></div> <div>75%</div> <div>20%</div> <div></div> </div> <div></div> </div>
2	B	523	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>11%</div> <div></div> </div> <div></div> </div>
2	D	523	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>10%</div> <div></div> </div> <div></div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 31202 atoms, of which 15166 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 Nitrogenase molybdenum-iron protein alpha chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	473	Total	C	H	N	O	S	0	0	0
			7290	2362	3582	629	693	24			
1	C	472	Total	C	H	N	O	S	0	0	0
			7220	2345	3539	627	684	25			

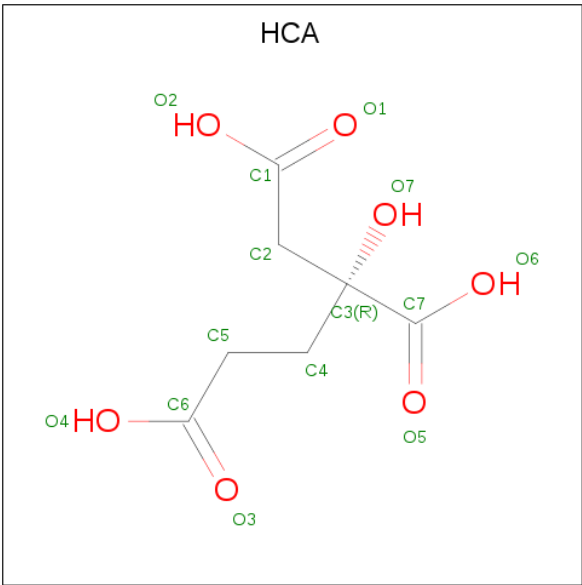
- Molecule 2 is a protein called Nitrogenase molybdenum-iron protein beta chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	522	Total	C	H	N	O	S	0	0	0
			8164	2648	4019	699	770	28			
2	D	522	Total	C	H	N	O	S	0	0	0
			8156	2646	4014	698	770	28			

There are 2 discrepancies between the modelled and reference sequences:

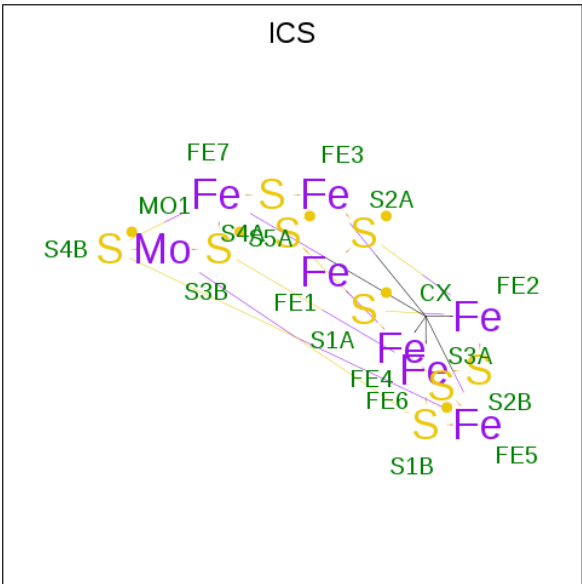
Chain	Residue	Modelled	Actual	Comment	Reference
B	188	ALA	SER	engineered mutation	UNP P07329
D	188	ALA	SER	engineered mutation	UNP P07329

- Molecule 3 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (three-letter code: HCA) (formula: C₇H₁₀O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			20	7	6	7		
3	C	1	Total	C	H	O	0	0
			20	7	6	7		

- Molecule 4 is iron-sulfur-molybdenum cluster with interstitial carbon (three-letter code: ICS) (formula: CFe₇MoS₉).



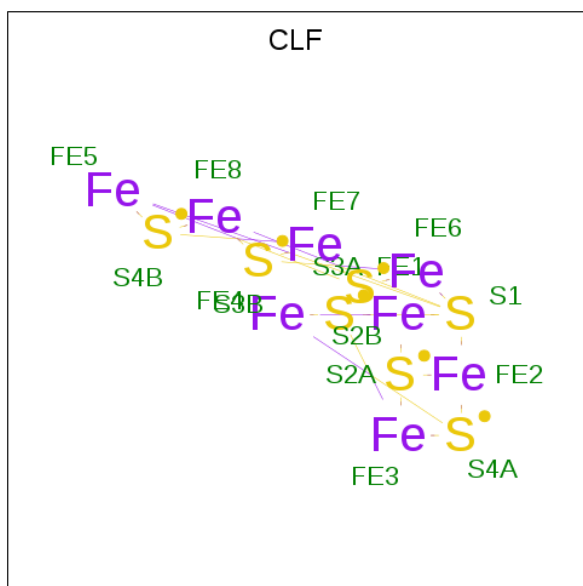
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	Mo	S	0	0
			18	1	7	1	9		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	Fe	Mo	S	
			18	1	7	1	9	
							0	0

- Molecule 5 is FE(8)-S(7) CLUSTER (three-letter code: CLF) (formula: Fe₈S₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	Fe	S		
			15	8	7		
						0	0
5	D	1	Total	Fe	S		
			15	8	7		
						0	0

- Molecule 6 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	2	Total	Fe		
			2	2		
					0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	53	Total	O		
			53	53		
					0	0
7	B	84	Total	O		
			84	84		
					0	0
7	C	38	Total	O		
			38	38		
					0	0

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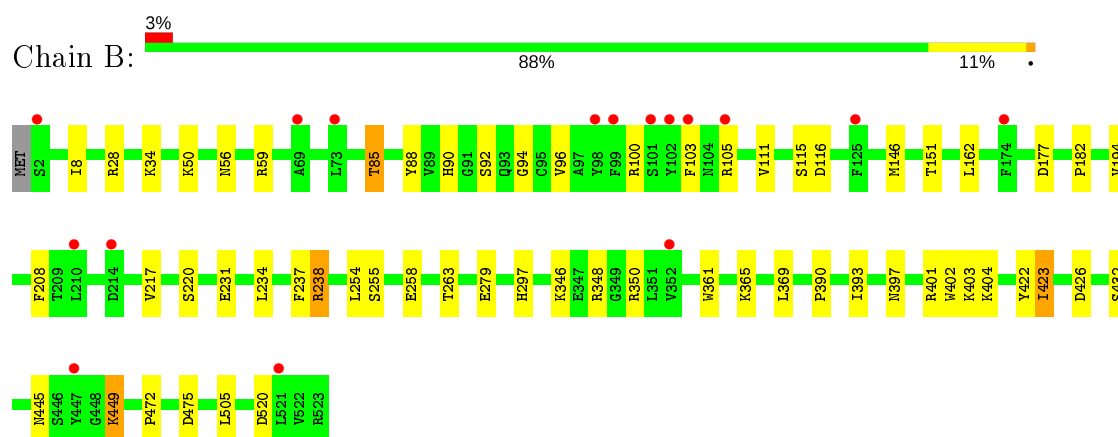
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	89	Total	O	0	0
			89	89		

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.

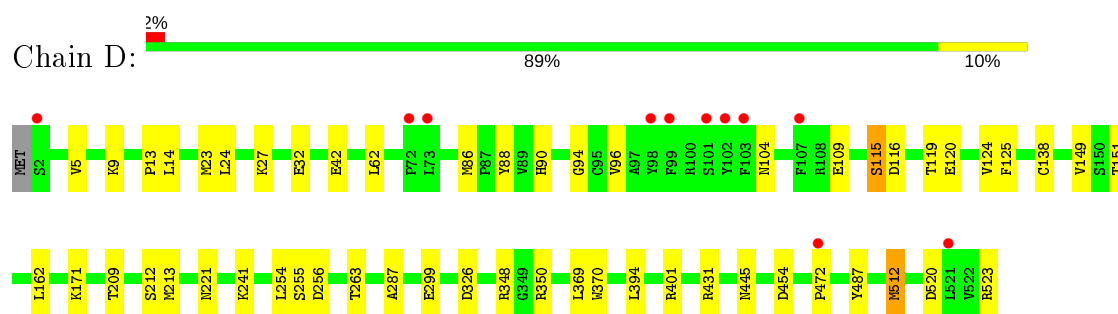
- Chain A:
-
- 6% 79% 15%
- MET THR GLY H4 S5 R6 V9 L12 V16 V19 K30 D36 P37 ALA VAL THR GLN S42 K43 K44 C45 I46 I47 K50 K60 G61 G62 G69 V70 D77 I81 S82 G87 C88 G89 Q90 I91 S92 R93 A94 R97 R98 T104 F125
- L134 S149 E153 E164 A172 E173 L174 T177 R182 L207 R210 D211 E212 D213 T219 P220 Y221 D222 V223 I226 N230 I231 A235 R239 E244 R248 Q252 W253 S254 S258 E263 L272 V273 H274 C275 I276 R277 S278 N279 I280
- R284 R289 F299 E318 K330 R343 Y354 I355 L358 R361 K362 V363 I364 E380 F381 A382 D385 D386 K391 M394 G395 D396 S397 T398 Y401 V404 Y407 E408 F409 E410 E411 F412 V413 K414 R415 G424 I425 K433 R439 H442 C443

- Chain C:
-

- 
- WORLD WIDE
PDB
PROTEIN DATA BANK



- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.56 Å 131.03 Å 107.62 Å 90.00° 110.85° 90.00°	Depositor
Resolution (Å)	49.42 – 2.26 49.42 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.42-2.26) 99.9 (49.42-2.26)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.27 Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.208 , 0.254 0.204 , 0.250	Depositor DCC
R_{free} test set	9597 reflections (9.86%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.956	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 33.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.020 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	31202	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.77% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ICS, CLF, HCA, FE

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	0.26	0/3795	0.46	0/5127
1	C	0.28	0/3768	0.46	0/5096
2	B	0.27	0/4251	0.43	0/5755
2	D	0.26	0/4248	0.43	0/5752
All	All	0.27	0/16062	0.45	0/21730

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3708	3582	3584	47	0
1	C	3681	3539	3539	68	0
2	B	4145	4019	4022	37	0
2	D	4142	4014	4013	34	0
3	A	14	6	6	1	0
3	C	14	6	6	1	0
4	A	18	0	0	0	0
4	C	18	0	0	1	0
5	B	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	15	0	0	0	0
6	B	2	0	0	0	0
7	A	53	0	0	1	0
7	B	84	0	0	2	0
7	C	38	0	0	7	0
7	D	89	0	0	3	0
All	All	16036	15166	15170	176	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 6.

All (176) 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:C:221:TYR:OH	1:C:317:ASP:OD2	1.67	1.08
1:C:35:ASN:ND2	7:C:601:HOH:O	2.06	0.88
2:D:27:LYS:NZ	2:D:32:GLU:OE2	2.14	0.81
2:D:326:ASP:OD2	2:D:348:ARG:NH1	2.20	0.75
1:C:96:ARG:NH2	4:C:502:ICS:S5A	2.60	0.73
2:B:90:HIS:ND1	2:B:116:ASP:OD2	2.22	0.72
1:C:391:MET:O	7:C:601:HOH:O	2.09	0.69
2:D:241:LYS:NZ	2:D:256:ASP:OD2	2.28	0.66
1:C:445:ASP:OD1	7:C:602:HOH:O	2.13	0.65
1:A:207:LEU:O	7:A:601:HOH:O	2.13	0.65
1:C:159:ILE:O	7:C:603:HOH:O	2.14	0.65
2:D:104:ASN:ND2	2:D:109:GLU:O	2.31	0.62
1:C:44:LYS:N	7:C:605:HOH:O	2.33	0.61
1:A:30:LYS:HB3	1:A:47:ILE:CD1	2.31	0.61
3:C:501:HCA:O2	3:C:501:HCA:O7	2.17	0.60
2:D:32:GLU:OE1	7:D:702:HOH:O	2.17	0.59
2:D:119:THR:OG1	2:D:120:GLU:N	2.35	0.59
1:A:474:LYS:O	2:D:348:ARG:NH2	2.35	0.59
1:A:219:THR:HG23	1:A:221:TYR:H	1.68	0.58
1:C:350:ARG:NH2	1:C:416:ILE:O	2.36	0.58
2:B:105:ARG:NH1	7:B:706:HOH:O	2.36	0.58
1:C:237:SER:OG	1:C:451:HIS:O	2.22	0.58
1:C:145:ASN:O	1:C:176:LYS:NZ	2.37	0.57
1:C:225:ILE:HD11	1:C:228:ASP:HB2	1.86	0.57
2:B:85:THR:HB	2:B:146:MET:HG2	1.87	0.56
1:C:223:VAL:HB	1:C:272:LEU:HD11	1.87	0.56
1:C:306:ILE:HD12	1:C:328:ILE:HG23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:422:TYR:O	2:B:423:ILE:HD12	2.04	0.56
2:D:90:HIS:ND1	2:D:116:ASP:OD2	2.37	0.56
1:A:457:ALA:HB1	2:B:8:ILE:HD12	1.87	0.56
2:D:5:VAL:O	7:D:701:HOH:O	2.16	0.56
1:A:98:ASN:O	1:A:98:ASN:ND2	2.37	0.55
3:A:501:HCA:O1	3:A:501:HCA:O7	2.24	0.55
1:C:433:LYS:NZ	2:D:263:THR:O	2.39	0.55
2:B:361:TRP:O	2:B:365:LYS:NZ	2.40	0.54
1:C:77:ASP:OD2	7:C:604:HOH:O	2.18	0.54
1:C:225:ILE:CD1	1:C:297:TYR:OH	2.56	0.54
1:A:244:GLU:OE2	1:A:330:LYS:NZ	2.40	0.54
2:B:59:ARG:NH2	2:B:426:ASP:OD2	2.42	0.53
1:C:146:LYS:NZ	7:C:604:HOH:O	2.41	0.53
1:C:221:TYR:CE1	1:C:320:ILE:HG12	2.43	0.53
2:D:96:VAL:HG21	2:D:115:SER:HB2	1.91	0.53
2:B:146:MET:HE2	2:B:182:PRO:HD3	1.91	0.52
1:A:210:ARG:HG3	1:A:263:GLU:HB3	1.91	0.52
1:A:354:TYR:CZ	1:A:404:VAL:HG12	2.44	0.52
2:B:231:GLU:HB3	2:B:237:PHE:CZ	2.45	0.52
1:C:6:ARG:HA	1:C:9:VAL:HG22	1.92	0.52
2:B:100:ARG:HD2	2:B:111:VAL:O	2.09	0.51
1:A:82:SER:HB3	1:A:153:GLU:OE2	2.11	0.51
1:C:265:THR:O	1:C:268:VAL:HG22	2.11	0.51
1:C:5:SER:O	1:C:8:GLU:HB3	2.11	0.51
2:B:402:TRP:CZ3	2:B:423:ILE:HD11	2.46	0.50
2:B:151:THR:HG23	2:B:162:LEU:HD11	1.93	0.50
1:A:280:ASN:OD1	1:A:284:ARG:NH1	2.45	0.50
1:C:97:ARG:NH2	1:C:447:SER:O	2.38	0.49
2:D:254:LEU:O	2:D:255:SER:HB3	2.12	0.49
2:D:431:ARG:HD2	2:D:454:ASP:OD2	2.12	0.49
1:A:239:ARG:HD2	1:A:252:GLN:OE1	2.12	0.49
1:C:219:THR:HG22	1:C:221:TYR:H	1.78	0.49
1:A:60:ARG:HD2	1:A:380:GLU:O	2.12	0.48
2:B:520:ASP:OD2	1:C:97:ARG:HD2	2.12	0.48
2:B:238:ARG:NH1	2:B:258:GLU:OE1	2.41	0.48
1:A:164:GLU:OE1	1:A:182:ARG:NH1	2.47	0.48
2:B:403:LYS:NZ	7:B:712:HOH:O	2.46	0.48
1:C:218:SER:HG	1:C:269:LYS:HZ1	1.57	0.48
1:A:277:ARG:NH2	1:A:385:ASP:OD1	2.47	0.48
2:D:124:VAL:HG13	2:D:125:PHE:CD1	2.49	0.48
2:D:209:THR:HB	2:D:213:MET:HE3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:35:ASN:HB3	1:C:400:LEU:HD11	1.95	0.48
1:C:62:CYS:HB3	2:D:94:GLY:HA3	1.95	0.48
1:A:30:LYS:HB3	1:A:47:ILE:HD12	1.95	0.48
1:A:97:ARG:HD2	2:D:520:ASP:OD2	2.14	0.48
1:A:277:ARG:NE	1:A:386:ASP:OD2	2.37	0.47
2:B:449:LYS:HE2	2:B:475:ASP:OD2	2.14	0.47
2:D:299:GLU:OE1	2:D:401:ARG:NH1	2.47	0.47
1:A:433:LYS:NZ	2:B:263:THR:O	2.44	0.47
2:B:50:LYS:HD3	2:B:50:LYS:N	2.29	0.47
1:C:139:GLU:HG3	1:C:174:LEU:HD13	1.95	0.47
1:C:317:ASP:O	1:C:321:GLN:NE2	2.47	0.47
2:D:88:TYR:O	2:D:149:VAL:HA	2.13	0.47
1:A:275:CYS:HA	1:A:358:LEU:HD22	1.97	0.47
1:C:9:VAL:HG23	1:C:34:VAL:HG11	1.95	0.47
2:D:42:GLU:O	7:D:703:HOH:O	2.19	0.47
1:C:359:ARG:N	1:C:360:PRO:CD	2.78	0.47
2:D:9:LYS:HD2	2:D:13:PRO:HG2	1.96	0.47
2:B:445:ASN:HB2	2:B:472:PRO:O	2.14	0.47
1:C:225:ILE:HD12	1:C:297:TYR:OH	2.14	0.46
1:C:77:ASP:OD2	1:C:258:SER:HB2	2.15	0.46
1:A:230:ASN:HA	1:A:235:ALA:H	1.80	0.46
2:D:9:LYS:HE3	2:D:14:LEU:HA	1.97	0.46
2:B:390:PRO:HB2	2:B:393:ILE:HD11	1.98	0.46
1:A:394:MET:HE3	1:A:398:THR:OG1	2.15	0.45
2:B:279:GLU:OE2	2:B:279:GLU:N	2.45	0.45
1:C:280:ASN:O	1:C:284:ARG:HG3	2.16	0.45
1:A:447:SER:OG	1:A:448:GLY:N	2.46	0.45
2:B:254:LEU:O	2:B:255:SER:HB3	2.16	0.45
1:C:190:SER:HB2	1:C:381:PHE:HB3	1.97	0.45
1:C:53:GLN:HB2	1:C:56:LEU:HD12	1.98	0.45
1:A:396:ASP:OD1	1:A:397:SER:N	2.50	0.45
1:C:302:PRO:O	1:C:306:ILE:HG12	2.16	0.45
1:C:219:THR:CG2	1:C:221:TYR:H	2.29	0.45
2:D:86:MET:HG2	2:D:138:CYS:SG	2.56	0.45
1:C:101:ILE:HG13	2:D:24:LEU:HD13	1.98	0.44
2:B:234:LEU:O	2:B:238:ARG:HG3	2.17	0.44
1:A:364:ILE:HD13	1:A:394:MET:HG2	2.00	0.44
1:C:135:ILE:HD13	1:C:178:ILE:HD13	1.99	0.44
1:C:17:LEU:HD22	1:C:20:TYR:CE2	2.53	0.44
1:A:62:CYS:HB3	2:B:94:GLY:HA3	1.98	0.44
1:C:356:GLY:O	1:C:379:TYR:HB3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:326:ASP:OD1	2:D:487:TYR:OH	2.22	0.44
1:C:26:LYS:O	1:C:30:LYS:HD2	2.18	0.44
1:C:207:LEU:HD22	1:C:282:ILE:HD11	2.00	0.44
1:A:12:LEU:HD13	1:A:415:ARG:HG3	2.00	0.43
2:B:397:ASN:N	2:B:397:ASN:OD1	2.49	0.43
1:C:328:ILE:HD12	1:C:328:ILE:H	1.83	0.43
1:A:211:ASP:OD2	1:A:289:LYS:NZ	2.46	0.43
2:D:445:ASN:HB2	2:D:472:PRO:O	2.18	0.43
1:A:361:ARG:HA	1:A:364:ILE:HD12	2.01	0.43
1:C:221:TYR:CE1	1:C:320:ILE:CG1	3.02	0.43
1:A:97:ARG:NH2	1:A:447:SER:O	2.43	0.43
1:C:69:GLY:O	1:C:96:ARG:HD3	2.19	0.43
1:A:81:ILE:HG12	1:A:134:LEU:HD21	2.00	0.43
1:C:203:ARG:HD2	1:C:204:ASP:OD2	2.19	0.43
2:B:346:LYS:O	2:B:350:ARG:HG3	2.19	0.43
1:C:413:VAL:HG13	1:C:418:PRO:HD2	2.01	0.42
1:A:407:TYR:O	1:A:411:GLU:HG2	2.19	0.42
2:D:88:TYR:OH	2:D:116:ASP:HB3	2.18	0.42
2:D:23:MET:SD	2:D:24:LEU:HD23	2.60	0.42
1:A:439:ARG:NH2	1:A:462:ASP:OD1	2.53	0.42
1:C:275:CYS:HA	1:C:358:LEU:HD22	2.01	0.42
2:D:212:SER:OG	2:D:212:SER:O	2.26	0.42
1:C:219:THR:HB	1:C:222:ASP:OD2	2.19	0.42
1:A:410:GLU:HG2	1:A:414:LYS:HZ2	1.85	0.42
2:D:221:ASN:OD1	2:D:287:ALA:HA	2.20	0.42
2:B:50:LYS:H	2:B:50:LYS:HE2	1.84	0.42
2:B:50:LYS:CD	2:B:50:LYS:N	2.83	0.42
2:B:217:VAL:HG13	2:B:220:SER:HB3	2.01	0.42
1:A:104:THR:N	2:D:512:MET:HE2	2.35	0.41
1:C:88:CYS:HB2	1:C:153:GLU:OE2	2.20	0.41
1:C:226:ILE:HB	1:C:273:VAL:HG12	2.01	0.41
1:C:328:ILE:N	1:C:328:ILE:HD12	2.35	0.41
2:B:348:ARG:NH2	1:C:474:LYS:O	2.52	0.41
2:B:103:PHE:HB3	2:B:111:VAL:HG21	2.01	0.41
1:C:148:ILE:O	1:C:178:ILE:HA	2.20	0.41
1:A:97:ARG:O	1:A:231:ILE:HA	2.20	0.41
1:A:223:VAL:HG11	1:A:272:LEU:HD11	2.03	0.41
1:A:50:LYS:HA	1:A:50:LYS:HD3	1.94	0.41
1:C:364:ILE:HD12	1:C:374:VAL:HG21	2.01	0.41
2:D:151:THR:HG23	2:D:162:LEU:HD11	2.03	0.41
1:A:30:LYS:HB3	1:A:47:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:370:TRP:HA	2:D:394:LEU:O	2.21	0.41
1:A:253:TRP:HA	1:A:254:SER:HA	1.88	0.41
1:C:412:PHE:O	1:C:416:ILE:HG12	2.20	0.41
1:A:177:THR:HG23	1:A:177:THR:O	2.20	0.41
1:A:222:ASP:OD1	1:A:248:ARG:NE	2.47	0.41
1:A:274:HIS:HE1	1:A:299:PHE:H	1.68	0.41
2:B:146:MET:HE3	2:B:208:PHE:CZ	2.56	0.41
1:A:226:ILE:HG22	1:A:279:MET:HB3	2.03	0.41
1:C:324:CYS:O	1:C:327:VAL:N	2.54	0.41
1:C:76:LYS:HA	1:C:110:VAL:HG23	2.01	0.41
2:B:96:VAL:HG21	2:B:115:SER:HB2	2.03	0.41
2:B:56:ASN:O	2:B:59:ARG:HD3	2.21	0.41
1:C:221:TYR:HE1	1:C:320:ILE:HG12	1.85	0.41
1:C:302:PRO:HD2	1:C:369:ASP:OD2	2.21	0.40
2:B:194:VAL:HB	2:B:297:HIS:CG	2.56	0.40
1:C:97:ARG:O	1:C:231:ILE:HA	2.21	0.40
1:C:239:ARG:HH21	1:C:252:GLN:HG3	1.86	0.40
1:A:77:ASP:OD2	1:A:258:SER:HB2	2.22	0.40
1:C:134:LEU:HG	2:D:62:LEU:HB2	2.03	0.40
1:C:234:ASP:HB3	1:C:451:HIS:ND1	2.36	0.40
1:A:382:ALA:HB1	1:A:386:ASP:HB2	2.04	0.40
2:B:28:ARG:HG3	2:B:34:LYS:HD2	2.04	0.40
1:C:253:TRP:HA	1:C:254:SER:HA	1.89	0.40
1:C:324:CYS:O	1:C:328:ILE:HD12	2.21	0.40
1:A:477:ALA:C	1:A:479:TRP:H	2.25	0.40
2:B:88:TYR:OH	2:B:116:ASP:HB3	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	469/492 (95%)	443 (94%)	23 (5%)	3 (1%)	25	25
1	C	468/492 (95%)	440 (94%)	27 (6%)	1 (0%)	47	55
2	B	520/523 (99%)	501 (96%)	19 (4%)	0	100	100
2	D	520/523 (99%)	502 (96%)	18 (4%)	0	100	100
All	All	1977/2030 (97%)	1886 (95%)	87 (4%)	4 (0%)	47	55

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	ARG
1	A	44	LYS
1	C	355	ILE
1	A	355	ILE

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	388/415 (94%)	372 (96%)	16 (4%)	30	36
1	C	381/415 (92%)	362 (95%)	19 (5%)	24	26
2	B	445/454 (98%)	434 (98%)	11 (2%)	47	56
2	D	444/454 (98%)	438 (99%)	6 (1%)	67	76
All	All	1658/1738 (95%)	1606 (97%)	52 (3%)	40	49

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	SER
1	A	19	VAL
1	A	44	LYS
1	A	47	ILE
1	A	98	ASN
1	A	149	SER
1	A	252	GLN

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Mol	Chain	Res	Type
1	A	254	SER
1	A	277	ARG
1	A	343	ARG
1	A	362	HIS
1	A	394	MET
1	A	397	SER
1	A	401	TYR
1	A	409	PHE
1	A	445	ASP
2	B	85	THR
2	B	92	SER
2	B	177	ASP
2	B	238	ARG
2	B	369	LEU
2	B	401	ARG
2	B	404	LYS
2	B	423	ILE
2	B	432	SER
2	B	449	LYS
2	B	505	LEU
1	C	6	ARG
1	C	19	VAL
1	C	30	LYS
1	C	36	ASP
1	C	44	LYS
1	C	98	ASN
1	C	121	LYS
1	C	146	LYS
1	C	177	THR
1	C	219	THR
1	C	225	ILE
1	C	254	SER
1	C	277	ARG
1	C	315	LYS
1	C	319	SER
1	C	362	HIS
1	C	401	TYR
1	C	409	PHE
1	C	445	ASP
2	D	115	SER
2	D	171	LYS
2	D	350	ARG

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Mol	Chain	Res	Type
2	D	369	LEU
2	D	512	MET
2	D	523	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	ICS	A	502	1	18,30,30	2.58	11 (61%)	-		
3	HCA	A	501	-	4,13,13	0.61	0	4,18,18	1.51	1 (25%)
3	HCA	C	501	-	4,13,13	0.82	0	4,18,18	1.51	1 (25%)
4	ICS	C	502	1	18,30,30	2.58	10 (55%)	-		
5	CLF	D	601	1,2	0,24,24	0.00	-	-		
5	CLF	B	601	1,2	0,24,24	0.00	-	-		

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
5	CLF	D	601	1,2	-	-	0/12/10/10
3	HCA	A	501	-	-	4/7/17/17	-
5	CLF	B	601	1,2	-	-	0/12/10/10
3	HCA	C	501	-	-	7/7/17/17	-

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	502	ICS	S4B-FE7	-4.25	2.21	2.32
4	A	502	ICS	S4B-FE7	-4.10	2.22	2.32
4	A	502	ICS	S3B-FE6	-4.03	2.22	2.32
4	C	502	ICS	S3B-FE6	-4.02	2.22	2.32
4	A	502	ICS	S1B-FE6	-3.94	2.22	2.32
4	C	502	ICS	S1B-FE6	-3.81	2.23	2.32
4	C	502	ICS	S3B-FE7	-3.21	2.24	2.32
4	A	502	ICS	S4B-FE5	-3.18	2.24	2.32
4	C	502	ICS	S4B-FE5	-3.13	2.24	2.32
4	A	502	ICS	S3B-FE7	-3.04	2.24	2.32
4	A	502	ICS	S2A-FE2	-3.03	2.24	2.32
4	C	502	ICS	S2A-FE2	-3.01	2.24	2.32
4	A	502	ICS	S2B-FE6	-2.94	2.18	2.24
4	C	502	ICS	S4A-FE3	-2.85	2.25	2.32
4	A	502	ICS	S4A-FE3	-2.79	2.25	2.32
4	C	502	ICS	S2B-FE6	-2.77	2.18	2.24
4	A	502	ICS	S1A-FE2	-2.51	2.26	2.32
4	C	502	ICS	S1A-FE2	-2.35	2.26	2.32
4	A	502	ICS	S1B-FE5	-2.29	2.26	2.32
4	C	502	ICS	S1B-FE5	-2.21	2.26	2.32
4	A	502	ICS	S2A-FE3	-2.05	2.27	2.32

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	HCA	C3-C2-C1	-2.89	110.35	114.98
3	C	501	HCA	C3-C2-C1	-2.70	110.66	114.98

There are no chirality outliers.

All (11) torsion outliers are listed below:

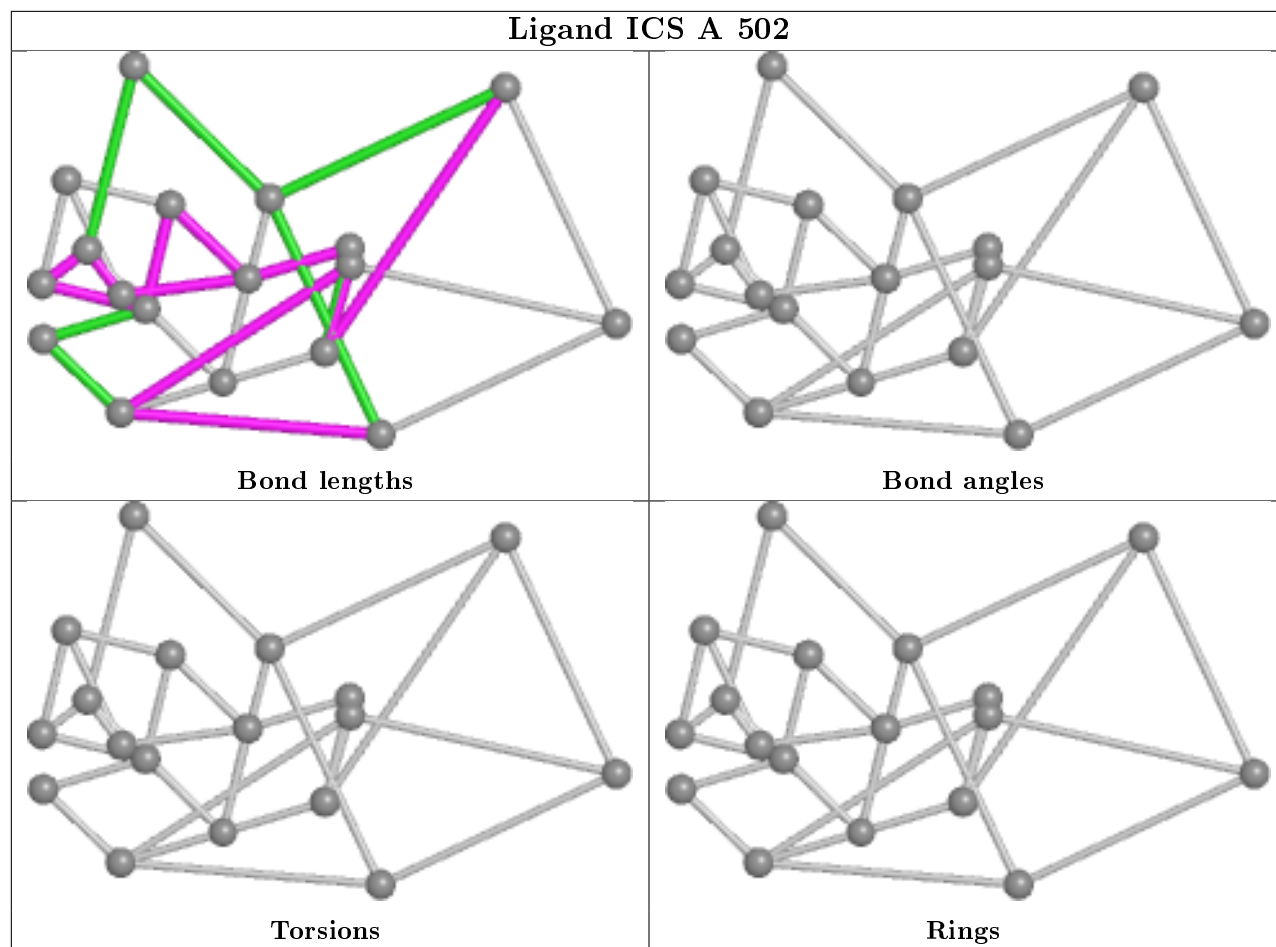
Mol	Chain	Res	Type	Atoms
3	A	501	HCA	C2-C3-C4-C5
3	A	501	HCA	C7-C3-C4-C5
3	A	501	HCA	O7-C3-C4-C5
3	C	501	HCA	C2-C3-C4-C5
3	C	501	HCA	C7-C3-C4-C5
3	C	501	HCA	O7-C3-C4-C5
3	C	501	HCA	C3-C4-C5-C6
3	C	501	HCA	C1-C2-C3-C7
3	C	501	HCA	C1-C2-C3-C4
3	A	501	HCA	C1-C2-C3-C4
3	C	501	HCA	C1-C2-C3-O7

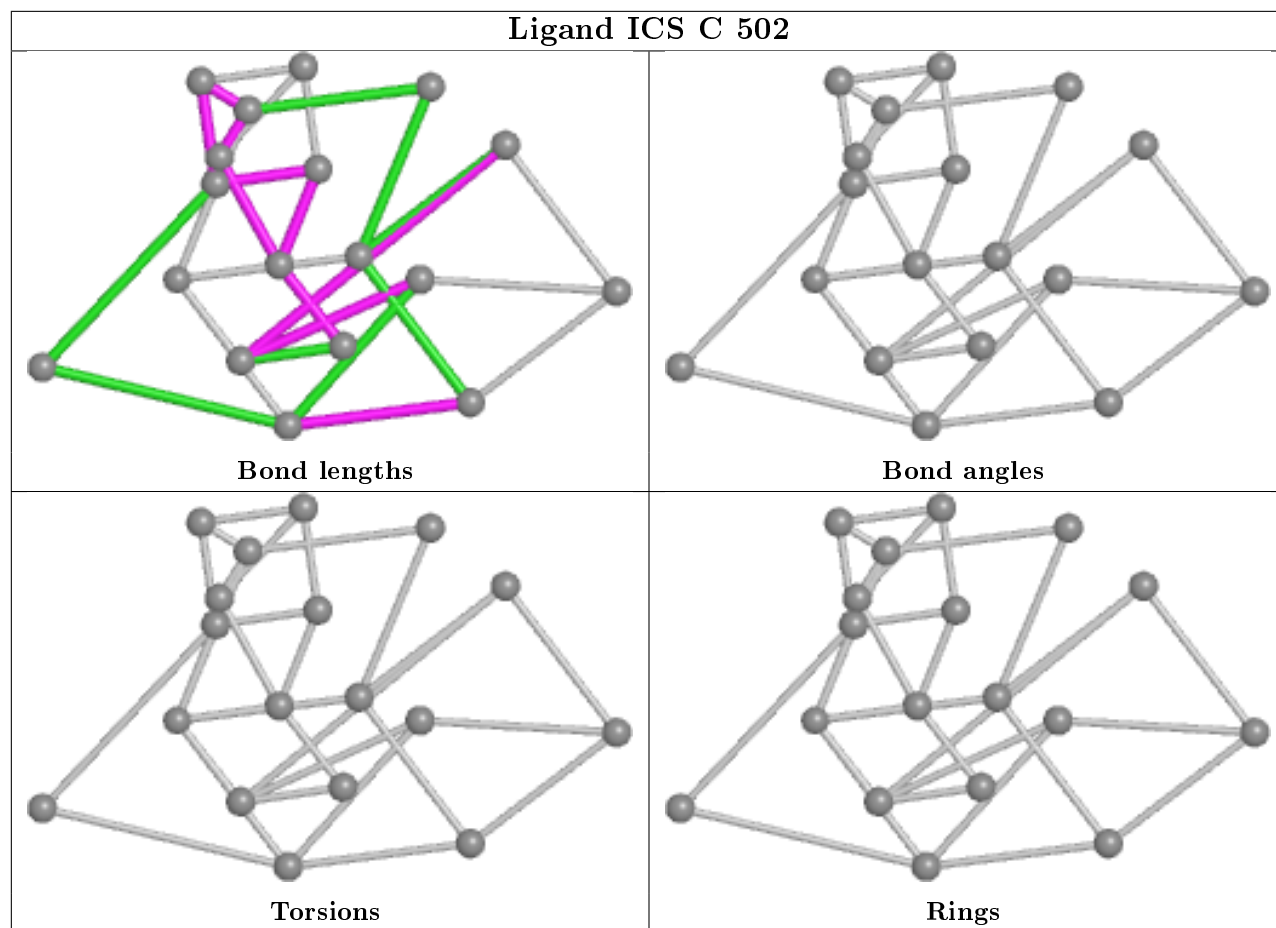
There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	HCA	1	0
3	C	501	HCA	1	0
4	C	502	ICS	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	473/492 (96%)	0.37	30 (6%)	20 22	37, 50, 70, 86	0
1	C	472/492 (95%)	0.53	32 (6%)	17 18	37, 54, 74, 99	0
2	B	522/523 (99%)	0.20	16 (3%)	49 52	36, 48, 63, 81	0
2	D	522/523 (99%)	0.17	11 (2%)	63 66	33, 47, 62, 71	0
All	All	1989/2030 (97%)	0.31	89 (4%)	33 36	33, 50, 67, 99	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	37	PRO	5.5
1	C	175	SER	4.3
1	C	37	PRO	4.0
1	A	91	TYR	3.9
2	B	174	PHE	3.8
1	C	91	TYR	3.8
1	C	46	ILE	3.8
2	D	102	TYR	3.7
1	C	45	CYS	3.6
2	B	102	TYR	3.6
1	A	172	ALA	3.5
1	A	9	VAL	3.4
2	D	98	TYR	3.4
2	B	98	TYR	3.3
1	C	95	GLY	3.2
1	A	87	GLY	3.1
1	A	45	CYS	3.1
1	A	36	ASP	3.0
1	C	13	ILE	2.9
1	A	318	GLU	2.8
1	A	425	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	19	VAL	2.7
1	C	225	ILE	2.7
2	D	103	PHE	2.7
2	B	101	SER	2.6
1	A	16	VAL	2.6
1	C	481	ALA	2.6
1	A	444	TRP	2.6
1	A	443	SER	2.5
1	C	250	VAL	2.5
1	C	213	ASP	2.5
1	C	442	HIS	2.4
2	B	210	LEU	2.4
1	A	125	PHE	2.4
2	B	105	ARG	2.4
1	C	221	TYR	2.4
1	A	174	LEU	2.4
1	A	70	VAL	2.4
1	A	94	ALA	2.4
1	C	391	MET	2.4
1	C	16	VAL	2.4
1	A	42	SER	2.4
1	C	446	TYR	2.4
1	A	442	HIS	2.4
1	C	394	MET	2.4
1	A	213	ASP	2.3
1	C	400	LEU	2.3
1	A	92	SER	2.3
1	C	36	ASP	2.3
2	D	2	SER	2.3
1	C	217	ALA	2.3
1	C	173	GLU	2.3
2	D	472	PRO	2.3
1	A	88	CYS	2.3
1	A	424	GLY	2.3
1	C	425	ILE	2.3
1	C	476	GLN	2.3
1	A	412	PHE	2.2
2	B	99	PHE	2.2
2	D	101	SER	2.2
1	A	415	ARG	2.2
1	A	446	TYR	2.2
1	C	388	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	34	VAL	2.2
1	C	444	TRP	2.2
2	D	73	LEU	2.2
2	B	447	TYR	2.2
2	D	72	PRO	2.2
2	D	99	PHE	2.2
1	A	391	MET	2.2
1	A	93	ARG	2.1
1	C	273	VAL	2.1
2	D	521	LEU	2.1
1	C	92	SER	2.1
2	B	521	LEU	2.1
2	B	125	PHE	2.1
2	B	214	ASP	2.1
2	B	2	SER	2.1
2	B	352	VAL	2.1
2	D	107	PHE	2.1
2	B	103	PHE	2.1
2	B	73	LEU	2.0
1	C	384	ASN	2.0
1	A	89	GLY	2.0
1	A	69	GLY	2.0
2	B	69	ALA	2.0
1	C	375	VAL	2.0
1	C	480	GLU	2.0
1	A	90	GLN	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](#)

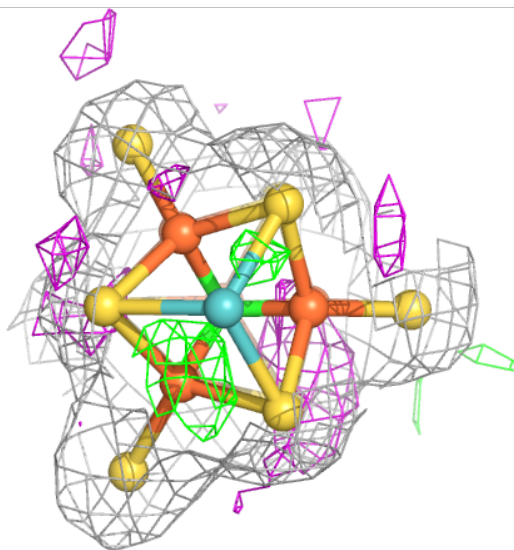
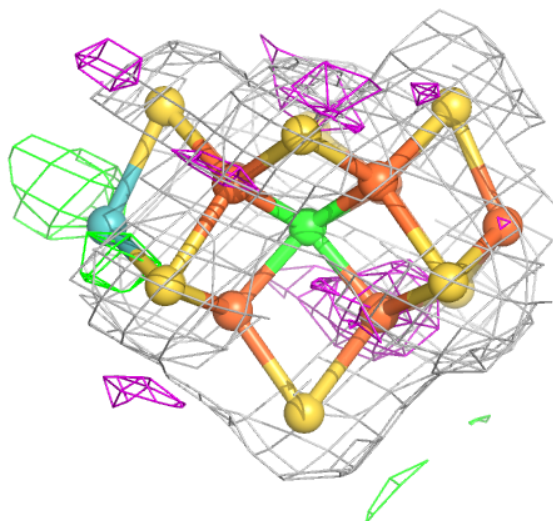
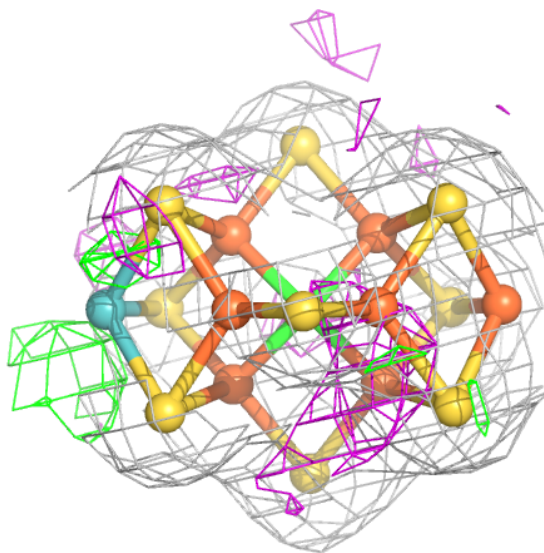
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	FE	B	603	1/1	0.80	0.26	53,53,53,53	1
3	HCA	C	501	14/14	0.93	0.21	41,45,54,54	0
3	HCA	A	501	14/14	0.95	0.19	36,42,46,46	0
5	CLF	D	601	15/15	0.96	0.11	33,47,57,59	0
5	CLF	B	601	15/15	0.96	0.12	41,48,59,59	0
4	ICS	C	502	18/18	0.98	0.10	36,47,58,62	0
4	ICS	A	502	18/18	0.98	0.11	34,44,54,57	0
6	FE	B	602	1/1	0.98	0.23	52,52,52,52	1

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.

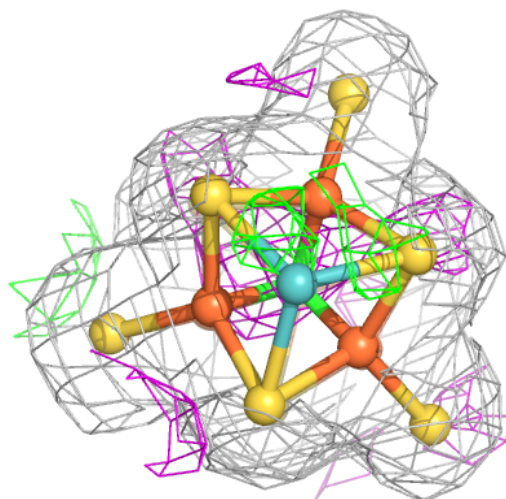
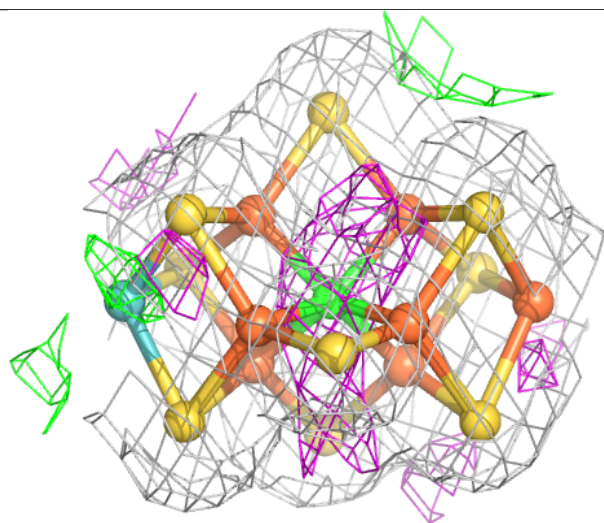
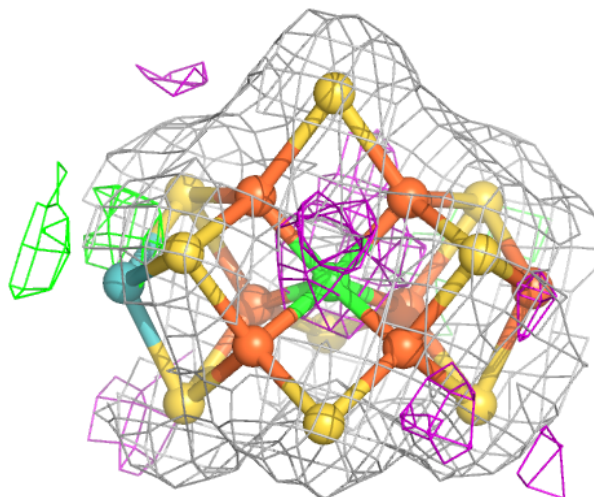
Electron density around ICS C 502:

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



Electron density around ICS A 502:

$2mF_o-DF_c$ (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.