



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:59 AM UTC

PDB ID : 1CVS / pdb_00001cvs
Title : CRYSTAL STRUCTURE OF A DIMERIC FGF2-FGFR1 COMPLEX
Authors : Plotnikov, A.N.; Schlessinger, J.; Hubbard, S.R.; Mohammadi, M.
Deposited on : 1999-08-24
Resolution : 2.80 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

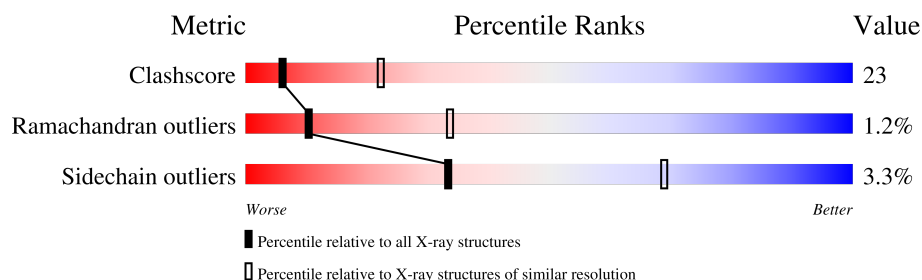
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	132	 59% 36% . .
1	B	132	 58% 38% . . .
2	C	225	 53% 35% 5% 6%
2	D	225	 46% 38% . 13%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5173 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 FIBROBLAST GROWTH FACTOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			1040	660	190	186	4			
1	B	129	Total	C	N	O	S	0	0	0
			1040	660	190	186	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	SER	CYS	engineered mutation	UNP P09038
A	87	SER	CYS	engineered mutation	UNP P09038
B	69	SER	CYS	engineered mutation	UNP P09038
B	87	SER	CYS	engineered mutation	UNP P09038

- Molecule 2 is a protein called FIBROBLAST GROWTH FACTOR RECEPTOR 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	211	Total	C	N	O	S	0	0	0
			1588	1015	270	294	9			
2	D	196	Total	C	N	O	S	0	0	0
			1485	951	252	273	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	185	GLN	ASN	engineered mutation	UNP P11362
D	185	GLN	ASN	engineered mutation	UNP P11362

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

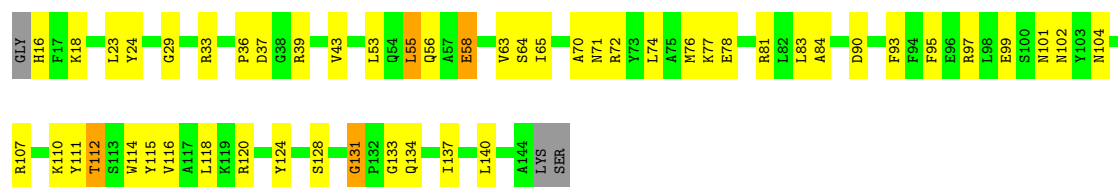
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

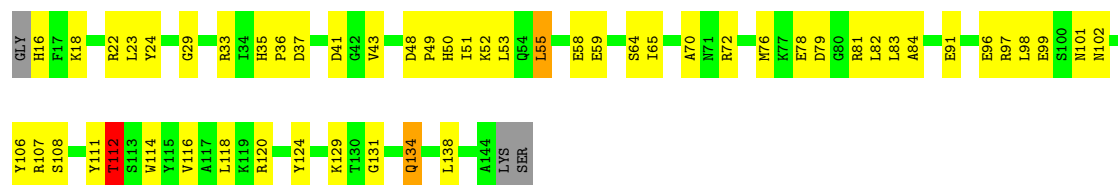
• Molecule 1: FIBROBLAST GROWTH FACTOR 2

Chain A: 



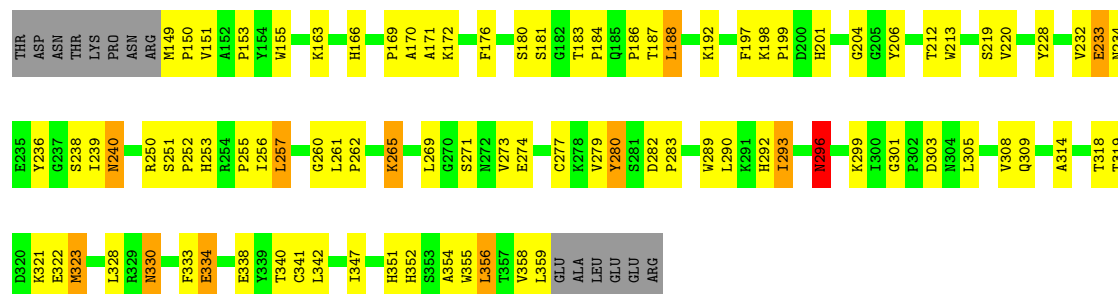
• Molecule 1: FIBROBLAST GROWTH FACTOR 2

Chain B: 

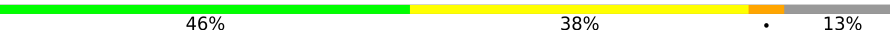


• Molecule 2: FIBROBLAST GROWTH FACTOR RECEPTOR 1

Chain C: 



• Molecule 2: FIBROBLAST GROWTH FACTOR RECEPTOR 1

Chain D: 

THR	ASP	ASN	THR	LYS	PRO	ASN	ARG	M149	P153	Y154	W155	T156	M161	E162	K163	K164	L165	H166	A170	A171	K175	F176	K177	C178	P179	S180	S181	G182	T183	P184	Q185	P186	T187	L188	R189	W190	F197	K198	F199	D200	H201	R202	I203	Y206	T212	I215	D218	S219	V220	V221											
	K225			C230	I231	V232	E233	N234	E235	Y236			I239		L245	D246	V247		R250	S251	P252	H253	R254	P255	I256	L257		P262		K265		L269	G270	S271	N272	V273	E274	F275		V279	Y280	S281	D282	P283	Q284	P285	H286	I287	Q288		K291	H292	ILE	GLU	VAL	ASN	GLY	SER	LYS	ILE	GLY
PRO	ASP	ASN	LEU	PRO	PRO	TYR	V308	L311	K312	T313	A314		T318	T319	D320	K321	E322	M323	E324	V325	L326	H327	L328	R329	M330		E338	Y339	T340	C341	L342	N345		H351	H352	S353	A354	W355	L356	T357	V358	L359	GLU	ALA	LEU	GLU	GLU	ARG													

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.45 Å 98.45 Å 197.03 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.80	Depositor
% Data completeness (in resolution range)	96.9 (25.00-2.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.240 , 0.281	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5173	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.49	0/1063	1.02	6/1425 (0.4%)
1	B	0.50	0/1063	0.99	5/1425 (0.4%)
2	C	0.54	0/1635	1.00	7/2244 (0.3%)
2	D	0.52	0/1528	0.94	2/2092 (0.1%)
All	All	0.52	0/5289	0.98	20/7186 (0.3%)

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	C	0	1
2	D	0	1
All	All	0	2

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	299	LYS	N-CA-C	-8.22	102.29	113.30
1	A	116	VAL	N-CA-C	-7.81	99.53	109.30
1	B	116	VAL	N-CA-C	-7.37	100.09	109.30
1	B	64	SER	N-CA-C	-6.76	98.70	109.59
1	A	64	SER	N-CA-C	-6.65	98.89	109.59
2	C	301	GLY	CA-C-N	6.41	127.86	119.84
2	C	301	GLY	C-N-CA	6.41	127.86	119.84
1	B	58	GLU	N-CA-C	-6.25	105.78	113.41
1	A	131	GLY	CA-C-N	6.23	125.96	119.05
1	A	131	GLY	C-N-CA	6.23	125.96	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	221	VAL	N-CA-CB	-6.13	107.60	111.83
1	A	58	GLU	N-CA-C	-6.07	106.03	113.50
2	D	323	MET	N-CA-C	5.95	120.14	113.01
1	B	112	THR	N-CA-C	5.58	122.68	110.80
2	C	293	ILE	N-CA-C	5.53	117.36	108.85
1	A	112	THR	N-CA-C	5.48	122.47	110.80
2	C	323	MET	N-CA-C	5.37	119.08	112.54
2	C	296	ASN	N-CA-C	-5.28	99.55	110.80
1	B	134	GLN	N-CA-C	5.17	117.67	109.24
2	C	233	GLU	N-CA-C	5.00	116.84	108.99

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	280	TYR	Sidechain
2	D	280	TYR	Sidechain

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	1040	0	1040	39	0
1	B	1040	0	1040	46	0
2	C	1588	0	1499	69	0
2	D	1485	0	1409	87	0
3	A	10	0	0	1	0
3	B	10	0	0	1	0
All	All	5173	0	4988	230	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 23.

All (230) 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:C:240:ASN:C	2:C:240:ASN:HD22	1.82	0.87
1:B:82:LEU:HD12	1:B:124:TYR:HB2	1.59	0.84
2:C:293:ILE:HD11	2:C:309:GLN:HB2	1.61	0.82
2:D:342:LEU:HD22	2:D:351:HIS:CB	2.13	0.79
1:A:133:GLY:HA3	2:D:200:ASP:HA	1.65	0.78
2:C:260:GLY:O	2:C:261:LEU:HD23	1.83	0.78
1:A:140:LEU:HD13	2:C:169:PRO:HD3	1.66	0.78
2:D:319:THR:HG22	2:D:321:LYS:H	1.50	0.76
2:D:190:TRP:CZ3	2:D:230:CYS:HB3	2.23	0.73
2:D:203:ILE:HD13	2:D:203:ILE:N	2.04	0.73
2:D:161:MET:HE3	2:D:178:CYS:HA	1.71	0.72
2:D:185:GLN:HA	2:D:185:GLN:NE2	2.03	0.72
2:D:342:LEU:HD22	2:D:351:HIS:HB3	1.72	0.70
2:C:172:LYS:O	2:C:220:VAL:HG22	1.92	0.70
2:D:203:ILE:HD13	2:D:203:ILE:H	1.56	0.69
1:B:76:MET:HE2	1:B:108:SER:HB2	1.73	0.68
2:C:282:ASP:HB3	2:C:283:PRO:CD	2.22	0.68
2:C:233:GLU:HG3	2:C:238:SER:HB3	1.76	0.68
2:C:314:ALA:HB2	2:C:323:MET:HG3	1.75	0.68
2:D:262:PRO:HG2	2:D:354:ALA:HB2	1.75	0.68
2:D:203:ILE:H	2:D:203:ILE:CD1	2.07	0.67
2:D:282:ASP:HB3	2:D:283:PRO:CD	2.26	0.66
1:B:76:MET:HE3	1:B:114:TRP:HB2	1.80	0.64
1:B:33:ARG:NH1	1:B:43:VAL:HG11	2.13	0.64
2:D:292:HIS:HD2	2:D:338:GLU:HG2	1.64	0.63
2:D:342:LEU:HD22	2:D:351:HIS:HB2	1.80	0.63
2:C:256:ILE:N	2:C:256:ILE:HD12	2.13	0.63
2:C:240:ASN:C	2:C:240:ASN:ND2	2.54	0.63
1:B:79:ASP:CG	1:B:81:ARG:HH11	2.07	0.62
2:C:253:HIS:CE1	2:C:256:ILE:HD11	2.35	0.62
1:A:72:ARG:HD3	1:A:84:ALA:O	1.99	0.62
1:A:24:TYR:OH	2:C:163:LYS:HE3	2.00	0.62
2:D:257:LEU:CD2	2:D:279:VAL:HG22	2.30	0.61
1:B:98:LEU:HD13	2:D:250:ARG:CZ	2.30	0.61
1:B:131:GLY:N	1:B:134:GLN:NE2	2.48	0.61
1:A:118:LEU:HD23	1:A:124:TYR:HA	1.80	0.61
2:D:225:LYS:HE2	2:D:247:VAL:O	2.00	0.61
1:A:83:LEU:HD12	1:A:83:LEU:C	2.26	0.61
1:B:76:MET:CE	1:B:114:TRP:HB2	2.30	0.61
1:B:59:GLU:HA	2:D:286:HIS:ND1	2.16	0.60
2:D:271:SER:O	2:D:330:ASN:HA	2.01	0.60
2:C:340:THR:HG22	2:C:342:LEU:HD12	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:185:GLN:HA	2:D:185:GLN:HE21	1.67	0.60
1:B:55:LEU:CD1	1:B:65:ILE:HG12	2.31	0.60
2:D:358:VAL:O	2:D:359:LEU:HD23	2.02	0.59
2:C:192:LYS:HE2	2:C:228:TYR:OH	2.03	0.59
1:A:76:MET:HE3	1:A:114:TRP:HB2	1.84	0.59
2:D:319:THR:HG22	2:D:321:LYS:HG3	1.83	0.59
1:B:138:LEU:HD11	2:C:204:GLY:HA2	1.84	0.59
2:C:153:PRO:HA	2:C:181:SER:O	2.03	0.59
2:D:199:PRO:HA	2:D:206:TYR:CE1	2.38	0.59
2:C:170:ALA:O	2:C:171:ALA:HB3	2.02	0.59
2:C:199:PRO:HA	2:C:206:TYR:CE1	2.39	0.58
2:D:319:THR:HG21	2:D:321:LYS:HE3	1.84	0.58
2:D:170:ALA:O	2:D:171:ALA:HB3	2.03	0.58
2:C:257:LEU:HD13	2:C:277:CYS:SG	2.44	0.58
2:D:319:THR:CG2	2:D:321:LYS:HG3	2.34	0.57
2:C:255:PRO:C	2:C:256:ILE:HD12	2.28	0.57
2:C:273:VAL:HG13	2:C:328:LEU:HB2	1.86	0.57
2:C:319:THR:HG22	2:C:321:LYS:HG3	1.86	0.57
2:C:265:LYS:HB2	2:C:356:LEU:HD23	1.87	0.57
1:B:96:GLU:HG3	1:B:106:TYR:CE1	2.40	0.57
2:D:197:PHE:O	2:D:206:TYR:OH	2.23	0.57
2:C:338:GLU:HB2	2:C:355:TRP:CZ3	2.40	0.56
2:D:251:SER:HB2	2:D:282:ASP:HB2	1.88	0.56
2:C:197:PHE:O	2:C:206:TYR:OH	2.23	0.56
2:C:257:LEU:HB2	2:C:352:HIS:CE1	2.40	0.56
2:D:312:LYS:HG2	2:D:323:MET:SD	2.46	0.56
1:A:78:GLU:HA	1:A:111:TYR:CZ	2.41	0.56
2:C:180:SER:OG	2:C:232:VAL:HG11	2.06	0.56
2:D:203:ILE:N	2:D:203:ILE:CD1	2.68	0.56
2:D:163:LYS:HE2	2:D:166:HIS:CD2	2.40	0.55
2:D:282:ASP:HB3	2:D:283:PRO:HD3	1.87	0.55
1:A:71:ASN:O	1:A:71:ASN:ND2	2.40	0.55
2:C:303:ASP:OD2	2:C:305:LEU:HB2	2.07	0.55
2:D:153:PRO:HA	2:D:181:SER:O	2.07	0.55
2:D:340:THR:HG22	2:D:342:LEU:HD23	1.88	0.55
2:D:185:GLN:HE21	2:D:185:GLN:CA	2.18	0.55
2:D:292:HIS:CD2	2:D:338:GLU:HG2	2.41	0.54
1:B:98:LEU:HD13	2:D:250:ARG:NH2	2.22	0.54
2:D:189:ARG:HG3	2:D:231:ILE:HB	1.90	0.54
2:D:161:MET:CE	2:D:178:CYS:HA	2.37	0.54
1:A:134:GLN:O	1:A:137:ILE:HG12	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:LEU:HG	1:B:53:LEU:HD12	1.90	0.54
2:D:314:ALA:HB2	2:D:323:MET:HG3	1.88	0.54
1:A:78:GLU:HA	1:A:111:TYR:CE1	2.42	0.54
1:B:55:LEU:N	1:B:55:LEU:HD22	2.22	0.53
2:D:165:LEU:HD12	2:D:166:HIS:N	2.22	0.53
2:D:279:VAL:HG12	2:D:280:TYR:N	2.22	0.53
2:C:282:ASP:HB3	2:C:283:PRO:HD3	1.92	0.52
2:D:342:LEU:CD2	2:D:351:HIS:HB2	2.39	0.52
2:C:261:LEU:HA	2:C:262:PRO:C	2.33	0.52
1:A:101:ASN:O	1:A:102:ASN:HB2	2.10	0.52
1:A:104:ASN:OD1	2:C:250:ARG:NH2	2.37	0.52
2:C:234:ASN:OD1	2:C:234:ASN:C	2.53	0.52
1:A:33:ARG:CZ	1:A:43:VAL:HG11	2.40	0.51
1:B:101:ASN:O	1:B:102:ASN:HB2	2.09	0.51
2:C:150:PRO:HB3	2:C:236:TYR:CZ	2.45	0.51
1:B:37:ASP:C	1:B:37:ASP:OD1	2.54	0.51
1:B:59:GLU:HA	2:D:286:HIS:CE1	2.46	0.51
2:C:166:HIS:CG	2:C:176:PHE:HE1	2.29	0.51
2:C:319:THR:CG2	2:C:321:LYS:HG3	2.42	0.50
2:D:325:VAL:HG13	2:D:325:VAL:O	2.11	0.50
1:B:79:ASP:OD2	1:B:81:ARG:HG2	2.12	0.50
1:A:76:MET:HE3	1:A:114:TRP:CB	2.42	0.49
1:B:107:ARG:HD2	1:B:112:THR:O	2.13	0.49
1:B:35:HIS:HE2	1:B:41:ASP:CG	2.20	0.49
2:C:149:MET:O	2:C:149:MET:HG3	2.11	0.49
2:C:319:THR:HG21	2:C:321:LYS:HE3	1.95	0.49
2:D:318:THR:HG22	2:D:323:MET:SD	2.52	0.49
2:C:155:TRP:CE2	2:C:239:ILE:HD12	2.48	0.49
2:C:293:ILE:CD1	2:C:309:GLN:HB2	2.38	0.49
2:C:338:GLU:HB2	2:C:355:TRP:CE3	2.47	0.49
1:A:90:ASP:OD2	1:A:110:LYS:HD2	2.12	0.49
2:C:358:VAL:O	2:C:359:LEU:HD23	2.13	0.49
2:C:290:LEU:HD23	2:C:308:VAL:HG11	1.95	0.49
2:C:262:PRO:HG2	2:C:354:ALA:HB2	1.95	0.48
1:B:48:ASP:CG	1:B:49:PRO:HD2	2.38	0.48
2:C:296:ASN:N	2:C:296:ASN:OD1	2.45	0.48
1:A:58:GLU:HG2	1:A:93:PHE:CE1	2.49	0.48
2:D:183:THR:HA	2:D:184:PRO:C	2.37	0.48
1:A:33:ARG:CZ	1:A:43:VAL:CG1	2.92	0.48
1:A:36:PRO:HA	1:A:70:ALA:CB	2.44	0.48
2:D:234:ASN:OD1	2:D:234:ASN:C	2.57	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:ASP:HB3	1:B:51:ILE:HG23	1.96	0.48
2:D:156:THR:HG23	2:D:180:SER:C	2.38	0.47
1:B:120:ARG:HG3	3:B:2:SO4:O2	2.14	0.47
1:A:55:LEU:N	1:A:55:LEU:CD2	2.77	0.47
1:B:83:LEU:C	1:B:83:LEU:HD12	2.39	0.47
2:C:183:THR:HA	2:C:184:PRO:C	2.38	0.47
2:C:198:LYS:H	2:C:201:HIS:CE1	2.32	0.47
2:C:257:LEU:HD12	2:C:352:HIS:HB2	1.97	0.47
2:D:170:ALA:O	2:D:171:ALA:CB	2.63	0.47
1:A:65:ILE:HD12	1:A:74:LEU:HD23	1.97	0.47
2:C:271:SER:O	2:C:330:ASN:HA	2.15	0.47
1:A:81:ARG:HB2	1:A:124:TYR:OH	2.16	0.46
2:D:269:LEU:HD23	2:D:270:GLY:N	2.31	0.46
1:B:131:GLY:H	1:B:134:GLN:NE2	2.13	0.46
2:C:253:HIS:CE1	2:C:256:ILE:CD1	2.98	0.46
2:D:178:CYS:N	2:D:179:PRO:HD3	2.31	0.46
2:D:155:TRP:CZ3	2:D:178:CYS:HB3	2.50	0.46
2:D:189:ARG:CG	2:D:231:ILE:HB	2.45	0.46
2:D:273:VAL:HG13	2:D:328:LEU:HB2	1.97	0.46
2:D:291:LYS:HB2	2:D:311:LEU:HD11	1.96	0.46
1:B:124:TYR:CD1	1:B:124:TYR:C	2.94	0.46
1:B:82:LEU:HD12	1:B:124:TYR:CB	2.37	0.46
2:D:255:PRO:HD3	2:D:345:ASN:ND2	2.31	0.46
2:D:212:THR:O	2:D:212:THR:HG22	2.16	0.46
1:A:97:ARG:HD3	1:A:99:GLU:OE1	2.16	0.45
1:B:36:PRO:HA	1:B:70:ALA:CB	2.46	0.45
2:C:233:GLU:HG3	2:C:238:SER:CB	2.45	0.45
2:D:287:ILE:HG22	2:D:288:GLN:N	2.30	0.45
2:D:356:LEU:HD23	2:D:357:THR:N	2.30	0.45
2:C:252:PRO:C	2:C:347:ILE:HD13	2.41	0.45
1:B:16:HIS:CE1	1:B:18:LYS:CB	3.00	0.45
2:C:170:ALA:O	2:C:171:ALA:CB	2.64	0.45
2:D:272:ASN:OD1	2:D:329:ARG:HA	2.17	0.45
2:C:233:GLU:CG	2:C:238:SER:HB3	2.46	0.45
2:D:184:PRO:HD2	2:D:236:TYR:HE1	1.81	0.45
2:D:265:LYS:HG2	2:D:275:PHE:CE1	2.51	0.45
1:B:48:ASP:OD2	1:B:49:PRO:HD2	2.16	0.45
2:D:318:THR:HG23	2:D:322:GLU:HG3	1.97	0.45
1:B:24:TYR:CZ	1:B:29:GLY:HA2	2.52	0.45
1:B:76:MET:O	1:B:91:GLU:HB3	2.17	0.45
1:A:115:TYR:HB2	1:A:137:ILE:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:356:LEU:C	2:D:356:LEU:CD2	2.90	0.45
1:B:59:GLU:HA	2:D:286:HIS:CG	2.52	0.44
2:C:319:THR:HG22	2:C:321:LYS:H	1.82	0.44
2:C:334:GLU:H	2:C:334:GLU:HG3	1.52	0.44
2:D:163:LYS:HE2	2:D:166:HIS:CG	2.52	0.44
2:D:190:TRP:CH2	2:D:230:CYS:HB3	2.53	0.44
2:D:318:THR:CG2	2:D:323:MET:SD	3.05	0.44
2:C:279:VAL:HG12	2:C:280:TYR:N	2.31	0.44
2:D:163:LYS:O	2:D:163:LYS:HG2	2.17	0.44
2:D:281:SER:HB3	2:D:285:PRO:HD3	2.00	0.44
1:B:81:ARG:HB2	1:B:124:TYR:OH	2.16	0.44
2:D:187:THR:O	2:D:232:VAL:HA	2.18	0.44
1:A:33:ARG:NH1	1:A:43:VAL:HG11	2.33	0.44
1:A:55:LEU:N	1:A:55:LEU:HD22	2.33	0.43
2:C:187:THR:O	2:C:232:VAL:HA	2.18	0.43
1:A:124:TYR:CD1	1:A:124:TYR:C	2.95	0.43
2:D:327:HIS:O	2:D:328:LEU:HD23	2.19	0.43
1:A:120:ARG:HG3	3:A:3:SO4:O2	2.19	0.43
2:C:188:LEU:HD12	2:C:213:TRP:HA	2.00	0.43
2:D:288:GLN:HG3	2:D:312:LYS:O	2.18	0.43
1:A:55:LEU:HD13	1:A:65:ILE:HG12	2.00	0.43
1:B:22:ARG:HH12	1:B:52:LYS:HE2	1.84	0.43
1:B:41:ASP:OD2	1:B:41:ASP:C	2.61	0.43
2:D:177:LYS:C	2:D:179:PRO:HD3	2.44	0.43
1:B:72:ARG:HB3	1:B:84:ALA:HB1	2.00	0.43
1:B:99:GLU:HB2	1:B:101:ASN:OD1	2.19	0.43
1:A:23:LEU:HG	1:A:53:LEU:HD12	2.01	0.43
2:D:175:LYS:HA	2:D:215:ILE:O	2.19	0.43
1:B:78:GLU:HA	1:B:111:TYR:CZ	2.55	0.42
2:C:314:ALA:CB	2:C:323:MET:HG3	2.48	0.42
1:A:95:PHE:HD1	1:A:107:ARG:CZ	2.33	0.42
1:B:36:PRO:HA	1:B:70:ALA:HB1	2.02	0.42
2:D:257:LEU:HB2	2:D:352:HIS:CE1	2.54	0.42
1:A:36:PRO:HA	1:A:70:ALA:HB1	2.00	0.42
2:C:282:ASP:HB3	2:C:283:PRO:HD2	2.02	0.42
1:B:49:PRO:HG2	1:B:50:HIS:CD2	2.54	0.42
2:C:269:LEU:HD12	2:C:333:PHE:CD2	2.55	0.42
2:D:218:ASP:O	2:D:219:SER:C	2.62	0.42
2:C:250:ARG:HB3	2:C:282:ASP:OD1	2.20	0.42
2:D:279:VAL:CG1	2:D:280:TYR:N	2.83	0.42
2:C:341:CYS:O	2:C:351:HIS:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:HIS:CE1	1:A:18:LYS:CB	3.03	0.41
1:B:97:ARG:HD3	1:B:99:GLU:OE1	2.20	0.41
1:A:37:ASP:OD2	1:A:39:ARG:NE	2.53	0.41
2:C:273:VAL:HG22	2:C:274:GLU:N	2.35	0.41
1:A:24:TYR:CZ	1:A:29:GLY:HA2	2.55	0.41
2:C:155:TRP:CD2	2:C:239:ILE:HD12	2.55	0.41
2:D:257:LEU:HD23	2:D:279:VAL:HG22	2.01	0.41
1:A:56:GLN:O	1:A:63:VAL:HA	2.21	0.41
1:A:77:LYS:HG2	1:A:81:ARG:O	2.21	0.41
2:D:188:LEU:HD22	2:D:189:ARG:N	2.36	0.41
2:D:189:ARG:HE	2:D:231:ILE:HG21	1.86	0.41
1:B:129:LYS:HB2	1:B:129:LYS:HE3	1.91	0.41
2:C:292:HIS:CD2	2:C:338:GLU:HG2	2.55	0.41
1:A:131:GLY:O	1:A:137:ILE:HD13	2.21	0.41
1:B:55:LEU:HD12	1:B:65:ILE:HG12	1.99	0.41
2:C:186:PRO:HB2	2:C:232:VAL:HG12	2.03	0.41
2:D:155:TRP:HZ3	2:D:178:CYS:HB3	1.86	0.41
2:D:254:ARG:HG2	2:D:254:ARG:HH11	1.84	0.41
1:B:118:LEU:HD23	1:B:124:TYR:HA	2.02	0.41
2:C:149:MET:O	2:C:151:VAL:HG23	2.21	0.41
2:D:253:HIS:CE1	2:D:256:ILE:HD13	2.55	0.40
1:A:133:GLY:HA2	2:D:202:ARG:O	2.21	0.40
2:C:289:TRP:C	2:C:290:LEU:HD12	2.46	0.40
2:D:166:HIS:O	2:D:245:LEU:HD12	2.22	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	127/132 (96%)	121 (95%)	5 (4%)	1 (1%)	16 44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	127/132 (96%)	121 (95%)	5 (4%)	1 (1%)	16	44
2	C	209/225 (93%)	195 (93%)	10 (5%)	4 (2%)	6	22
2	D	192/225 (85%)	183 (95%)	7 (4%)	2 (1%)	12	38
All	All	655/714 (92%)	620 (95%)	27 (4%)	8 (1%)	10	34

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	THR
1	B	112	THR
2	C	330	ASN
2	D	330	ASN
2	C	296	ASN
2	D	219	SER
2	C	219	SER
2	C	251	SER

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	110/113 (97%)	108 (98%)	2 (2%)	51	82
1	B	110/113 (97%)	109 (99%)	1 (1%)	70	89
2	C	168/198 (85%)	159 (95%)	9 (5%)	20	51
2	D	158/198 (80%)	152 (96%)	6 (4%)	29	64
All	All	546/622 (88%)	528 (97%)	18 (3%)	33	69

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	LEU
1	A	128	SER
1	B	55	LEU

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Mol	Chain	Res	Type
2	C	188	LEU
2	C	212	THR
2	C	240	ASN
2	C	257	LEU
2	C	265	LYS
2	C	318	THR
2	C	322	GLU
2	C	334	GLU
2	C	356	LEU
2	D	188	LEU
2	D	203	ILE
2	D	239	ILE
2	D	342	LEU
2	D	355	TRP
2	D	356	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	B	71	ASN
2	C	185	GLN
2	C	240	ASN
2	C	241	HIS
2	C	317	ASN
2	D	166	HIS
2	D	185	GLN
2	D	241	HIS
2	D	284	GLN
2	D	317	ASN
2	D	327	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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	$\# Z > 2$
3	SO4	A	3	-	4,4,4	0.35	0	6,6,6	0.08	0
3	SO4	B	1	-	4,4,4	0.37	0	6,6,6	0.04	0
3	SO4	A	4	-	4,4,4	0.38	0	6,6,6	0.11	0
3	SO4	B	2	-	4,4,4	0.38	0	6,6,6	0.11	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3	SO4	1	0
3	B	2	SO4	1	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.