



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:24 AM UTC

PDB ID : 3GZD / pdb_00003gzd
Title : Human selenocysteine lyase, P1 crystal form
Authors : Karlberg, T.; Hogbom, M.; Arrowsmith, C.H.; Berglund, H.; Bountra, C.; Collins, R.; Edwards, A.M.; Flodin, S.; Flores, A.; Graslund, S.; Hammarstrom, M.; Johansson, A.; Johansson, I.; Kotenyova, T.; Moche, M.; Nordlund, P.; Nyman, T.; Persson, C.; Sagemark, J.; Schutz, P.; Siponen, M.I.; Thorsell, A.G.; Tresaugues, L.; Van Den Berg, S.; Weigelt, J.; Welin, M.; Wisniewska, M.; Schuler, H.; Structural Genomics Consortium (SGC)
Deposited on : 2009-04-07
Resolution : 1.80 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)	:	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)

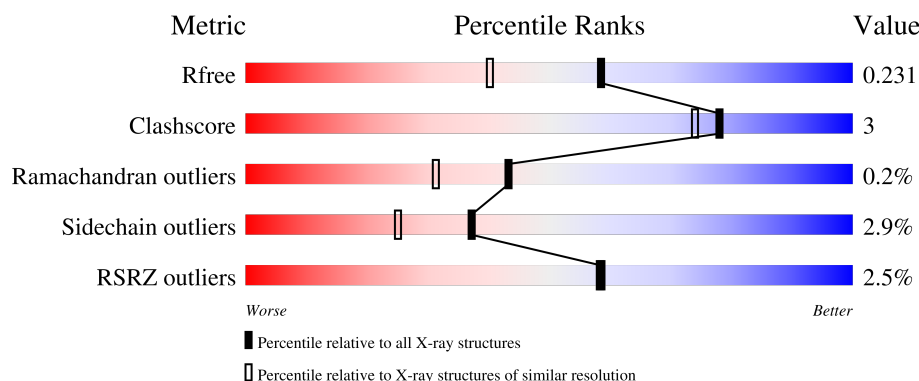
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 $\leq 5\%$. 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	440	82% 7% 10%
1	B	440	83% 6% 11%
1	D	440	83% 7% 10%

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
2	C	440	2% 82% 8% • 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13184 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 Selenocysteine lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	397	Total	C	N	O	S	0	2	0
			3064	1929	549	571	15			
1	B	392	Total	C	N	O	S	0	1	0
			3027	1906	540	568	13			
1	D	397	Total	C	N	O	S	0	2	0
			3063	1927	547	574	15			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	SER	-	expression tag	UNP Q96I15
A	7	MET	-	expression tag	UNP Q96I15
A	175	THR	ALA	SEE REMARK 999	UNP Q96I15
B	6	SER	-	expression tag	UNP Q96I15
B	7	MET	-	expression tag	UNP Q96I15
B	175	THR	ALA	SEE REMARK 999	UNP Q96I15
D	6	SER	-	expression tag	UNP Q96I15
D	7	MET	-	expression tag	UNP Q96I15
D	175	THR	ALA	SEE REMARK 999	UNP Q96I15

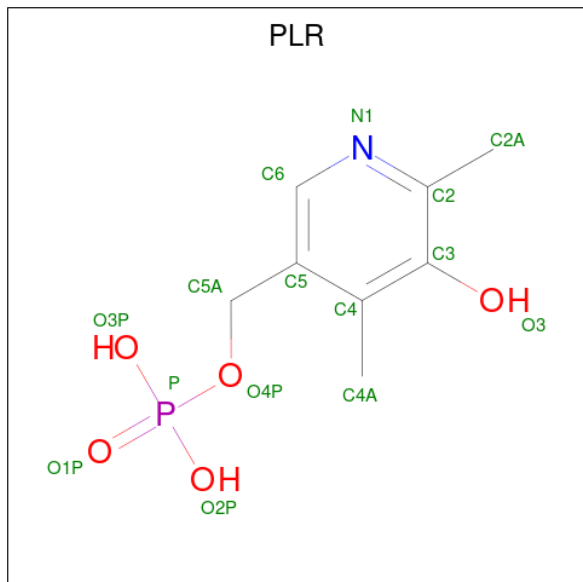
- Molecule 2 is a protein called Selenocysteine lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	396	Total	C	N	O	S	0	2	0
			3056	1923	547	572	14			

There are 3 discrepancies between the modelled and reference sequences:

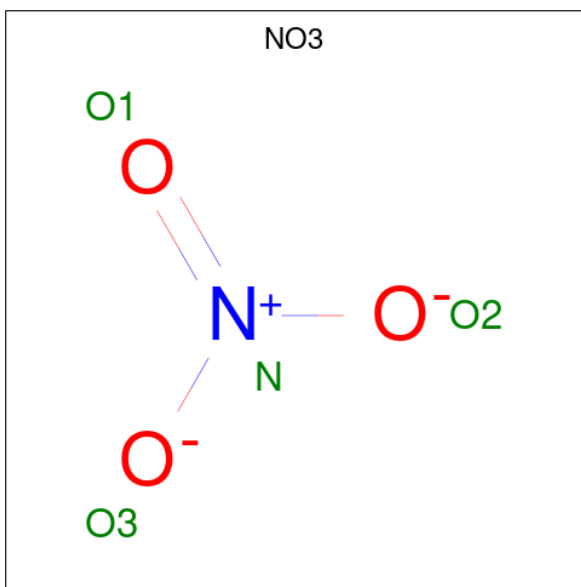
Chain	Residue	Modelled	Actual	Comment	Reference
C	6	SER	-	expression tag	UNP Q96I15
C	7	MET	-	expression tag	UNP Q96I15
C	175	THR	ALA	SEE REMARK 999	UNP Q96I15

- Molecule 3 is (5-HYDROXY-4,6-DIMETHYLPYRIDIN-3-YL)METHYL DIHYDROGEN PHOSPHATE (CCD ID: PLR) (formula: $C_8H_{12}NO_5P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 4 is NITRATE ION (CCD ID: NO3) (formula: NO_3).



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

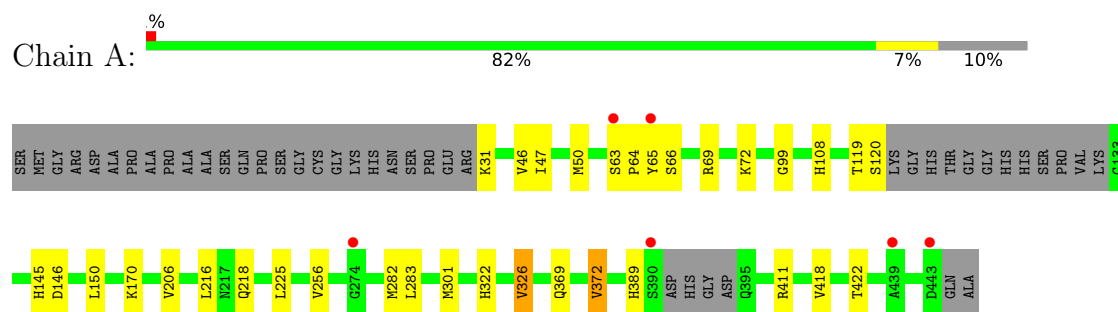
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	252	Total	O	0	0
			252	252		
5	B	208	Total	O	0	0
			208	208		
5	C	234	Total	O	0	0
			234	234		
5	D	204	Total	O	0	0
			204	204		

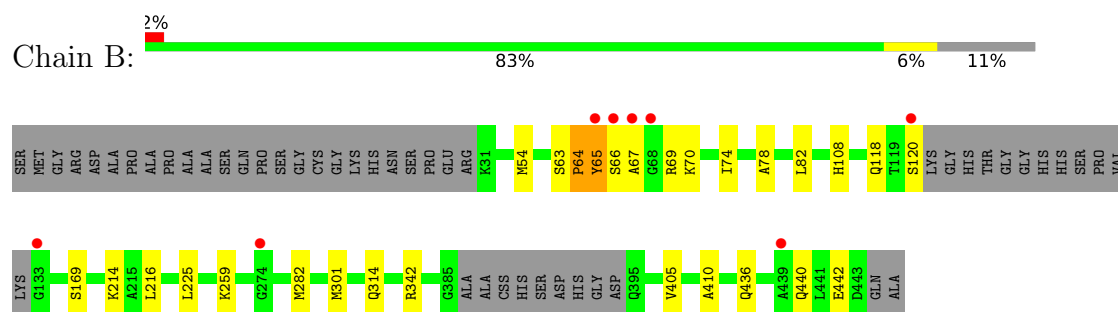
3 Residue-property plots [i](#)

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.

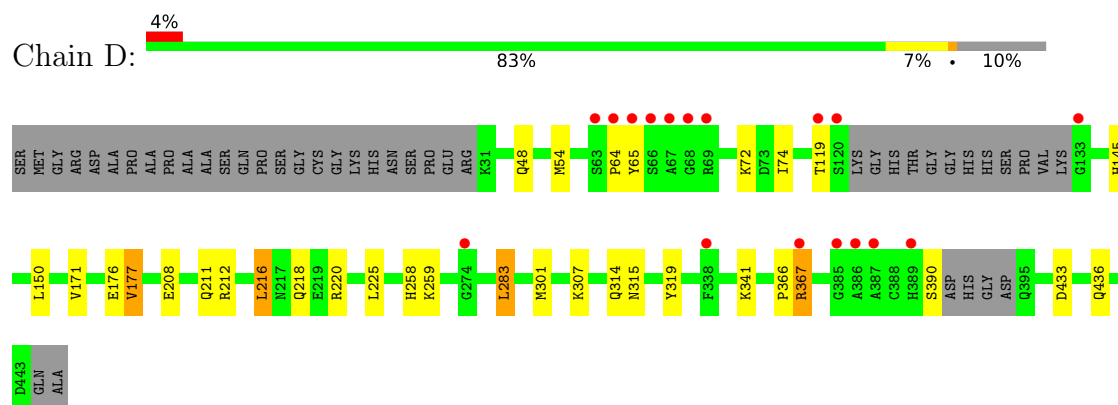
- Molecule 1: Selenocysteine lyase



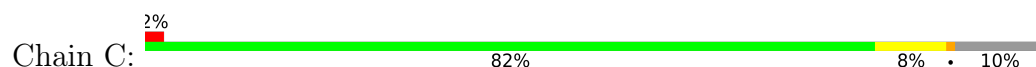
- Molecule 1: Selenocysteine lyase

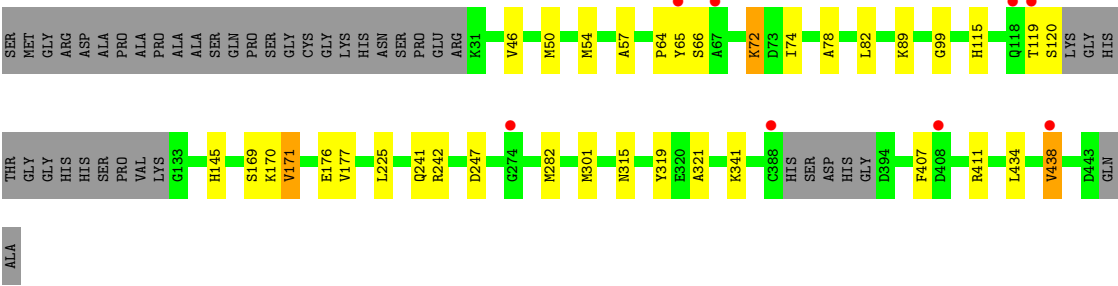


- Molecule 1: Selenocysteine lyase



- Molecule 2: Selenocysteine lyase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.64Å 72.20Å 89.43Å 83.91° 68.39° 86.96°	Depositor
Resolution (Å)	29.59 – 1.80 29.59 – 1.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.59-1.80) 94.2 (29.59-1.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.5.0035	Depositor
R, R_{free}	0.184 , 0.217 0.198 , 0.231	Depositor DCC
R_{free} test set	6724 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13184	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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: PLR, NO3, CSS

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	0.85	1/3121 (0.0%)	0.88	2/4234 (0.0%)
1	B	0.88	2/3085 (0.1%)	0.95	3/4187 (0.1%)
1	D	0.83	0/3120	0.88	0/4233
2	C	0.85	0/3120	0.87	1/4234 (0.0%)
All	All	0.85	3/12446 (0.0%)	0.90	6/16888 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	206	VAL	CA-CB	-6.55	1.49	1.53
1	B	63	SER	C-O	-6.49	1.16	1.23
1	B	69	ARG	C-O	-5.62	1.17	1.24

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	TYR	O-C-N	-6.72	116.94	123.26
1	B	67	ALA	N-CA-C	-6.25	105.50	113.01
1	B	64	PRO	N-CA-C	5.88	124.58	112.47
2	C	64	PRO	N-CA-C	5.29	123.38	112.47
1	A	150	LEU	CA-C-N	-5.16	113.33	119.05
1	A	150	LEU	C-N-CA	-5.16	113.33	119.05

There are no chirality outliers.

There are no planarity outliers.

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	3064	0	3083	23	0
1	B	3027	0	3036	17	0
1	D	3063	0	3072	16	0
2	C	3056	0	3071	24	0
3	A	15	0	7	3	0
3	B	15	0	8	1	0
3	C	15	0	7	3	0
3	D	15	0	9	1	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	D	4	0	0	0	0
5	A	252	0	0	0	0
5	B	208	0	0	0	0
5	C	234	0	0	3	0
5	D	204	0	0	0	0
All	All	13184	0	12293	68	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (68) 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:50:MET:HE3	1:B:54:MET:HE3	1.22	1.16
1:A:50:MET:HE3	1:B:54:MET:CE	1.79	1.11
1:A:50:MET:CE	1:B:54:MET:HE3	1.94	0.97
2:C:301:MET:HE3	1:D:301:MET:HE3	1.50	0.93
1:A:301:MET:HE3	1:B:301:MET:HE3	1.51	0.91
1:A:369:GLN:HG3	1:A:411:ARG:HG2	1.77	0.65
1:B:65:TYR:O	1:B:66:SER:C	2.37	0.64
2:C:115:HIS:O	2:C:119:THR:HG23	1.98	0.63
2:C:321:ALA:HB2	5:C:497:HOH:O	1.97	0.62
1:A:326:VAL:CG2	1:A:418:VAL:HG21	2.33	0.58
1:A:50:MET:HE3	1:B:54:MET:HE1	1.81	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:145:HIS:HB2	3:C:500:PLR:H2A3	1.85	0.57
2:C:99:GLY:HA3	3:C:500:PLR:H5A1	1.86	0.57
1:A:218:GLN:NE2	1:D:218:GLN:OE1	2.38	0.57
2:C:241:GLN:NE2	5:C:530:HOH:O	2.36	0.56
1:A:369:GLN:O	1:A:372:VAL:HG13	2.05	0.56
1:D:366:PRO:HD2	1:D:367:ARG:NH1	2.21	0.55
2:C:242:ARG:NH1	2:C:247:ASP:OD2	2.42	0.53
2:C:54:MET:HE3	1:D:54:MET:HE1	1.91	0.53
1:A:119:THR:O	1:A:119:THR:HG22	2.10	0.52
2:C:170:LYS:O	2:C:170:LYS:HG3	2.10	0.51
1:A:99:GLY:HA3	3:A:500:PLR:H5A1	1.93	0.51
2:C:65:TYR:O	2:C:66:SER:C	2.53	0.51
1:D:177:VAL:HG22	1:D:212:ARG:NH1	2.26	0.50
1:A:46:VAL:HG12	1:A:50:MET:HE2	1.92	0.50
1:D:367:ARG:H	1:D:367:ARG:CD	2.26	0.49
1:D:216:LEU:HD22	1:D:220:ARG:HG3	1.94	0.48
1:A:145:HIS:HB2	3:A:500:PLR:H2A3	1.95	0.48
1:B:118:GLN:C	1:B:120:SER:H	2.22	0.48
2:C:46:VAL:HG12	2:C:50:MET:HE2	1.95	0.48
1:B:78:ALA:O	1:B:82:LEU:HD23	2.14	0.47
2:C:54:MET:CE	1:D:54:MET:HE1	2.44	0.47
2:C:78:ALA:O	2:C:82:LEU:HD23	2.14	0.47
1:A:64:PRO:HA	1:A:69:ARG:CD	2.46	0.46
1:A:326:VAL:HG23	1:A:418:VAL:HG21	1.96	0.46
1:A:47:ILE:HG12	1:B:54:MET:HE2	1.97	0.46
2:C:282:MET:HE1	1:D:283:LEU:CD1	2.46	0.46
2:C:434:LEU:O	2:C:438:VAL:HG13	2.16	0.45
2:C:315:ASN:HB2	2:C:319:TYR:CZ	2.51	0.45
1:D:177:VAL:HG11	1:D:208:GLU:CD	2.40	0.45
1:D:433:ASP:O	1:D:436:GLN:HG3	2.16	0.45
1:A:256:VAL:HG11	3:A:500:PLR:H5A2	1.99	0.44
1:B:405:VAL:HG12	1:B:410:ALA:HB2	1.99	0.44
1:B:436:GLN:OE1	1:B:440:GLN:NE2	2.49	0.44
1:D:258:HIS:CE1	1:D:259:LYS:HE3	2.52	0.44
1:A:108:HIS:CG	1:A:282:MET:HG2	2.52	0.44
1:D:145:HIS:HB2	3:D:500:PLR:H2A3	2.00	0.43
2:C:282:MET:HE2	2:C:282:MET:HB3	1.82	0.43
1:B:342:ARG:NH1	1:B:442:GLU:OE2	2.50	0.43
2:C:57:ALA:CB	2:C:74:ILE:HD12	2.49	0.43
1:A:64:PRO:HA	1:A:69:ARG:HD3	2.01	0.43
1:B:70:LYS:O	1:B:74:ILE:HG12	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:407:PHE:O	2:C:411:ARG:HG3	2.19	0.42
1:A:50:MET:HB2	1:B:54:MET:HE1	2.00	0.42
2:C:119:THR:O	2:C:120:SER:C	2.61	0.42
1:A:65:TYR:O	1:A:66:SER:C	2.62	0.42
1:B:108:HIS:CG	1:B:282:MET:HG2	2.54	0.42
2:C:72:LYS:HE3	2:C:72:LYS:HA	2.00	0.42
1:B:108:HIS:CD2	1:B:282:MET:HG2	2.54	0.42
1:A:322:HIS:NE2	1:A:422:THR:O	2.51	0.42
2:C:169:SER:OG	2:C:171:VAL:HG13	2.20	0.42
2:C:177:VAL:HG23	5:C:607:HOH:O	2.19	0.42
1:D:315:ASN:HB2	1:D:319:TYR:CZ	2.55	0.42
1:B:259:LYS:NZ	3:B:500:PLR:O3	2.51	0.41
1:D:150:LEU:HD23	1:D:150:LEU:HA	1.94	0.41
2:C:145:HIS:HB2	3:C:500:PLR:C2A	2.50	0.40
1:D:367:ARG:H	1:D:367:ARG:HD2	1.85	0.40
1:A:146:ASP:OD2	1:A:389:HIS:NE2	2.55	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	392/440 (89%)	383 (98%)	9 (2%)	0	100	100
1	B	387/440 (88%)	374 (97%)	12 (3%)	1 (0%)	36	25
1	D	392/440 (89%)	382 (97%)	8 (2%)	2 (0%)	24	14
2	C	392/440 (89%)	381 (97%)	11 (3%)	0	100	100
All	All	1563/1760 (89%)	1520 (97%)	40 (3%)	3 (0%)	43	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	119	THR
1	B	64	PRO
1	D	64	PRO

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	330/359 (92%)	320 (97%)	10 (3%)	36	24
1	B	327/359 (91%)	322 (98%)	5 (2%)	57	49
1	D	330/359 (92%)	313 (95%)	17 (5%)	21	9
2	C	330/360 (92%)	323 (98%)	7 (2%)	47	36
All	All	1317/1437 (92%)	1278 (97%)	39 (3%)	37	24

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LYS
1	A	63	SER
1	A	72	LYS
1	A	120	SER
1	A	170	LYS
1	A	216	LEU
1	A	225	LEU
1	A	283	LEU
1	A	326	VAL
1	A	372	VAL
1	B	169	SER
1	B	214	LYS
1	B	216	LEU
1	B	225	LEU
1	B	314	GLN
2	C	72	LYS
2	C	89	LYS
2	C	171	VAL
2	C	176	GLU

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Mol	Chain	Res	Type
2	C	225	LEU
2	C	341	LYS
2	C	438	VAL
1	D	48[A]	GLN
1	D	48[B]	GLN
1	D	65	TYR
1	D	72	LYS
1	D	74	ILE
1	D	171	VAL
1	D	176	GLU
1	D	177	VAL
1	D	211	GLN
1	D	216	LEU
1	D	225	LEU
1	D	283	LEU
1	D	307	LYS
1	D	314	GLN
1	D	341	LYS
1	D	367	ARG
1	D	390	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	108	HIS
1	A	118	GLN
1	A	346	ASN
1	B	118	GLN
1	B	315	ASN
1	B	346	ASN
1	B	395	GLN
2	C	154	HIS
2	C	346	ASN
2	C	360	ASN
2	C	440	GLN
1	D	117	ASN
1	D	211	GLN
1	D	314	GLN
1	D	346	ASN
1	D	432	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	CSS	A	388	1	4,6,7	0.88	0	2,6,8	0.87	0
1	CSS	D	388	1	4,6,7	0.87	0	2,6,8	0.49	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSS	A	388	1	-	0/1/5/7	-
1	CSS	D	388	1	-	0/1/5/7	-

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.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

8 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	PLR	A	500	1	15,15,15	1.29	3 (20%)	21,22,22	2.47	5 (23%)
3	PLR	C	500	2	15,15,15	0.77	0	21,22,22	1.52	4 (19%)
3	PLR	D	500	1	15,15,15	0.89	1 (6%)	21,22,22	1.74	6 (28%)
4	NO3	C	600	-	1,3,3	3.52	1 (100%)	0,3,3	-	-
4	NO3	B	600	-	1,3,3	3.27	1 (100%)	0,3,3	-	-
4	NO3	A	600	-	1,3,3	2.91	1 (100%)	0,3,3	-	-
4	NO3	D	600	-	1,3,3	3.37	1 (100%)	0,3,3	-	-
3	PLR	B	500	1	15,15,15	0.81	0	21,22,22	2.07	6 (28%)

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	PLR	A	500	1	-	4/6/6/6	0/1/1/1
3	PLR	D	500	1	-	0/6/6/6	0/1/1/1
3	PLR	B	500	1	-	0/6/6/6	0/1/1/1
3	PLR	C	500	2	-	1/6/6/6	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	600	NO3	O1-N	3.52	1.41	1.24
4	D	600	NO3	O1-N	3.37	1.40	1.24
4	B	600	NO3	O1-N	3.27	1.40	1.24
3	A	500	PLR	C4A-C4	2.99	1.57	1.51
4	A	600	NO3	O1-N	2.91	1.38	1.24
3	D	500	PLR	C3-C2	-2.08	1.38	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	PLR	C6-C5	2.07	1.41	1.37
3	A	500	PLR	C5-C4	2.06	1.42	1.40

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	500	PLR	C4A-C4-C5	7.02	128.18	120.94
3	B	500	PLR	C4A-C4-C5	5.78	126.89	120.94
3	A	500	PLR	C6-C5-C4	4.83	122.05	118.10
3	A	500	PLR	C5A-C5-C6	-4.34	112.29	119.36
3	D	500	PLR	O3P-P-O4P	-4.15	95.86	106.67
3	A	500	PLR	C3-C4-C5	-3.83	113.99	118.59
3	B	500	PLR	C5A-C5-C6	-3.75	113.24	119.36
3	C	500	PLR	O3P-P-O4P	-3.16	98.42	106.67
3	C	500	PLR	C5-C6-N1	-2.92	119.08	123.83
3	B	500	PLR	C4A-C4-C3	-2.69	116.03	120.52
3	D	500	PLR	C4A-C4-C5	2.62	123.64	120.94
3	D	500	PLR	C5A-C5-C6	-2.57	115.17	119.36
3	B	500	PLR	O4P-C5A-C5	2.51	114.06	109.36
3	C	500	PLR	C6-C5-C4	2.50	120.14	118.10
3	D	500	PLR	C5-C6-N1	-2.39	119.94	123.83
3	B	500	PLR	O3P-P-O4P	-2.32	100.61	106.67
3	D	500	PLR	O3P-P-O2P	2.31	116.46	107.80
3	B	500	PLR	C5A-C5-C4	2.22	127.03	122.64
3	D	500	PLR	O2P-P-O1P	2.14	119.18	110.83
3	A	500	PLR	C5-C6-N1	-2.13	120.36	123.83
3	C	500	PLR	C6-N1-C2	2.09	122.99	119.20

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	500	PLR	C5A-O4P-P-O2P
3	A	500	PLR	C5A-O4P-P-O3P
3	C	500	PLR	C5A-O4P-P-O3P
3	A	500	PLR	C5A-O4P-P-O1P
3	A	500	PLR	C4-C5-C5A-O4P

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	500	PLR	3	0
3	C	500	PLR	3	0
3	D	500	PLR	1	0
3	B	500	PLR	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 ⓘ

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	396/440 (90%)	-0.17	6 (1%)	72 72	5, 13, 30, 39	2 (0%)
1	B	392/440 (89%)	-0.00	8 (2%)	65 65	3, 13, 29, 38	1 (0%)
1	D	396/440 (90%)	-0.02	17 (4%)	40 39	4, 13, 32, 39	2 (0%)
2	C	396/440 (90%)	0.01	8 (2%)	65 65	3, 14, 31, 41	2 (0%)
All	All	1580/1760 (89%)	-0.04	39 (2%)	58 58	3, 13, 31, 41	7 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	64	PRO	4.0
1	D	65	TYR	3.8
1	B	65	TYR	3.8
1	B	274	GLY	3.7
2	C	65	TYR	3.6
2	C	274	GLY	3.5
1	D	119	THR	3.5
1	A	65	TYR	3.2
1	D	274	GLY	3.2
1	A	274	GLY	3.2
1	A	390	SER	2.9
2	C	67	ALA	2.9
1	A	439	ALA	2.8
1	B	67	ALA	2.8
1	B	439	ALA	2.7
1	D	387	ALA	2.7
1	B	66	SER	2.7
1	D	63	SER	2.7
1	A	63	SER	2.6
1	D	67	ALA	2.6
1	D	66	SER	2.6

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Mol	Chain	Res	Type	RSRZ
2	C	408	ASP	2.6
1	D	338	PHE	2.5
1	D	68	GLY	2.4
1	D	133	GLY	2.4
1	D	385	GLY	2.4
2	C	388	CYS	2.4
1	B	120	SER	2.3
1	D	386	ALA	2.2
1	D	389	HIS	2.2
2	C	118	GLN	2.2
1	B	133	GLY	2.2
1	A	443	ASP	2.1
2	C	119	THR	2.1
1	D	367	ARG	2.1
1	D	69	ARG	2.1
1	B	68	GLY	2.1
1	D	120	SER	2.0
2	C	438	VAL	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CSS	A	388	7/8	0.87	0.11	31,32,35,38	0
1	CSS	D	388	7/8	0.87	0.13	26,26,29,33	0

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($\text{\AA}^2$)	Q<0.9
4	NO3	B	600	4/4	0.84	0.14	33,33,33,33	0
4	NO3	C	600	4/4	0.85	0.14	31,31,31,31	0
4	NO3	D	600	4/4	0.86	0.15	25,26,26,26	0
4	NO3	A	600	4/4	0.88	0.14	45,45,46,47	0
3	PLR	B	500	15/15	0.91	0.10	20,21,22,23	0
3	PLR	D	500	15/15	0.92	0.10	17,21,22,23	0
3	PLR	C	500	15/15	0.94	0.09	19,20,21,22	0
3	PLR	A	500	15/15	0.96	0.08	13,18,24,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.